

Query Match	73.3%	Score 22;	DB 1;	Length 23;
Best Local Similarity	100.0%	Pred. No. 8;		
Matches 22; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
Qy      1 CTGACAGAGCCCACTCTTCG 22
Db      22 CTGACAGAGCCCACTCTTCG 1

RESULT 2
PCT-US03-04088-540/c
Sequence 540, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwigen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 540
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc_feature
LOCATION: (20)..(21)
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 548
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc_feature
LOCATION: (1)..(1)

Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGACAGAGCCCACTCTTC 20
Db      19 TGACAGAGCCCACTCTTC 1

RESULT 3
PCT-US03-04088-544
Sequence 544, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwigen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 548
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc_feature
LOCATION: (1)..(1)

Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGACAGAGCCCACTCTTC 20
Db      1 TGACAGAGCCCACTCTTC 19

RESULT 4
PCT-US03-04088-548/c
Sequence 548, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwigen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 548
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc_feature
LOCATION: (1)..(1)
```



```
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-548
```

```
Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 TGACGAGCCCAACTCTTC 20
Db      19 TGACGAGCCCAACTCTTC 1
```

## RESULT 5

```
PCT-US03-04088-552
; Sequence 552, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSwigen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 552
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
```

```
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorochioate 3'-Internucleotide Linkage
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-552
```

```
Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 TGACGAGCCCAACTCTTC 20
Db      1 UGACGAGCCCAACUUCUUC 19
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## RESULT 6

```
PCT-US03-04088-556/C
; Sequence 556, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSwigen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 556
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: 2'-deoxy
```

```
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)..(16)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety
PCT-US03-04088-556
```

```
Query Match 63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 TGACAGAGCCCACTCTTC 20
Db 19 TGACAGAGCCCACTCTTC 1
```

```
RESULT 7
PCT-US03-04088-560
Sequence 560, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
```

```
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 560
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(3)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)..(8)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(13)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-internucleotide linkage
PCT-US03-04088-560
```

```
Query Match 63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 TGACAGAGCCCACTCTTC 20
Db 1 UGACAGAGCCCACTCTTC 19
```

```
RESULT 8
PCT-US03-04088-23/C
Sequence 23, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
```

PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 23  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
PCT-US03-04088-23

Query Match 60.0%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCT 18  
DB 18 CTGACAGAGCCCACTCT 1

## RESULT 9

PCT-US03-04088-287  
Sequence 287, Application PC/TUS0304088  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwigen, James  
APPLICANT: Beigelman, Leonid  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)  
FILE REFERENCE: 02-708-A (400/080)  
CURRENT APPLICATION NUMBER: PCT/US03/04088  
PRIOR FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: US 60/396,600  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 287  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense  
PCT-US03-04088-287

Query Match 60.0%; Score 18; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 4.6e+02;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTGACAGAGCCCACTCT 18  
DB 2 CTGACAGAGCCCACTCT 19

## RESULT 10

US-10-325-899-7470/c  
Sequence 7470, Application US/10325899  
GENERAL INFORMATION:  
APPLICANT: Wohlgemuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Ly, Ngoc  
APPLICANT: Woodward, Robert  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT  
TITLE OF INVENTION: REJECTION  
FILE REFERENCE: 506612000122  
CURRENT APPLICATION NUMBER: US/10/325,899  
CURRENT FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 10/131,831  
PRIOR FILING DATE: 2002-04-24  
NUMBER OF SEQ ID NOS: 9966  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7470  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Human adenovirus type 2  
US-10-325-899-7470

Query Match 56.7%; Score 17; DB 9; Length 50;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 AGAGCCCACTCTGCGGTGGCAG 30  
DB 31 AGAGCCCACTCTGCGGTGGCAG 7

## RESULT 11

US-60-427-808-503841  
Sequence 503841, Application US/60427808  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Method of Genetic Analysis of Mouse  
FILE REFERENCE: 3528  
CURRENT APPLICATION NUMBER: US/60/427,808  
CURRENT FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 503841  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-60-427-808-503841

Query Match 56.0%; Score 16.8; DB 12; Length 25;  
Best Local Similarity 90.0%; Pred. No. 1.6e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCACTCTTGG 21  
DB 6 TGACAGAGCCCACTCTTGG 25

## RESULT 12

US-60-427-808-699316  
Sequence 699316, Application US/60427808  
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528  
CURRENT APPLICATION NUMBER: US/60/427,808  
CURRENT FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 699316  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-60-427-808-699316

Query Match 55.3%; Score 16.6; DB 12; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 GAGCCCACTCTTCGCGTGCA 29  
DB 3 GAGCCCACTCTTCAGGCGCA 25

## RESULT 13

PCT-US03-04088-588/c  
Sequence 588, Application PC/TUS0304088  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: McSwiggen, James  
APPLICANT: Beigelman, Leonid  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
FILE REFERENCE: 02-708-A (400/080)  
CURRENT APPLICATION NUMBER: PCT/US03/04088  
CURRENT FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: US 60/396,600  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 588  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
PCT-US03-04088-588

Query Match 53.3%; Score 16; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 CTCTTCGCGGTGGCGAG 30  
DB 21 CTCTTCGCGGTGGCGAG 6

RESULT 14  
PCT-US03-04088-530/c  
Sequence 530, Application PC/TUS0304088

GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: McSwiggen, James  
APPLICANT: Beigelman, Leonid  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
FILE REFERENCE: 02-708-A (400/080)  
CURRENT APPLICATION NUMBER: PCT/US03/04088  
CURRENT FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: US 60/396,600  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 530  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
PCT-US03-04088-530

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Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
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DB 23 CTCTTCGCGGTGGCGAG 8

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US-60-427-836-550603/c  
Sequence 550603, Application US/60427836  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
FILE REFERENCE: 3527  
CURRENT APPLICATION NUMBER: US/60/427,836  
CURRENT FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 699466  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 550603  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-60-427-836-550603

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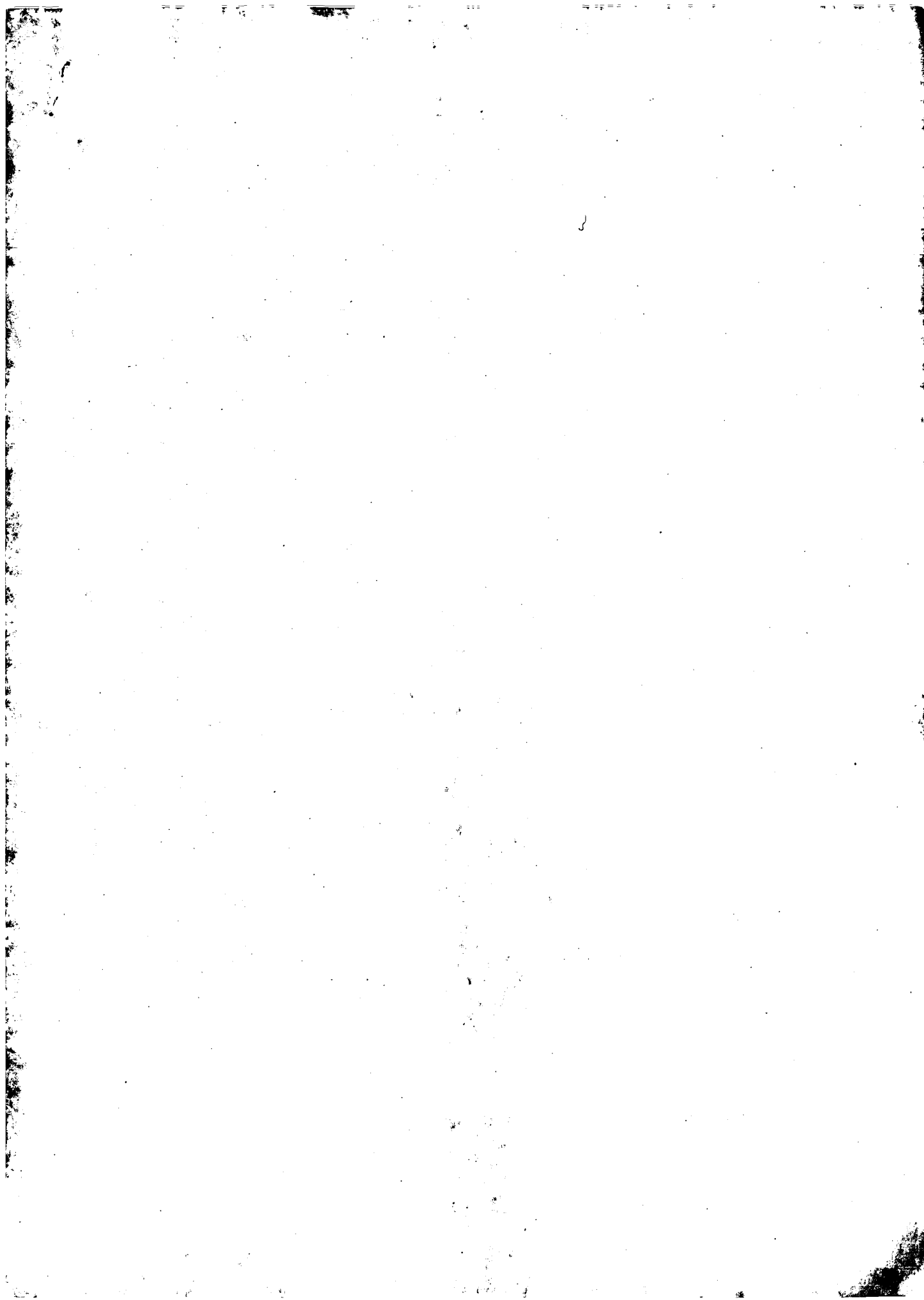
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DB 25 TGACAGAGCAACACTTCGCGGT 2

Search completed: June 26, 2003, 04:15:14  
Job time : 719.961 secs

Fri Jun 27 07:42:47 2003

us-08-770-564a-5.rnpn

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 139.554 Seconds  
(without alignments)  
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Title: US-08-770-564A-4

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Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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4	12	100.0	20	6	AR079894
5	12	100.0	30	6	AR063826
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7	11	91.7	20	6	AR079898
8	11	91.7	20	6	I21035
9	11	91.7	20	6	I21062
10	11	91.7	42	6	AX166899
11	10	83.3	14	6	AR036791
12	10	83.3	15	6	A35610
13	10	83.3	15	6	AR192969
14	10	83.3	16	6	AX073744
15	10	83.3	16	6	AX073745
16	10	83.3	17	6	AR101699
17	10	83.3	17	6	AR187031
18	10	83.3	17	6	AR187032
19	10	83.3	17	6	AR187033
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23	10	83.3	18	6	AX012429
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28	10	83.3	19	6	AX128977
29	10	83.3	19	6	AX128978
30	10	83.3	19	6	AX128979
31	10	83.3	19	6	AX128980
32	10	83.3	20	4	BOVINE30
33	10	83.3	20	6	AR067594
34	10	83.3	20	6	AR126656
35	10	83.3	20	6	AR160506
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# ALIGNMENTS

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DEFINITION Sequence 4 from patent US 5846723.

ACCESSION AR063828

VERSION AR063828.1 GI:5993136

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.

TITLE Methods for detecting the RNA component of telomerase

JOURNAL Patent: US 5846723-A 4 08-DEC-1998;

FEATURES Location/Qualifiers

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DEFINITION Sequence 14 from Patent WO9845450.
ACCESSION  A84604.
VERSION     A84604.1 GI:6733517
KEYWORDS
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Ackinson,E.M. and Kealey,J.T.
TITLE      PURIFIED TELOMERASE
JOURNAL    Patent: WO 9845450-A 14 15-OCT-1998;
GERON CORP (US)
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ACCESSION  A8063827
VERSION     A8063827.1 GI:5993135
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methode for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 3 08-DEC-1998;
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Db
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ACCESSION  A8079894
VERSION     A8079894.1 GI:10006647
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vassero,A.P.,
            Pruzan,R.A. and Kealey,J.T.
TITLE      Purified telomerase
JOURNAL    Patent: US 5965506-A 7 19-OCT-1999;
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Db
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ACCESSION  A8063826
VERSION     A8063826.1 GI:5993134
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methode for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 2 08-DEC-1998;
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DEFINITION Sequence 7 from Patent WO9845450.
ACCESSION  A84597
VERSION     A84597.1 GI:6733513
KEYWORDS
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Atkinson,E.M. and Kealey,J.T.
TITLE      PURIFIED TELOMERASE

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JOURNAL Patent: WO 9845450-A 7 15-OCT-1998;  
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 ACCESSION AR079898  
 VERSION AR079898.1 GI:10006651  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Weinrich,S.L., Atkinson,B.M. III, Lichtsteiner,S.P., Vassero,A.P.,  
 Puzan,R.A. and Kealey,J.T.  
 TITLE Purified telomerase  
 JOURNAL Patent: US 5968506-A 14 19-OCT-1999;  
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 DEFINITION Sequence 6 from patent US 5518880.  
 ACCESSION 121035  
 VERSION 121035.1 GI:1601389  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Leonard,W.J., Noguchi,M. and McBride,O.Wesley,  
 TITLE Methods for diagnosis of XSCID and kits thereof  
 JOURNAL Patent: US 5518880-A 6 21-MAY-1996;  
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 VERSION 121062.1 GI:1601416  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Leonard,W.J., Noguchi,M. and McBride,O.Wesley,  
 TITLE Methods for diagnosis of XSCID and kits thereof  
 JOURNAL Patent: US 5518880-A 33 21-MAY-1996;  
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 DEFINITION Sequence 12 from Patent WO0141811.  
 ACCESSION AX166899  
 VERSION AX166899.1 GI:14596492  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 42)  
 AUTHORS Horton,J.K., Smith,J.A., Teeear,M.L., Kendall,J.M. and Michael,N.P.  
 TITLE Carrier peptide and method for delivery of molecules into cells  
 JOURNAL Patent: WO 0141811-A 12 14-JUN-2001;  
 FEATURES location/Qualifiers  
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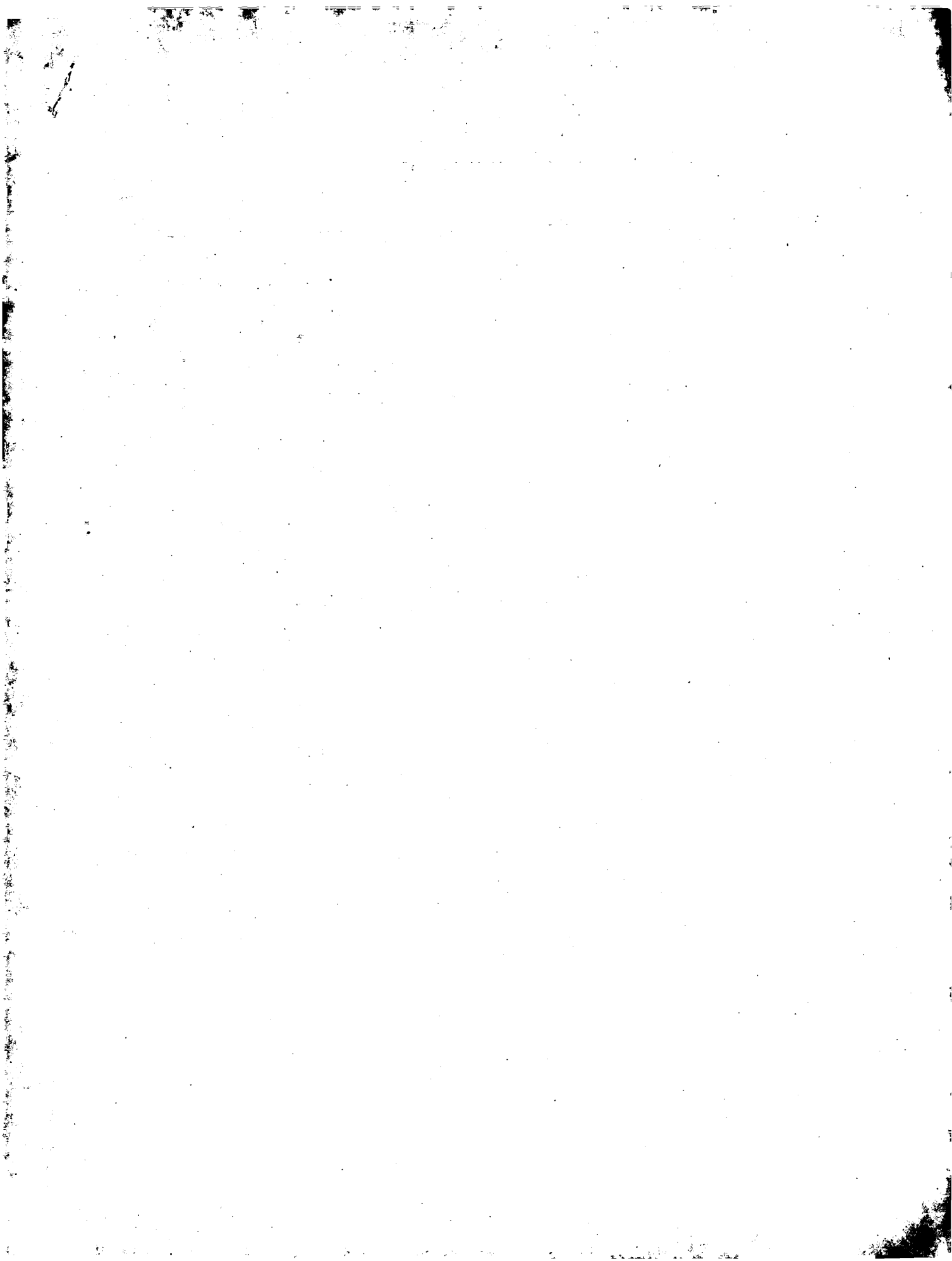
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 ACCESSION AR036791

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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Vary,C.P.H.  
TITLE Nucleic acid sequence detection by triple helix formation at primer  
JOURNAL site in amplification reactions  
FEATURES Patent: US 5800984-A 33 01-SEP-1998;  
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ACCESSION A35610  
VERSION A35610.1 GI:1926992  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Camble,R. and Edge,M.D.  
TITLE Analogous interferon polypeptides, process for their preparation  
JOURNAL and pharmaceutical compositions containing them  
Patent: EP 0194006-A 55 10-SEP-1986;  
IMPERIAL CHEMICAL INDUSTRIES PLC  
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ACCESSION AR192869  
VERSION AR192869.1 GI:20238934  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Payco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
JOURNAL related to levels of vascular endothelial growth factor receptor  
Patent: US 6346398-A 8457 12-FEB-2002;  
FEATURES Location/Qualifiers

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AX073744 AX073744 16 bp DNA linear PAT 06-FEB-2001  
LOCUS Sequence 4 from Patent WO0104290.  
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ACCESSION AX073744  
VERSION AX073744.1 GI:12710156  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Jin,Y.X. and Liu,J.S.  
TITLE Triplex-forming oligonucleotides and their use in therapy  
JOURNAL Patent: WO 0104290-A 4 18-JAN-2001;  
Shanghai Institute of Biochemistry Chinese Academy of Sciences (CN)  
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LOCUS Sequence 5 from Patent WO0104290.  
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ACCESSION AX073745  
VERSION AX073745.1 GI:12710157  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Jin,Y.X. and Liu,J.S.  
TITLE Triplex-forming oligonucleotides and their use in therapy  
JOURNAL Patent: WO 0104290-A 5 18-JAN-2001;  
Shanghai Institute of Biochemistry Chinese Academy of Sciences (CN)  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 79.745 Seconds  
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Perfect score: 12  
Sequence: 1 CGTTCCTCTCC 12

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	12	100.0	20	AA509477	Antisense oligonuc
7	12	100.0	20	AA509480	Antisense oligonuc
8	12	100.0	30	AAV41169	RNA component of h
9	11	91.7	20	AAQ71941	Human IL-2R gamma

C	10	11	91.7	20	15	AAQ71914	Human IL-2R gamma
	11	11	91.7	20	21	AAA07908	Hs-UNC-53/2 specif
	12	11	91.7	21	21	AAAI1686	Human GABA-B recep
	13	11	91.7	21	21	AAZ89497	Human GABA-B recep
	14	11	91.7	21	22	AAH62356	RBBP2 polymorphism
	15	11	91.7	22	24	ABU43752	Human chromosome 1
	16	11	91.7	27	20	AAZ23809	Mouse Kv6.2 DNA co
	17	11	91.7	40	17	AAZ70784	Stenotic carotid a
	18	11	91.7	40	17	AAZ70788	Stenotic carotid a
	19	11	91.7	40	17	AAZ70789	Stenotic carotid a
	20	10	83.3	12	23	AB117903	Oligonucleotide pr
	21	10	83.3	12	23	AB145722	Oligonucleotide pr
	22	10	83.3	14	13	AAQ26598	Predicted HPV-18 e
	23	10	83.3	15	18	AAZ75707	Human flt-1 and KD
	24	10	83.3	16	22	AAZ5892	Human c-sis/PDGF-B
	25	10	83.3	16	22	AAZ5893	Human c-sis/PDGF-B
	26	10	83.3	17	18	AAZ69769	Human flt1 VEGF re
	27	10	83.3	17	18	AAZ69770	Human flt1 VEGF re
	28	10	83.3	17	18	AAZ69771	Human flt1 VEGF re
	29	10	83.3	17	18	AAZ69772	Human flt1 VEGF re
	30	10	83.3	17	19	AAZ20569	Human BRCA1 probe
	31	10	83.3	17	19	AAZ20570	Human BRCA1 probe
	32	10	83.3	17	20	AAZ80263	Human BRCA1 wild t
	33	10	83.3	17	22	ABA78053	BRCA1 mutation cor
	34	10	83.3	17	22	ABA78054	BRCA1 mutation cor
	35	10	83.3	18	14	AAQ52877	Cytomegalovirus ta
	36	10	83.3	18	21	AAZ30195	PCR primer M17 us
	37	10	83.3	18	24	ABH88411	Site gated incorpo
	38	10	83.3	19	21	AAH82608	cdk2 ribozyme bind
	39	10	83.3	19	21	AAH82609	cdk2 ribozyme bind
	40	10	83.3	19	21	AAH82610	cdk2 ribozyme bind
	41	10	83.3	19	21	AAH82611	cdk2 ribozyme bind
	42	10	83.3	19	21	AAH82612	cdk2 ribozyme bind
	43	10	83.3	19	22	AAH57770	Cell-cycle depende
	44	10	83.3	19	22	AAH57771	Cell-cycle depende
	45	10	83.3	19	22	AAH57772	Cell-cycle depende

#### ALIGNMENTS

RESULT 1	
AAV41171	standard; DNA; 12 BP.
ID	AAV41171
XX	XX
AC	AAV41171:
XX	XX
DT	08-OCT-1998. (first entry)
XX	XX
DE	RNA component of human telomerase (hTR) antisense oligo 14d.
XX	XX
KW	RNA component; human telomerase; antisense oligonucleotide; infection;
KW	neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW	contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW	immune system down-regulation; anti-inflammatory therapy; ss.
XX	XX
OS	Synthetic.
OS	Homo sapiens.
XX	XX
PN	WO9828442-A1.
XX	XX
PD	02-JUL-1998.
XX	XX
PF	19-DEC-1997; 97WO-US23619.
XX	XX
PR	20-DEC-1996; 96US-0770565.
XX	XX
PR	20-DEC-1996; 96US-0770564.
XX	XX
PA	(GERO-) GERON CORP.
XX	XX
PI	Kaaley JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX	XX
DR	WPI; 1998-377670/32.



CC Sequences shown in AAV41169 to AAV41181 represent antisense  
CC oligonucleotides to the RNA component of human telomerase (hTR). These  
CC antisense oligonucleotides specifically hybridize to a nucleotide  
CC sequence within an accessible region of the hTR, but that does not  
CC hybridize to a sequence within the template region of hTR. These  
CC oligonucleotides may specifically be used for detection of an RNA  
CC component of human telomerase in a sample. This is useful for diagnosing  
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),  
CC and providing prognosis for a cancer patient. The inhibitory  
CC oligonucleotides can inhibit the telomerase activity level in a cell by  
CC interfering with transcription of the RNA component, decreasing the  
CC half-life of the telomerase RNA component transcript, inhibiting the  
CC of the RNA component into the telomerase holoenzyme, or inhibiting the  
CC polymerase activity of telomerase. These antisense oligonucleotides can  
CC be used for inhibiting telomerase activity in both cultured cells and in  
CC cells in vivo. They can be used in therapeutics for treating or  
CC preventing cancer, for contraception or sterilisation, for  
CC immunosuppression, and for selectively down-regulating specific branches  
CC of the immune system, e.g. a specific subset of T-cells, in  
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,  
CC parasites or fungi.

SO Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 12; DB 19; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCC 12  
Db 1 CGTTCCTCTCC 12

RESULT 4

AAZ23632 standard; DNA; 20 BP.

AAZ23632;

07-JAN-2000 (first entry)

Human clone 28-1 telomerase oligonucleotide 14ab.

Telomerase; human; immune response; cancer; vaccine; treatment;  
disease; primer; ss.

Synthetic.

Homo sapiens.

US5968506-A.

19-OCT-1999.

04-APR-1997; 97US-0833377.

04-AUG-1995; 95US-0510736.

(GERO-) GERON CORP.

Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT,  
Vassero AP;

WPI; 1999-590379/50.

Compositions comprising human telomerase, useful for treating diseases  
associated with overexpression of telomerase e.g. cancer -

Disclosure; Column 45-46; 34pp; English.

This invention describes a novel composition comprising human telomerase  
having at least 2000-fold (preferably at least 6000-fold) increased  
relative purity compared with crude extract of cells from  
adenovirus-transformed kidney cell line. The composition is useful for

CC eliciting an immune response in animals and may therefore be used as a  
CC vaccine for treating diseases associated with the overexpression of  
CC telomerase e.g. cancer. AAZ23626-223637 represent oligonucleotides used  
CC in the isolation of human clone 28-1 which contains a fragment of the  
CC human telomerase described in the method of the invention.

SO Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCC 12  
Db 1 CGTTCCTCTCC 12

RESULT 5

AAZ23636 standard; DNA; 20 BP.

AAZ23636;

07-JAN-2000 (first entry)

Human clone 28-1 telomerase oligonucleotide oligo 14ab.

Telomerase; human; immune response; cancer; vaccine; treatment;  
disease; primer; ss.

Synthetic.

Homo sapiens.

Key Location/Qualifiers

modified\_base 1 /tag= a

/note= "5'-biotinylated cytidine"

US5968506-A.

19-OCT-1999.

04-APR-1997; 97US-0833377.

04-AUG-1995; 95US-0510736.

(GERO-) GERON CORP.

Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT,  
Vassero AP;

WPI; 1999-590379/50.

Compositions comprising human telomerase, useful for treating diseases  
associated with overexpression of telomerase e.g. cancer -

Disclosure; Column 49-50; 34pp; English.

This invention describes a novel composition comprising human telomerase  
having at least 2000-fold (preferably at least 6000-fold) increased  
relative purity compared with crude extract of cells from  
adenovirus-transformed kidney cell line. The composition is useful for  
CC eliciting an immune response in animals and may therefore be used as a  
CC vaccine for treating diseases associated with the overexpression of  
CC telomerase e.g. cancer. AAZ23626-223637 represent oligonucleotides used  
CC in the isolation of human clone 28-1 which contains a fragment of the  
CC human telomerase described in the method of the invention.

SO Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12  
 Db 1 CGTTCCTCTCC 12

## RESULT 6

AAS09477  
 ID AAS09477 standard; DNA; 20 BP.

XX AAS09477;  
 XX 24-OCT-2001 (first entry)

DE Antisense oligonucleotide for human telomerase, Oligo 14ab #1.

XX Human; Telomerase; vaccine; antibody; cancer; EF2H;  
 KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

XX Homo sapiens.

OS US6261556-B1.

PN 17-JUL-2001.

PD 18-OCT-1999; 99US-0420056.

PF 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

XX Weinrich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA;  
 PI Kealey JT;

DR WPI: 2001-450477/48.

XX Purified human telomerase, useful for inducing immune response in  
 PT animals, comprises several thousand folds increased purity compared  
 PT with cytoplasmic crude cell preparations -  
 XX  
 PS Disclosure; Column 2; 29pp; English.

XX The sequence represents an antisense oligonucleotide used in  
 CC the purification of human telomerase. The invention relates  
 CC to a purified human telomerase core enzyme protein comprising  
 CC 2000-fold increased purity compared with a crude extract of cells from  
 CC adenovirus-transformed kidney cell line (293 cells) and when associated  
 CC with telomerase RNA component has DNA polymerase activity and a molecular  
 CC weight of 200-2000 Kilo Daltons (kDa). The purified telomerase is useful  
 CC for inducing a humoral or cell-mediated immune response in an animal.  
 CC Purified telomerase or immunogenic fragments are useful as vaccines for  
 CC treating diseases associated with over-expression of telomerase, such as  
 CC cancer and for producing antibodies that recognize telomerase, which are  
 CC useful as affinity agents in isolating the proteins and for detecting the  
 CC presence of proteins in a sample, such as cell or tissue. Identification  
 CC of telomerase aids in diagnosis of cancer or pre-cancerous states.  
 CC Telomerase and/or telomerase associated proteins are also useful for  
 CC screening compounds to identify agents that alter the association of  
 CC telomerase-associated proteins, such as nucleolin or EF2H with  
 CC telomerase.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

SQ Query Match 100.0%; Score 12; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CGTTCCTCTCC 12  
 Db 1 CGTTCCTCTCC 12

RESULT 7  
 AAS09480  
 ID AAS09480 standard; DNA; 20 BP.

XX AAS09480;

XX 24-OCT-2001 (first entry)

DE Antisense oligonucleotide for human telomerase, Oligo 14ab #2.

XX Human; Telomerase; vaccine; antibody; cancer; EF2H;  
 KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FT modified\_base 1  
 FT /tag= a  
 FT /mod\_base= C  
 FT /note= "C is biotinylated"

PN US6261556-B1.

PD 17-JUL-2001.

PF 18-OCT-1999; 99US-0420056.

PR 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

XX Weinrich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA;  
 PI Kealey JT;

DR WPI: 2001-450477/48.

XX Purified human telomerase, useful for inducing immune response in  
 PT animals, comprises several thousand folds increased purity compared  
 PT with cytoplasmic crude cell preparations -  
 XX  
 PS Disclosure; Column 18; 29pp; English.

XX The sequence represents a biotinylated antisense oligonucleotide  
 CC used in the purification of human telomerase. The invention  
 CC relates to a purified human telomerase core enzyme protein comprising  
 CC 2000-fold increased purity compared with a crude extract of cells from  
 CC adenovirus-transformed kidney cell line (293 cells) and when associated  
 CC with telomerase RNA component has DNA polymerase activity and a molecular  
 CC weight of 200-2000 Kilo Daltons (kDa). The purified telomerase is useful  
 CC for inducing a humoral or cell-mediated immune response in an animal.  
 CC Purified telomerase or immunogenic fragments are useful as vaccines for  
 CC treating diseases associated with over-expression of telomerase, such as  
 CC cancer and for producing antibodies that recognize telomerase, which are  
 CC useful as affinity agents in isolating the proteins and for detecting the  
 CC presence of proteins in a sample, such as cell or tissue. Identification  
 CC of telomerase aids in diagnosis of cancer or pre-cancerous states.  
 CC Telomerase and/or telomerase associated proteins are also useful for  
 CC screening compounds to identify agents that alter the association of  
 CC telomerase-associated proteins, such as nucleolin or EF2H with  
 CC telomerase.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

SQ Query Match 100.0%; Score 12; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CGTTCCTCTCC 12  
 Db 1 CGTTCCTCTCC 12



## RESULT 8

AAV41169 standard; DNA; 30 BP.

AAV41169;

08-OCT-1998 (first entry)

RNA component of human telomerase (hTR) antisense oligo 14.

RNA component; human telomerase; antisense oligonucleotide; infection; neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer; contraception; sterilisation; immunosuppression; therapeutic; hTR; immune system down-regulation; anti-inflammatory therapy; ss.

Synthetic.

Homo sapiens.

MO9828442-A1.

02-JUL-1998.

19-DEC-1997; 97WO-US23619.

20-DEC-1996; 96US-0770565.

20-DEC-1996; 96US-0770564.

(GERO-) GERON CORP.

Kealey JT, Kim NM, Pruzan R, Weinrich SL, Wu F;

WPI; 1998-377670/32.

New polynucleotide(s) anti:sense to human telomerase - used for detecting or inhibiting human telomerase, e.g. for treating cancers, contraception, immuno-suppression or treating infection

Claim 11; Page 65; 80pp; English.

Sequences shown in AAV41169 to AAV41181 represent antisense oligonucleotides to the RNA component of human telomerase (hTR). These antisense oligonucleotides specifically hybridise to a nucleotide sequence within an accessible region of the hTR, but that does not hybridise to a sequence within the template region of hTR. These oligonucleotides may specifically be used for detection of an RNA component of human telomerase in a sample. This is useful for diagnosing cancer (especially neuroblastoma, bladder, colon and prostate cancer), and providing prognosis for a cancer patient. The inhibitory oligonucleotides can inhibit the telomerase activity level in a cell by interfering with transcription of the RNA component, decreasing the half-life of the telomerase RNA component transcript, inhibiting the assembly of the RNA component into the telomerase holoenzyme, or inhibiting the polymerase activity of telomerase. These antisense oligonucleotides can be used for inhibiting telomerase activity in both cultured cells and in cells in vivo. They can be used in therapeutics for treating or preventing cancer, for contraception or sterilisation, for immunosuppression, and for selectively down-regulating specific branches of the immune system, e.g. a specific subset of T-cells, in anti-inflammatory therapies or for treating infections by, e.g. yeast, parasites or fungi.

Sequence 30 BP; 4 A; 10 C; 8 G; 8 T; 0 other;

Query Match 100.0%; Score 12; DB 19; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTTCCTCTTCC 12

1 CGTTCCTCTTCC 12

## RESULT 9

AAQ71941 standard; DNA; 20 BP.

AAQ71941;

03-MAY-1995 (first entry)

Human IL-2R gamma gene exon 3 Nsense primer.

Human IL-2R gamma gene; X-linked severe combined immunodeficiency; XSCID; interleukin; ss.

Homo sapiens.

Key Location/Qualifiers

FT modified\_base 1

FT /tag= a

FT /mod\_base= OTHER

FT /note= "Biotin covalently bound to cytosine"

MO9420641-A.

15-SEP-1994.

10-MAR-1994; 94WO-US02891.

12-MAR-1993; 93US-0031143.

14-SEP-1993; 93US-0121435.

(USSH) US DEPT HEALTH &amp; HUMAN SERVICES.

Leonard WJ, McBride WO, Noguchi M;

WPI; 1994-303046/37.

Diagnosis of X-linked severe combined immunodeficiency (XSCID) - comprises detecting mutated IL-2R gamma gene, also vectors and transgenic animals containing the mutated gene

Claim 12; Page 88; 98pp; English.

AAQ71911 to AAQ71975 are primers for the human IL-2R gamma gene, these were used to amplify DNA from mutated and normal IL-2R gamma genes. The mutated gene DNA was obtained either from female carriers or male sufferers of X-linked severe combined immunodeficiency (XSCID). The amplified DNA from normal and affected individuals was then compared using a variety of methods including northern blotting and dot and slot hybridisation. From this a claimed method for the diagnosis of XSCID carriers and sufferers was developed.

Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 other;

Query Match 91.7%; Score 11; DB 15; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.6e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 GTTCCCTTCC 12

3 GTTCCCTTCC 13

## RESULT 10

AAQ71914/C standard; DNA; 20 BP.

AAQ71914;

03-MAY-1995 (first entry)

Human IL-2R gamma gene intron 2 antisense primer.

Human IL-2R gamma gene; X-linked severe combined immunodeficiency; XSCID; interleukin; ss.

```

OS Homo sapiens.
XX
XX MO9420641-A.
XX
XX 15-SEP-1994.
XX
XX 10-MAR-1994; 94MO-US02891.
XX
XX 12-MAR-1993; 93US-0031143.
XX
XX 14-SEP-1993; 93US-0121435.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Leonard WJ, McBride WO, Noguchi M;
XX
XX WPI; 1994-303046/37.
XX
XX
XX Diagnosis of X-linked severe combined immunodeficiency (XSCID) -
XX comprises detecting mutated IL-2R gamma gene, also vectors and
XX transgenic animals containing the mutated gene
XX
XX Claim 12; Page 87; 98pp; English.
XX
XX AA071911 to AA071975 are primers for the human IL-2R gamma gene, these
XX were used to amplify DNA from mutated and normal IL-2R gamma genes.
XX The mutated gene DNA was obtained either from female carriers or
XX male sufferers of X-linked severe combined immunodeficiency (XSCID).
XX The amplified DNA from normal and affected individuals was then
XX compared using a variety of methods including northern blotting and
XX dot and slot hybridisation. From this a claimed method for the
XX diagnosis of XSCID carriers and sufferers was developed.
XX
XX Sequence 20 BP; 8 A; 1 C; 9 G; 2 T; 0 other;
XX
XX
XX Query Match 91.7%; Score 11; DB 15; Length 20;
XX Best Local Similarity 100.0%; Pred.No. 4.6e+03;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 2 GTTCTCTTCC 12
XX |||||
XX 18 GTTCTCTTCC 8
XX
XX
XX RESULT 11
XX ID AAA07908 standard; DNA; 20 BP.
XX
XX AC AAA07908;
XX
XX DT 07-JUL-2000 (first entry)
XX
XX DE Hs-UNC-53/2 specific RT-PCR forward primer.
XX
XX KW UNC-53; Caenorhabditis elegans; microtubule; neural regeneration;
XX anticancer; anti-neurodegeneration; antifibrotic; anti-adhesive; human;
XX KW antisclerotic; antimetastatic; anti-arthritis; autoimmune disease;
XX RT-PCR; primer; ss.
XX
XX OS Homo sapiens.
XX
XX FN WO9963080-A1.
XX
XX PD 09-DEC-1999.
XX
XX PF 02-JUN-1999; 99WO-EP03848.
XX
XX PR 03-JUN-1998; 98GB-0011962.
XX
XX PA (JANC ) JANSSEN PHARM NV.
XX
XX PI Layten WHM, De Raeymaeker WC, Geysen JGH, Bogaert TROE;
XX Maerten LJS, Verhasselt P, Van De Craen M;
XX

```

```

XX
XX DR WPI; 2000-116370/10.
XX
XX PT Novel proteins and nucleic acids e.g. for treating neurodegeneration
XX
XX PS Disclosure; Fig 6b; 146pp; English.
XX
XX
XX The invention provides vertebrate (human) protein homologue of a UNC-53
XX protein of Caenorhabditis elegans. The UNC-53 binds to microtubules or
XX their plus ends. The UNC-53 sequences are used to promote neural
XX regeneration, revascularization and wound healing; also for treating
XX neurodegenerative disease, acute traumatic injury, fibrotic disease and
XX autoimmune diseases (e.g. rheumatoid arthritis and sclerosis). The
XX UNC-53 polynucleotides can be used for recombinant production of the
XX proteins, as a source of probes for detecting allelic variants and
XX polymorphisms, for sequencing genomic DNA and for detecting UNC-53
XX expression; and as source of therapeutic antisense sequences. Cells that
XX express the protein are used to identify regulators of cell shape,
XX growth, motility and migration. They can also be used to identify
XX proteins that are involved in signal transduction pathways also involving
XX UNC-53, and to identify compounds that alter attachment of UNC-53 to
XX microtubules. A target gene coupled to a UNC-53 encoding sequence may be
XX used to deliver the target gene to a cellular microtubule or its plus
XX ends. Sequences AA07902-7911 represent primers specific for Hs-UNC-53/2,
XX used in RT-PCR studies of Hs-UNC-53/2 expression.
XX
XX Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 other;
XX
XX
XX Query Match 91.7%; Score 11; DB 21; Length 20;
XX Best Local Similarity 100.0%; Pred.No. 4.6e+03;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 2 GTTCTCTTCC 12
XX |||||
XX 8 GTTCTCTTCC 18
XX
XX
XX RESULT 12
XX ID AAA11686 standard; DNA; 21 BP.
XX
XX AC AAA11686;
XX
XX DT 14-JUL-2000 (first entry)
XX
XX DE Human GABA-B receptor PCR primer GRI6as (hs).
XX
XX KW GABA receptor; GABA-B receptor; neuroprotective; metabotropic receptor;
XX human disease marker; gene therapy; central nervous system; epilepsy;
XX KW stroke; psychological disease; stress; manic depression; schizophrenia;
XX migraine; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200015786-A1.
XX
XX PD 23-MAR-2000.
XX
XX PF 11-SEP-1999; 99WO-EP06742.
XX
XX PR 14-SEP-1998; 98DE-1041941.
XX
XX PR 04-DEC-1998; 98DE-1056066.
XX
XX PA (BADI ) BASF-LYNX BIOSCIENCE AG.
XX
XX PI Kornau H, Eisenhardt G, Kuner R, Hirschfeld K;
XX
XX DR WPI; 2000-283281/24.
XX
XX PT A novel metabotropic receptor complex from the central nervous system,
XX related coding sequences and methods of identifying binding substances,
XX ligands and interactions with other proteins
XX

```

PS Example 5; Page 27; 66pp; German.

XX This invention describes a novel protein heteromer, containing at least

CC a GABA-B receptor protein and at least a protein (A) or a sequence which

CC has a substitution, inversion, insertion or deletion of one or more amino

CC acid residues and which retains the biological activity of the protein

CC heteromer and which has neuroprotective activity. The encoding nucleic

CC acid (1), the construct, (A) or the protein heteromer are useful for

CC identifying proteins (or nucleic acids encoding such proteins) that show

CC specific binding affinity to (A) or the protein heteromer. The two-hybrid

CC system or biochemical methods can be used to identify interaction domains

CC of metabotropic receptors and use for pharmacotherapeutic intervention.

CC Structural information from the protein or protein complex is useful for

CC identifying and manufacture of substances which have specific binding

CC activity to the protein or protein complex. The protein heteromer and

CC (A), or fragments of these are useful as antigens to generate specific

CC mono- or polyclonal antibodies. (1) is useful for identifying and for

CC isolating homologous sequences, as a marker for human disease and for

CC gene therapy. The methods can be used to identify substances, which bind

CC to (A) or (1) and that cause inhibition or activation of functional

CC effects of the GABAergic signal messages in neurons of the central

CC nervous system. The method can also identify substances that inhibit or

CC amplify interactions of (A) with other metabotropic receptors or

CC interaction of ligands with the protein heteromer or (A) or interactions

CC of (A) with G-proteins or other signal transduction molecules. The

CC analysis of the interactions of (A) and GABA-B receptors is important

CC for identifying potential active substances against diseases such as

CC epilepsy, stroke and psychological diseases such as stress, manic

CC depression, schizophrenia, migraine and others. This sequence

CC represents a PCR primer used in the method of the invention.

SQ Sequence 21 BP; 1 A; 9 C; 2 G; 9 T; 0 other;

QY Query Match 91.7%; Score 11; DB 21; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.6e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 CGTTCCTCTTC 21

1 CGTTCCTCTTC 11

|||||

11 CGTTCCTCTTC 21

RESULT 13

AAZ89497

ID AAZ89497 standard; DNA; 21 BP.

XX

AC AAZ89497;

XX

DT 22-JUN-2000 (first entry)

XX

DE Human GABA-B receptor cDNA PCR primer GB16as (hs).

XX

KW GABA-B receptor; neuroprotectant; gene therapy; central nervous system;

KW metabotropic receptor; signal transduction; epilepsy; stroke; migraine;

KW psychological disease; stress; manic depression; schizophrenia; human;

KW PCR primer; ss.

XX

OS Homo sapiens.

XX

PN DE19841941-A1.

XX

PD 16-MAR-2000.

XX

PF 14-SEP-1998; 98DE-1041941.

XX

PR 14-SEP-1998; 98DE-1041941.

XX

PA (BADI) BASF-LYX BIOSCIENCE AG.

XX

PI Kornau H, Eisenhardt G, Kuner R, Hirschfeld K;

XX

DR WPI; 2000-257875/23.

XX

PT A novel metabotropic receptor complex from the central nervous system,

PT related coding sequences and methods of identifying binding substances,

PT ligands and interactions with other proteins

XX

PS Example 5; Page 11; 32pp; German.

XX This invention describes a novel protein heteromer, containing at least

CC a GABA-B receptor protein and at least a protein (A) or its derivative

CC which retains the biological activity of the protein heteromer. The

CC protein of the invention has neuroprotective activity and can be used

CC for gene therapy. (A) or the protein heteromer are useful for identifying

CC proteins (or nucleic acids encoding such proteins) that show specific

CC binding affinity to (A) or the protein heteromer. The two-hybrid system

CC or biochemical methods can be used to identify interaction domains of

CC metabotropic receptors and use for pharmacotherapeutic intervention.

CC Structural information from the protein or protein complex is useful for

CC identifying and manufacture of substances which have specific binding

CC activity to the protein or protein complex. The protein heteromer and (A)

CC or fragments of these are useful as antigens to generate specific mono-

CC or polyclonal antibodies. The encoding nucleic acid (1) is useful for

CC identifying and isolating homologous sequences, as a marker for human

CC disease and for gene therapy. The methods can be used to identify

CC substances, which bind to (A) or (1) and that cause inhibition or

CC activation of functional effects of the GABAergic signal messages in

CC neurons of the central nervous system. The method can also identify

CC substances that inhibit or amplify interactions of (A) with other

CC metabotropic receptors or interaction of ligands with the protein

CC heteromer or (A) or interactions of (A) with G-proteins or other signal

CC transduction molecules. The analysis of the interactions of (A) and

CC GABA-B receptors is important for identifying potential active substances

CC against diseases such as epilepsy, stroke and psychological diseases such

CC as stress, manic depression, schizophrenia, migraine and others. This

CC sequence represents a PCR primer used in the amplification of the human

CC GABA-B receptor described in the method of the invention.

SQ Sequence 21 BP; 1 A; 9 C; 2 G; 9 T; 0 other;

QY Query Match 91.7%; Score 11; DB 21; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.6e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 CGTTCCTCTTC 21

1 CGTTCCTCTTC 11

|||||

11 CGTTCCTCTTC 21

RESULT 14

AAH62356

ID AAH62356 standard; DNA; 21 BP.

XX

AC AAH62356;

XX

DT 12-SEP-2001 (first entry)

XX

DE RBBP2 polymorphism containing DNA fragment #257.

XX

KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;

KW heart disease; paternally testing; forensic science; ds.

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT Variation replace(11,G)

FT /tag= a

FT /standard\_name= "single nucleotide polymorphism"

PN WO200138576-A2.

XX

PD 31-MAY-2001.

XX

PF 17-NOV-2000; 2000WO-US31639.

XX

PR 24-NOV-1999; 99US-0167334.

XX

XX (WHEB) WHITEHEAD INST BIOMEDICAL RES.  
 XX Cargill M, Ireland JS, Lander ES;  
 PI WPI; 2001-367705/38.  
 XX  
 DR New nucleic acid segments of the human genome, particularly from genes  
 PT including polymorphic sites, for phenotype correlation, forensics,  
 PT paternity testing, medicine and genetic analysis  
 XX  
 PS Claim 1; Page 50; 80pp; English.  
 XX  
 CC DNA sequences AAH62100 - AAH62688 represent segments of human genes which  
 CC contain single nucleotide polymorphisms (SNPs). A method is included in  
 CC the invention for analysing a nucleic acid sample, which consists of  
 CC determining the base occupying any one of the polymorphic sites given in  
 CC the SNP containing sequences. The nucleotide sequences can be used in the  
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart  
 CC diseases, diseases of the cardiovascular system, and infection by  
 CC microorganisms. The oligonucleotides are also useful in the manufacture  
 CC of a medicament for the treatment or prophylaxis of the diseases, and as  
 CC a pharmaceutical. SNP containing oligonucleotides are useful in  
 CC applications such as phenotype correlation, forensics, paternity testing,  
 CC medicine and genetic analysis.  
 XX  
 SQ Sequence 21 BP; 3 A; 7 C; 3 G; 8 T; 0 other;  
 Query Match 91.7%; Score 11; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 CGTCTCTCTCC 12  
 Db 8 GTTCTCTCTCC 18  
 RESULT 15  
 ABL43752/C  
 ID ABL43752 standard; DNA; 22 BP.  
 XX  
 AC ABL43752;  
 XX  
 DT 11-APR-2002 (first entry)  
 XX  
 DE Human chromosome 1p36-35 PCR primer SEQ ID NO:796.  
 XX  
 KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;  
 KW genome; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2001321190-A.  
 PD 20-NOV-2001.  
 PF 12-MAR-2001; 2001JP-0068285.  
 PR 10-MAR-2000; 2000JP-0066716.  
 PA (RIKA) RIKAGAKU KENKYUSHO.  
 PA (GENO-) GENOTEX YG.  
 XX  
 DR WPI; 2002-144136/19.  
 XX  
 PT Arraying genome clones  
 PS Claim 4; Page 20; 528pp; Japanese.  
 XX  
 CC The present invention describes a method of arraying genome clones. The  
 CC method comprises: (a) clones of the genomic libraries contained in  
 CC multitwell plates numbered for discrimination are mixed in each of the  
 CC multitwell plates; (b) a primer designed based on the chromosome marker

CC sequence is added to the mixture to carry out an amplification reaction;  
 CC (c) a signal corresponding to the marker is detected from the resultant  
 CC amplified product to specify the discrimination Nos. of the multitwell  
 CC plates containing the clones having said marker sequence; (d) the order  
 CC of the markers is changed so that the same discrimination Nos. succeed to  
 CC the maximum in the specified discrimination Nos. to array the multitwell  
 CC plates; (e) the clones in the multitwell plates of the specified  
 CC discrimination Nos. are mixed respectively in each well of longitudinal  
 CC and lateral directions; (f) the mixed clones are cultured and the  
 CC resultant cultures are amplified by using the above primer; (g) signals  
 CC are detected from the amplified products; (h) the clones in the multitwell  
 CC plates are specified from the detected result; and (i) the clones are  
 CC reconstituted as the positions on the chromosome and arrayed. The  
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
 CC represent PCR primers for human chromosome 21q22.1, which are  
 CC specifically claimed for use in the present invention.  
 XX  
 SQ Sequence 22 BP; 7 A; 4 C; 6 G; 5 T; 0 other;  
 Query Match 91.7%; Score 11; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 CGTCTCTCTTC 11  
 Db 13 CGTCTCTCTTC 3

Search completed: June 23, 2003, 05:43:34  
 Job time : 80.0527 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 18.7888 Seconds  
(without alignments)  
195.867 Million cell updates/sec

Title: US-08-770-564A-4

Perfect score: 12  
Sequence: 1 CGTTCCTCTTCC 12

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/prodata/2/ina/5A COMB. seq: \*  
2: /cgn2\_6/prodata/2/ina/5B COMB. seq: \*  
3: /cgn2\_6/prodata/2/ina/6A COMB. seq: \*  
4: /cgn2\_6/prodata/2/ina/6B COMB. seq: \*  
5: /cgn2\_6/prodata/2/ina/PCTUS COMB. seq: \*  
6: /cgn2\_6/prodata/2/ina/backfile1 seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	12	2	US-08-770-565-4
2	12	100.0	20	2	US-08-770-565-3
3	12	100.0	20	2	US-08-833-377-7
4	12	100.0	30	2	US-08-770-565-2
5	11	91.7	20	1	US-08-031-143B-6
6	11	91.7	20	1	US-08-031-143B-33
7	11	91.7	20	2	US-08-833-377-14
8	11	91.7	20	5	PCT-US94-02891-6
9	11	91.7	20	5	PCT-US94-02891-33
10	10	83.3	14	1	US-08-294-424-33
11	10	83.3	15	4	US-08-584-040-8457
12	10	83.3	17	3	US-08-988-706-54
13	10	83.3	17	4	US-08-584-040-2519
14	10	83.3	17	4	US-08-584-040-2520
15	10	83.3	17	4	US-08-584-040-2521
16	10	83.3	17	4	US-08-584-040-2522
17	10	83.3	18	4	US-09-306-595C-30
18	10	83.3	20	2	US-08-534-479-1
19	10	83.3	20	4	US-09-490-692-85
20	10	83.3	20	4	US-09-458-377-30
21	10	83.3	20	4	US-09-203-895-5
22	10	83.3	21	4	US-08-949-344C-18
23	10	83.3	22	1	US-07-820-412-8
24	10	83.3	22	1	US-08-488-144-4
25	10	83.3	22	1	US-08-611-155B-1
26	10	83.3	22	1	US-08-611-155B-2
27	10	83.3	22	1	US-08-611-155B-3

C 28	10	83.3	22	1	US-08-611-155B-4	Sequence 4, Appl1
C 29	10	83.3	22	1	US-08-611-155B-5	Sequence 5, Appl1
C 30	10	83.3	22	1	US-08-611-155B-6	Sequence 6, Appl1
C 31	10	83.3	22	2	US-08-916-120A-1	Sequence 1, Appl1
C 32	10	83.3	22	2	US-08-916-120A-2	Sequence 2, Appl1
C 33	10	83.3	22	2	US-08-916-120A-3	Sequence 3, Appl1
C 34	10	83.3	22	2	US-08-916-120A-4	Sequence 4, Appl1
C 35	10	83.3	22	2	US-08-916-120A-5	Sequence 5, Appl1
C 36	10	83.3	22	2	US-08-916-120A-6	Sequence 6, Appl1
C 37	10	83.3	24	5	PCT-US94-09851-66	Sequence 66, Appl1
C 38	10	83.3	26	2	US-08-646-367-27	Sequence 27, Appl1
C 39	10	83.3	28	3	US-08-884-324-17	Sequence 17, Appl1
C 40	10	83.3	28	3	US-08-884-324-19	Sequence 19, Appl1
C 41	10	83.3	30	1	US-08-210-880B-4	Sequence 4, Appl1
C 42	10	83.3	30	1	US-08-485-692-19	Sequence 19, Appl1
C 43	10	83.3	30	1	US-08-485-692-20	Sequence 20, Appl1
C 44	10	83.3	30	1	US-08-419-519-19	Sequence 19, Appl1
C 45	10	83.3	30	1	US-08-419-519-19	Sequence 19, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-770-565-4  
; Sequence 4, Application US/08770565  
; Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-4  
Query Match 100.0%; Score 12; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTCCTCTTCC 12

Db 1 CGTTCCTCTCC 12

RESULT 2  
US-08-770-565-3  
Sequence 3, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald L.  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-3

Query Match 100.0%; Score 12; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12  
Db 1 CGTTCCTCTCC 12

RESULT 3  
US-08-833-377-7  
Sequence 7, Application US/0883377  
Patent No. 586506  
GENERAL INFORMATION:  
APPLICANT: Weinrich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichtsteiner, Serge P.  
APPLICANT: Vaseerot, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,377  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note= "Oligo 14ab"  
US-08-833-377-7

Query Match 100.0%; Score 12; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12  
Db 1 CGTTCCTCTCC 12

RESULT 4  
US-08-770-565-2  
Sequence 2, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald L.  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565

FILED DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-2

Query Match 100.0%; Score 12; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCTTCC 12  
DB 1 GTTCTCTTCC 12

RESULT 5  
US-08-031-143B-6/C  
Sequence 6, Application US/08031143B  
Patent No. 551880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
APPLICANT: MCBIRDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,143B  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: HUMAN

INDIVIDUAL ISOLATE: IL-2R  
US-08-031-143B-6  
Query Match 91.7%; Score 11; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCC 12  
DB 18 GTTCTCTTCC 8

RESULT 6  
US-08-031-143B-33  
Sequence 33, Application US/08031143B  
Patent No. 551880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
APPLICANT: MCBIRDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,143B  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R  
US-08-031-143B-33

Query Match 91.7%; Score 11; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCC 12  
DB 3 GTTCTCTTCC 13

RESULT 7  
US-08-833-377-14  
Sequence 14, Application US/08833377

Patent No. 5968506  
GENERAL INFORMATION:  
APPLICANT: Weinlich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichtesteiner, Serge P.  
APPLICANT: Vassero, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,377  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1  
OTHER INFORMATION: /mod base= OTHER  
FEATURE: OTHER INFORMATION: /note= "N = 5' biotinylated cytidine"  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note= "biotinylated Oligo 14ab"  
US-08-833-377-14  
Query Match 91.7%; Score 11; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 2 GTTCTCTTCC 12  
Db 2 GTTCTCTTCC 12  
RESULT 8  
PCT-US94-02891-6/c  
Sequence 6, Application PC/TUS9402891  
GENERAL INFORMATION:  
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN  
APPLICANT: SERVICES  
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL  
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: XSCID  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02891  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/031,143  
FILING DATE: 12-MAR-1993  
APPLICATION NUMBER: 08/121,435  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FETLER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: OLIGONUCLEOTIDE  
DESCRIPTION: NO  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R  
PCT-US94-02891-6  
Query Match 91.7%; Score 11; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 2 GTTCTCTTCC 12  
Db 18 GTTCTCTTCC 8  
RESULT 9  
PCT-US94-02891-33  
Sequence 33, Application PC/TUS9402891  
GENERAL INFORMATION:  
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN  
APPLICANT: SERVICES  
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL  
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA



ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02891  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/031,133  
FILING DATE: 12-MAR-1993  
APPLICATION NUMBER: 08/121,435  
FILING DATE: 14-SEPT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R  
PCT-US94-02891-33

Query Match 91.7%; Score 11; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCC 12  
|||||||  
Db 3 GTTCCTCTTCC 13

RESULT 10  
US-08-294-424-33/c  
Sequence 33, Application US/08294424  
Patent No. 5800984  
GENERAL INFORMATION:  
APPLICANT: VARY, Calvin  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE DETECTION BY  
TITLE OF INVENTION: TRIPLE HELIX FORMATION  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/294,424  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/000,922  
FILING DATE: 16 JAN 1993  
APPLICATION NUMBER: US/07/629,601B  
FILING DATE: 17-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00088-037001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-294-424-33

Query Match 83.3%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTCCTCTTCC 12  
|||||||  
Db 12 TTTCCTCTTCC 3

RESULT 11  
US-08-584-040-8457  
Sequence 8457, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwiggan, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 216/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 8457:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-8457

Query Match 83.3%; Score 10; DB 4; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.9e+03;  
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTC 11  
|:|:|:|:|:  
DB 5 GUUCCUCCUCC 14

## RESULT 12

US-08-988-706-54/C  
Sequence 54, Application US/08988706  
Patent No. 6083698

## GENERAL INFORMATION:

APPLICANT: OLSEN, Sheri J.  
APPLICANT: ANGELLY, Tracy S.  
APPLICANT: LAWRENCE, Tammy  
APPLICANT: LESCALLET, Jennifer L.  
APPLICANT: MURPHY, Patricia D.  
APPLICANT: ALLEN, Antoinette P.  
APPLICANT: THRUER, Denise B.  
APPLICANT: WHITE, Marga B.  
APPLICANT: ZENG, Bin  
APPLICANT: SADZEWICZ, Lisa K.  
TITLE OF INVENTION: CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oncomed, Inc.  
STREET: 205 Perry Parkway  
CITY: Galtherburg  
STATE: MD  
COUNTRY: USA  
ZIP: 20877  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,706  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: TARCA, John E.  
REGISTRATION NUMBER: 33,638  
REFERENCE/DOCKET NUMBER: PA-0108  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-208-1888  
TELEFAX: 301-926-6125  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "PROBE"  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: HOMO SAPIENS  
STRAIN: BRCA1  
US-08-988-706-54

Query Match 83.3%; Score 10; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTT 10  
|:|:|:|:|:  
DB 10 CGTTCCTCTT 1

## RESULT 13

US-08-584-040-2519  
Sequence 2519, Application US/08584040  
Patent No. 6346398

## GENERAL INFORMATION:

APPLICANT: Pavco, Pamela  
APPLICANT: MCSWIGEN, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2519:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-2519

Query Match 83.3%; Score 10; DB 4; Length 17;  
Best Local Similarity 50.0%; Pred. No. 1.9e+03;  
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTC 11  
|:|:|:|:|:  
DB 7 GUUCCUCCUCC 16

## RESULT 14

US-08-584-040-2520  
Sequence 2520, Application US/08584040

```

; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2520:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2520

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```

Query Match      83.3%; Score 10; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY      2 GTTCTCTTC 11
      ||:||:||:|
Db      6 GUUCUCUCUC 15

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RESULT 15
US-08-584-040-2521
; Sequence 2521, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2521:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2521

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Query Match      83.3%; Score 10; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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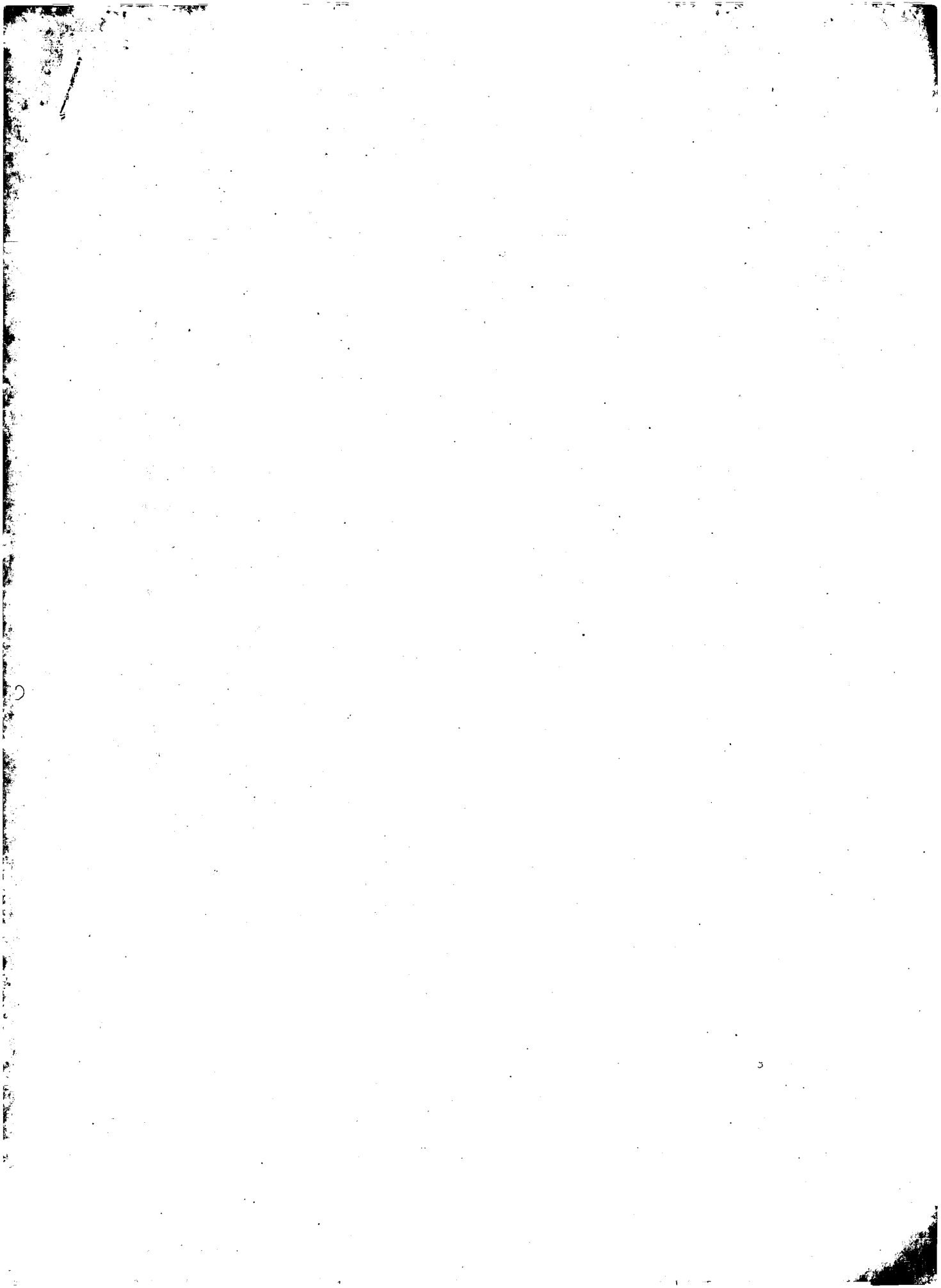
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Db      3 GUUCUCUCUC 12

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GenCore version 5.1.6  
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OM-nucleic - nucleic search, using sw model

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Title: US-08-770-564a-4  
Perfect score: 12  
Sequence: 1 CGTTCCTCTCC 12

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

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Minimum DB seq length: 0  
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Database :

Published Applications NA:\*

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- 2: /cgn2\_6/prodata/1/pubpna/PCR\_NEW\_PUB.seq:\*
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- 9: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:\*
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- 11: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	91.7	25	US-10-215-112-12736	Sequence 12736, A
C 2	11	91.7	25	US-10-098-2638-24096	Sequence 24096, A
C 3	11	91.7	25	US-10-098-2638-81647	Sequence 81647, A
C 4	11	91.7	25	US-10-098-2638-81648	Sequence 81648, A
C 5	11	91.7	25	US-10-098-2638-96226	Sequence 96226, A
C 6	11	91.7	25	US-10-098-2638-114611	Sequence 114611, A
C 7	10	83.3	17	US-09-818-875-899	Sequence 899, App
C 8	10	83.3	17	US-09-818-875-900	Sequence 900, App
C 9	10	83.3	17	US-10-163-552-930	Sequence 930, App
C 10	10	83.3	18	US-09-925-388-30	Sequence 30, Appl
C 11	10	83.3	18	US-09-969-373-3188	Sequence 3188, Ap
C 12	10	83.3	19	US-09-969-373-1794	Sequence 1794, Ap
C 13	10	83.3	20	US-10-139-496-25	Sequence 25, Appl
C 14	10	83.3	20	US-10-181-846-85	Sequence 85, Appl
C 15	10	83.3	20	US-09-953-047-40	Sequence 40, Appl
C 16	10	83.3	20	US-10-216-484-94	Sequence 94, Appl
C 17	10	83.3	20	US-10-216-484-98	Sequence 98, Appl
C 18	10	83.3	22	US-09-864-636A-1899	Sequence 1899, Ap
C 19	10	83.3	24	US-10-101-487-12	Sequence 12, Appl

20	10	83.3	24	9	US-10-101-487-13	Sequence 13, Appl
21	10	83.3	24	10	US-09-818-875-4	Sequence 4, Appl
C 22	10	83.3	24	10	US-09-037-657-4	Sequence 4, Appl
C 23	10	83.3	25	9	US-09-943-388-16	Sequence 16, Appl
C 24	10	83.3	25	9	US-09-754-853A-686	Sequence 686, App
C 25	10	83.3	25	9	US-10-215-112-2936	Sequence 2936, Ap
C 26	10	83.3	25	9	US-10-215-112-4629	Sequence 4629, Ap
C 27	10	83.3	25	9	US-10-215-112-4630	Sequence 4630, Ap
C 28	10	83.3	25	9	US-10-215-112-13297	Sequence 13297, A
C 29	10	83.3	25	9	US-10-098-2638-2814	Sequence 2814, Ap
C 30	10	83.3	25	9	US-10-098-2638-17568	Sequence 17568, A
C 31	10	83.3	25	9	US-10-098-2638-19683	Sequence 19683, A
C 32	10	83.3	25	9	US-10-098-2638-24706	Sequence 24706, A
C 33	10	83.3	25	9	US-10-098-2638-25145	Sequence 25145, A
C 34	10	83.3	25	9	US-10-098-2638-26377	Sequence 26377, A
C 35	10	83.3	25	9	US-10-098-2638-39832	Sequence 39832, A
C 36	10	83.3	25	9	US-10-098-2638-40293	Sequence 40293, A
C 37	10	83.3	25	9	US-10-098-2638-40300	Sequence 40300, A
C 38	10	83.3	25	9	US-10-098-2638-44698	Sequence 44698, A
C 39	10	83.3	25	9	US-10-098-2638-52287	Sequence 52287, A
C 40	10	83.3	25	9	US-10-098-2638-67887	Sequence 67887, A
C 41	10	83.3	25	9	US-10-098-2638-84565	Sequence 84565, A
C 42	10	83.3	25	9	US-10-098-2638-86229	Sequence 86229, A
C 43	10	83.3	25	9	US-10-098-2638-95971	Sequence 95971, A
C 44	10	83.3	25	9	US-10-098-2638-95972	Sequence 95972, A
C 45	10	83.3	25	9	US-10-098-2638-96589	Sequence 96589, A

#### ALIGNMENTS

RESULT 1  
US-10-215-112-12736/c  
Sequence 12736, Application US/10215112  
Publication No. US20030082596A1  
GENERAL INFORMATION:  
APPLICANT: Michael Miltman  
TITLE OF INVENTION: Method of Genetic Analysis of Probes:  
TITLE OF INVENTION: Test3  
FILE REFERENCE: 3119  
CURRENT APPLICATION NUMBER: US/10/215,112  
CURRENT FILING DATE: 2002-08-08  
NUMBER OF SEQ ID NOS: 14936  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12736  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
US-10-215-112-12736  
OTHER INFORMATION: Synthetic Oligonucleotide

Query Match 91.7%; Score 11; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 GTTCTCTTCC 12  
Db 18 GTTCTCTTCC 8

RESULT 2  
US-10-098-2638-24096/c  
Sequence 24096, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIORITY APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16

```
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-24096
```

```
Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 GTTCCTCTTCC 12
        |||||
Db      16 GTTCCTCTTCC 6
```

## RESULT 3

```
US-10-098-263B-81647
; Sequence 81647, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81647
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-81647
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```
Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 GTTCCTCTTCC 12
        |||||
Db      1 GTTCCTCTTCC 11
```

## RESULT 4

```
US-10-098-263B-81648
; Sequence 81648, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-81648
```

```
Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 GTTCCTCTTCC 12
        |||||
Db      1 GTTCCTCTTCC 11
```

```
RESULT 5
US-10-098-263B-96226
; Sequence 96226, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 96226
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-96226
```

```
Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 GTTCCTCTTCC 12
        |||||
Db      11 GTTCCTCTTCC 21
```

## RESULT 6

```
US-10-098-263B-114611
; Sequence 114611, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 114611
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-114611
```

```
Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 GTTCCTCTTCC 12
        |||||
Db      6 GTTCCTCTTCC 16
```

## RESULT 7

```
US-09-818-875-899/C
; Sequence 899, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; PRIOR FILING DATE: 2001-03-27
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```

; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedmann macro Napro4
; SEQ ID NO 899
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-818-875-899

Query Match      83.3%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTCCTCTT 10
DB      17 CGTTCCTCTT 8

RESULT 8
US-09-818-875-900
; Sequence 900, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedmann macro Napro4
; SEQ ID NO 900
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-818-875-900

Query Match      83.3%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTCCTCTT 10
DB      1 CGTTCCTCTT 10

RESULT 9
US-10-163-552-930/c
; Sequence 930, Application US/10163552
; Publication No. US2003015051A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggan, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; TITLE OF INVENTION: HER2
; FILE REFERENCE: MHB01-1653-A (400/014)
```

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; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 930
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-163-552-930

Query Match      83.3%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTCCCTCTC 11
DB      10 GTTCCCTCTC 1

RESULT 10
US-09-925-388-30/c
; Sequence 30, Application US/09925388
; Publication No. US20030054523A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOL PRODUCTION
; FILE REFERENCE: ISOPRENOL PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/925,388
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/306,595
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of 5'-adjacent region of MVK gene
; US-09-925-388-30

Query Match      83.3%; Score 10; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTCCTCTTCC 12
DB      10 TTCCTCTTCC 1

RESULT 11
US-09-969-373-3188/c
; Sequence 3188, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Eiferetz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3188
; LENGTH: 18
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;; TYPE: DNA  
;; ORGANISM: Glycine max  
US-09-969-373-3188

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 18;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTCTCTTTC 11  
DB 17 TTCTCTTTC 8

RESULT 12  
US-09-969-373-1794  
; Sequence 1794, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Effertz, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10132679A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 1794  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-1794

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 19;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTTC 12  
DB 6 TTCTCTTTC 15

RESULT 13  
US-10-139-496-25/c  
; Sequence 25, Application US/10139496  
; Publication No. US20030082646A1  
; GENERAL INFORMATION:  
; APPLICANT: Carey, Thomas E.  
; APPLICANT: Nair, Shankum S.  
; APPLICANT: Gray, Jennifer P.  
; TITLE OF INVENTION: Antisense Targets of Autoimmune Sensorineural Hearing Loss (AISNL)  
; FILE REFERENCE: UM-6982  
; CURRENT APPLICATION NUMBER: US/10/139,496  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 09/222,179  
; PRIOR FILING DATE: 1998-12-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-139-496-25

Query Match  
Best Local Similarity 100.0%; Score 10; DB 9; Length 20;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTTC 12  
DB 17 TTCTCTTTC 8

RESULT 14  
US-10-181-846-85/c  
; Sequence 85, Application US/10181846  
; Publication No. US20030083297A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Lex M. Cowart  
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION  
; FILE REFERENCE: RSP-0363  
; CURRENT APPLICATION NUMBER: US/10/181,846  
; CURRENT FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: PCT/US01/01416  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/490,692  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 85  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-181-846-85

Query Match  
Best Local Similarity 100.0%; Score 10; DB 9; Length 20;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTTC 12  
DB 10 TTCTCTTTC 1

RESULT 15  
US-09-953-047-40  
; Sequence 40, Application US/09953047  
; Publication No. US20030087854A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyalt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXP-  
; FILE REFERENCE: RTS-0157  
; CURRENT APPLICATION NUMBER: US/09/953,047  
; CURRENT FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 95  
; SEQ ID NO 40  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-953-047-40

Query Match  
Best Local Similarity 100.0%; Score 10; DB 9; Length 20;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTTC 12  
DB 11 TTCTCTTTC 20

Search completed: June 23, 2003, 20:01:29  
Job time : 97.4303 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: June 23, 2003, 05:20:00 ; Search time 1006.47 Seconds  
(without alignments)  
299.770 Million cell updates/sec

Title: US-08-770-564a-4  
Perfect score: 12  
Sequence: 1 CGTTCCTCTTCC 12

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

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Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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11: /cgn2\_6/ptodata/2/pna/US087 COMB.seq:\*

12: /cgn2\_6/ptodata/2/pna/US088 COMB.seq:\*

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16: /cgn2\_6/ptodata/2/pna/US092 COMB.seq:\*

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19: /cgn2\_6/ptodata/2/pna/US095 COMB.seq:\*

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21: /cgn2\_6/ptodata/2/pna/US097 COMB.seq:\*

22: /cgn2\_6/ptodata/2/pna/US098 COMB.seq:\*

23: /cgn2\_6/ptodata/2/pna/US099 COMB.seq:\*

24: /cgn2\_6/ptodata/2/pna/US100 COMB.seq:\*

25: /cgn2\_6/ptodata/2/pna/US101 COMB.seq:\*

26: /cgn2\_6/ptodata/2/pna/US102 COMB.seq:\*

27: /cgn2\_6/ptodata/2/pna/US103 COMB.seq:\*

28: /cgn2\_6/ptodata/2/pna/US104 COMB.seq:\*

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35: /cgn2\_6/ptodata/2/pna/US111 COMB.seq:\*

36: /cgn2\_6/ptodata/2/pna/US112 COMB.seq:\*

37: /cgn2\_6/ptodata/2/pna/US113 COMB.seq:\*

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39: /cgn2\_6/ptodata/2/pna/US115 COMB.seq:\*

40: /cgn2\_6/ptodata/2/pna/US116 COMB.seq:\*

41: /cgn2\_6/ptodata/2/pna/US117 COMB.seq:\*

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43: /cgn2\_6/ptodata/2/pna/US119 COMB.seq:\*

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	12	1 PCT-US97-23619-4	Sequence 4, Appl1
2	12	100.0	12	US-08-770-564a-4	Sequence 4, Appl1
3	12	100.0	20	1 PCT-US97-23619-3	Sequence 3, Appl1
4	12	100.0	20	US-08-770-564a-3	Sequence 3, Appl1
5	12	100.0	25	36 US-09-954-427-81691	Sequence 81691, A
6	12	100.0	25	36 US-09-956-584-18655	Sequence 18655, A
7	12	100.0	25	67 US-60-233-166-81691	Sequence 81691, A
8	12	100.0	25	67 US-60-233-620-45573	Sequence 45573, A
9	12	100.0	25	67 US-60-234-011-52883	Sequence 52883, A
10	12	100.0	25	79 US-60-353-987-139546	Sequence 139546, A
11	12	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appl1
12	12	100.0	30	US-08-770-564a-2	Sequence 2, Appl1
13	12	100.0	31	US-08-521-634-17	Sequence 17, Appl1
14	12	100.0	32	1 PCT-US02-25943-62884	Sequence 62884, A
15	12	100.0	32	US-10-227-565-62884	Sequence 62884, A
16	12	100.0	36	1 PCT-US02-35943-46617	Sequence 46617, A
17	11	91.7	16	US-10-227-565-46617	Sequence 46617, A
18	11	91.7	18	1 PCT-US02-25943-62885	Sequence 62885, A
19	11	91.7	18	US-10-227-565-62885	Sequence 62885, A
20	11	91.7	18	US-10-227-565-25195	Sequence 25195, A
21	11	91.7	18	US-10-227-565-62885	Sequence 62885, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

22 11 91.7 25 17 US-09-396-196F-95194 Sequence 95194, A  
23 11 91.7 25 17 US-09-396-196F-95195 Sequence 95195, A  
24 11 91.7 25 17 US-09-396-196F-95206 Sequence 95206, A  
25 11 91.7 25 17 US-09-396-196F-95206 Sequence 95206, A  
26 11 91.7 25 17 US-09-396-196G-95194 Sequence 95194, A  
27 11 91.7 25 17 US-09-396-196G-95195 Sequence 95195, A  
28 11 91.7 25 17 US-09-396-196G-95206 Sequence 95206, A  
29 11 91.7 25 17 US-09-396-196G-11937 Sequence 11937, A  
30 11 91.7 25 26 US-09-660-220-124398 Sequence 124398, A  
31 11 91.7 25 26 US-09-660-220-124402 Sequence 124402, A  
32 11 91.7 25 26 US-09-660-220-124403 Sequence 124403, A  
33 11 91.7 25 26 US-09-660-220-124417 Sequence 124417, A  
34 11 91.7 25 36 US-09-954-427-15992 Sequence 35992, A  
35 11 91.7 25 36 US-09-954-427-56129 Sequence 56129, A  
36 11 91.7 25 36 US-09-954-427-56129 Sequence 56129, A  
37 11 91.7 25 36 US-09-954-427-77982 Sequence 77982, A  
38 11 91.7 25 36 US-09-954-427-149911 Sequence 149911, A  
39 11 91.7 25 36 US-09-954-427-149920 Sequence 149920, A  
40 11 91.7 25 36 US-09-954-427-291192 Sequence 291192, A  
41 11 91.7 25 36 US-09-954-427-291302 Sequence 291302, A  
42 11 91.7 25 36 US-09-954-427-291352 Sequence 291352, A  
43 11 91.7 25 36 US-09-954-427-377727 Sequence 377727, A  
44 11 91.7 25 36 US-09-956-584-64807 Sequence 64807, A  
45 11 91.7 25 36 US-09-956-584-100805 Sequence 100805, A

## ALIGNMENTS

RESULT 1  
PCT-US97-23619-4  
Sequence 4, Application PC/TUS9723619  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: 1.12  
LOCATION: 1.12  
OTHER INFORMATION: /note="oligo 14d"  
PCT-US97-23619-4  
Query Match 100.0%; Score 12; DB 1; Length 12;  
Best local similarity 100.0%; Pred. No. 2e+04; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTTCCTCTCC 12  
Db 1 CGTTCCTCTCC 12  
RESULT 2  
US-08-770-564A-4  
Sequence 4, Application US/0870564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Krizan, Ron  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564A-4  
Query Match 100.0%; Score 12; DB 1; Length 12;  
Best local similarity 100.0%; Pred. No. 2e+04; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTTCCTCTCC 12  
Db 1 CGTTCCTCTCC 12  
RESULT 3  
PCT-US97-23619-3

; Sequence 3, Application PC/TUS9723619  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
; TITLE OF INVENTION: RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/23619  
; FILING DATE: Not yet assigned  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/770,564  
; FILING DATE: 20-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/770,565  
; FILING DATE: 20-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scorelila, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 15389-27PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY:  
; LOCATION: 1..20  
; OTHER INFORMATION: /note="oligo 14ab"  
PCT-US97-23619-3  
Query Match 100.0%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTCTCTTCC 12  
Db 1 CGTCTCTTCC 12  
RESULT 4  
US-08-770-564A-3  
; Sequence 3, Application US/0870564A  
; GENERAL INFORMATION:  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ron  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
; TITLE OF INVENTION: Against the RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,564A  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scorelila, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002200US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0300  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-770-564A-3  
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Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTCTCTTCC 12  
Db 1 CGTCTCTTCC 12

RESULT 5  
US-09-954-427-81691  
; Sequence 81691, Application US/09954427  
; GENERAL INFORMATION:  
; APPLICANT: Miltmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/09/954,427  
; CURRENT FILING DATE: 2001-09-17  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 81691  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819663  
US-09-954-427-81691  
Query Match 100.0%; Score 12; DB 36; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTCTCTTCC 12  
Db 5 CGTCTCTTCC 16

RESULT 6  
US-09-956-584-18655/c  
; Sequence 18655, Application US/09956584

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; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18655
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-18655

Query Match          100.0%; Score 12; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTCCCTCTTCC 12
        |||||
DB      18 CGTCCCTCTTCC 7

RESULT 7
; Sequence 81691, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/223,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819663
US-60-233-166-81691

Query Match          100.0%; Score 12; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTCCCTCTTCC 12
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DB      5 CGTCCCTCTTCC 16

RESULT 8
; Sequence 45573, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:

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; DATABASE ACCESSION NUMBER: GenBank AL034567
US-60-233-620-45573

Query Match          100.0%; Score 12; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTCCCTCTTCC 12
        |||||
DB      15 CGTCCCTCTTCC 4

RESULT 9
; Sequence 52883, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltman, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U41285
US-60-234-017-52883

Query Match          100.0%; Score 12; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTCCCTCTTCC 12
        |||||
DB      18 CGTCCCTCTTCC 7

RESULT 10
; Sequence 396546, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 396546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-396546

Query Match          100.0%; Score 12; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTCCCTCTTCC 12
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DB      24 CGTCCCTCTTCC 13

RESULT 11
; Sequence 2, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:

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APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY:  
LOCATION: 1..30  
OTHER INFORMATION: /note="oligo 14"  
PCT-US97-23619-2  
Query Match 100.0%; Score 12; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCC 12  
Db 1 CGTCTCTCTCC 12

RESULT 12  
US-08-770-564a-2  
Sequence 2, Application US/0870564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Prizant, Ron  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564a-2  
Query Match 100.0%; Score 12; DB 11; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCC 12  
Db 1 CGTCTCTCTCC 12

RESULT 13  
US-08-521-634-17/C  
Sequence 17, Application US/08521634  
GENERAL INFORMATION:  
APPLICANT: Villeneuve, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/521,634  
FILING DATE: 31-AUG-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,115  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/350,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102  
FILING DATE: 7-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy J.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 15389-000850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-521-634-17

Query Match 100.0%; Score 12; DB 9; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTC 12  
DB 31 CGTTCCTCTTC 20

RESULT 14  
PCT-US02-25943-62884/C  
Sequence 62884, Application PC/TUS0225943  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: PCT/US02/25943  
CURRENT FILING DATE: 2002-08-27  
NUMBER OF SEQ ID NOS: 64158  
SOFTWARE: Proprietary  
SEQ ID NO 62884  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
FEATURE:  
LOCATION: (6132858)...(6132888)  
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 67367  
PCT-US02-25943-62884

Query Match 100.0%; Score 12; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTC 12  
DB 22 CGTTCCTCTTC 11

RESULT 15  
US-10-227-565-62884/C  
Sequence 62884, Application US/10227565  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/227,565  
CURRENT FILING DATE: 2002-08-26  
NUMBER OF SEQ ID NOS: 64158  
SOFTWARE: Proprietary  
SEQ ID NO 62884  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
FEATURE:  
LOCATION: (6132858)...(6132888)

OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 6736  
US-10-227-565-62884

Query Match 100.0%; Score 12; DB 42; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTC 12  
DB 22 CGTTCCTCTTC 11

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Job time : 1006.55 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: June 23, 2003, 05:45:21 ; Search time 526.757 Seconds  
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Title: US-08-770-564A-4  
Perfect score: 12  
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Scoring table: OLIGO\_NUC  
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#### SUMMARIES

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C 2	12	100.0	25	9	US-10-355-577-396546
C 3	12	100.0	25	12	US-60-427-836-683575
C 4	11	91.7	17	9	US-10-303-778-7608
C 5	11	91.7	18	9	US-10-303-778-7627
C 6	11	91.7	18	9	US-10-310-188-6596
C 7	11	91.7	20	9	US-10-315-474-66
C 8	11	91.7	20	9	US-10-315-474-137
C 9	11	91.7	25	6	US-09-660-222-124398
C 10	11	91.7	25	6	US-09-660-222-124402
C 11	11	91.7	25	6	US-09-660-222-124403
C 12	11	91.7	25	6	US-09-660-222-124417
C 13	11	91.7	25	6	US-09-660-222-124417
C 14	11	91.7	25	7	US-09-953-570-131778
C 15	11	91.7	25	7	US-09-953-570-131778
C 16	11	91.7	25	7	US-09-954-445A-71403
C 17	11	91.7	25	7	US-09-954-445A-21805
C 18	11	91.7	25	7	US-09-954-445A-31524
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C 20	11	91.7	25	7	US-09-954-445A-79210
C 20	11	91.7	25	9	US-10-098-263B-24096

21	11	91.7	25	9	US-10-098-263B-81647	Sequence 81647, A
22	11	91.7	25	9	US-10-098-263B-81648	Sequence 81648, A
23	11	91.7	25	9	US-10-098-263B-96226	Sequence 96226, A
24	11	91.7	25	9	US-10-098-263B-114611	Sequence 114611, A
25	11	91.7	25	9	US-10-355-577-96775	Sequence 96775, A
26	11	91.7	25	9	US-10-355-577-101273	Sequence 101273, A
27	11	91.7	25	9	US-10-355-577-101274	Sequence 101274, A
28	11	91.7	25	9	US-10-355-577-164671	Sequence 164671, A
29	11	91.7	25	9	US-10-355-577-178073	Sequence 178073, A
30	11	91.7	25	9	US-10-355-577-198249	Sequence 198249, A
31	11	91.7	25	9	US-10-355-577-318084	Sequence 318084, A
32	11	91.7	25	9	US-10-355-577-394493	Sequence 394493, A
33	11	91.7	25	9	US-10-355-577-394494	Sequence 394494, A
34	11	91.7	25	9	US-10-355-577-396545	Sequence 396545, A
35	11	91.7	25	9	US-10-355-577-498091	Sequence 498091, A
36	11	91.7	25	9	US-10-355-577-581372	Sequence 581372, A
37	11	91.7	25	9	US-10-355-577-587426	Sequence 587426, A
38	11	91.7	25	9	US-10-355-577-650483	Sequence 650483, A
39	11	91.7	25	9	US-10-355-577-650484	Sequence 650484, A
40	11	91.7	25	9	US-10-355-577-653296	Sequence 653296, A
41	11	91.7	25	9	US-10-355-577-658872	Sequence 658872, A
42	11	91.7	25	9	US-10-355-577-667847	Sequence 667847, A
43	11	91.7	25	9	US-10-355-577-667848	Sequence 667848, A
44	11	91.7	25	9	US-10-355-577-730882	Sequence 730882, A
45	11	91.7	25	9	US-10-355-577-734855	Sequence 734855, A

#### ALIGNMENTS

```

RESULT 1
US-09-954-445A-45573/c
; Sequence 45573, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 45573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-45573

Query Match
Best Local Similarity 100.0%; Score 12; DB 7; Length 25;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
Db       15 CGTTCCTCTTCC 4

RESULT 2
US-10-355-577-396546/c
; Sequence 396546, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 396546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

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US-10-355-577-396546

Query Match 100.0%; Score 12; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12  
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Db 24 CGTTCCTCTCC 13

RESULT 3  
US-60-427-836-683575

Sequence 683575, Application US/60427836  
GENERAL INFORMATION:  
APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
FILE REFERENCE: 3527  
CURRENT APPLICATION NUMBER: US/60/427,836  
CURRENT FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 699466  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 683575  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Rattus norvegicus

Query Match 100.0%; Score 12; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12  
|||  
Db 12 CGTTCCTCTCC 23

RESULT 4  
US-10-303-778-7608

Sequence 7608, Application US/10303778  
GENERAL INFORMATION:  
APPLICANT: RosettaGenomics  
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL  
FILE REFERENCE: 47416  
CURRENT APPLICATION NUMBER: US/10/303,778  
CURRENT FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 17608  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7608  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Avian infectious bronchitis virus

Query Match 91.7%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCTCTCC 12  
|||  
Db 7 GTTCCTCTCC 17

RESULT 5  
US-10-303-778-7627

Sequence 7627, Application US/10303778  
GENERAL INFORMATION:  
APPLICANT: RosettaGenomics  
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL  
FILE REFERENCE: 47416  
CURRENT APPLICATION NUMBER: US/10/303,778

CURRENT FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 17608  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7627  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens

Query Match 91.7%; Score 11; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCTCTCC 12  
|||  
Db 7 GTTCCTCTCC 17

RESULT 6  
US-10-310-188-6596/c

Sequence 6596, Application US/10310188  
GENERAL INFORMATION:  
APPLICANT: RosettaGenomics  
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN  
FILE REFERENCE: 47487  
CURRENT APPLICATION NUMBER: US/10/310,188  
CURRENT FILING DATE: 2002-12-19  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6596  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens

Query Match 91.7%; Score 11; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCTCTCC 12  
|||  
Db 12 GTTCCTCTCC 2

RESULT 7  
US-10-315-474-66/c

Sequence 66, Application US/10315474  
GENERAL INFORMATION:  
APPLICANT: Brett P. Mont  
TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION  
FILE REFERENCE: RTS-0338  
CURRENT APPLICATION NUMBER: US/10/315,474  
CURRENT FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 156  
SEQ ID NO 66  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
OTHER INFORMATION: Antisense Oligonucleotide

Query Match 91.7%; Score 11; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCTCTCC 12  
|||  
Db 12 GTTCCTCTCC 2



```
RESULT 8
US-10-315-474-137
; Sequence 137, Application US/10315474
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
; FILE REFERENCE: RTS-0338
; CURRENT APPLICATION NUMBER: US/10/315,474
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 137
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-315-474-137

Query Match          91.7%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  CGTCTCTCTTC 12
Db      9  GTTCTCTCTTC 19

RESULT 9
US-09-660-222-124398
; Sequence 124398, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124398

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGTCTCTCTTC 11
Db     12  CGTCTCTCTTC 22

RESULT 10
US-09-660-222-124402
; Sequence 124402, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124402
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124402

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGTCTCTCTTC 11
Db      6  CGTCTCTCTTC 16

RESULT 11
US-09-660-222-124403
; Sequence 124403, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124403

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGTCTCTCTTC 11
Db      4  CGTCTCTCTTC 14

RESULT 12
US-09-660-222-124417
; Sequence 124417, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124417
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124417

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Fri Jun 27 07:42:34 2003

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Page 4

OY 1 GTTCCCTTTC 11  
|||  
Db 3 CGTCCCTTTC 13

RESULT 13  
US-09-953-570-22842/c  
; Sequence 22842, Application US/09953570  
; GENERAL INFORMATION:  
; APPLICANT: Miltmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast  
; FILE REFERENCE: 3110.1  
; CURRENT APPLICATION NUMBER: US/09/953,570  
; PRIOR FILING DATE: 2001-09-13  
; PRIOR APPLICATION NUMBER: 60/232,638  
; NUMBER OF SEQ ID NOS: 138410  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22842  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces Cerevisiae  
US-09-953-570-22842

Query Match 91.7%; Score 11; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTCCCTTTC 12  
|||  
Db 19 GTTCCCTTTC 9

RESULT 14  
US-09-953-570-131778/c  
; Sequence 131778, Application US/09953570  
; GENERAL INFORMATION:  
; APPLICANT: Miltmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast  
; FILE REFERENCE: 3110.1  
; CURRENT APPLICATION NUMBER: US/09/953,570  
; CURRENT FILING DATE: 2001-09-13  
; PRIOR APPLICATION NUMBER: 60/232,638  
; PRIOR FILING DATE: 2000-09-14  
; NUMBER OF SEQ ID NOS: 138410  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 131778  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces Cerevisiae  
US-09-953-570-131778

Query Match 91.7%; Score 11; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTCCCTTTC 12  
|||  
Db 17 GTTCCCTTTC 7

RESULT 15  
US-09-954-445A-7403/c  
; Sequence 7403, Application US/09954445A  
; GENERAL INFORMATION:  
; APPLICANT: Miltmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana  
; FILE REFERENCE: 3116.1  
; CURRENT APPLICATION NUMBER: US/09/954,445A  
; CURRENT FILING DATE: 2000-09-17  
; PRIOR APPLICATION NUMBER: 60/233,620  
; PRIOR FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 131820

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 7403  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-954-445A-7403

Query Match 91.7%; Score 11; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTCCCTTTC 12  
|||  
Db 12 GTTCCCTTTC 2

Search completed: June 23, 2003, 19:12:10  
Job time : 526.757 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 618.693 Seconds  
(without alignments)  
314.123 Million cell updates/sec

Title: US-08-770-564A-4  
Perfect score: 12  
Sequence: 1 CGTTCCTCTTCC 12

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estnu:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pla:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	10	83.3	26	17	AZ942099 2M0202C09
4	10	83.3	27	17	AZ630179 1M0483B10
5	10	83.3	28	14	N92455 2B63h01.81
6	10	83.3	33	17	BH850686 SALK_0716

C 7	10	83.3	37	17	A2392980	AZ392980 1M0155P13
C 8	10	83.3	38	17	A2974736	AZ974736 2M0249A03
C 9	10	83.3	43	17	A2419099	AZ419099 1M0195N23
C 10	10	83.3	43	17	A2830358	AZ830358 2M0109M04
C 11	10	83.3	46	9	AA052407	AA052407 mb70h06.r
C 12	10	83.3	49	9	AA902962	AA902962 ok44b09.f
C 13	10	83.3	50	9	AU102702	AU102702 AU102702
C 14	9	75.0	19	17	A2636812	AZ636812 1M0495B21
C 15	9	75.0	26	17	A2799780	AZ799780 2M0057K20
C 16	9	75.0	28	12	BG673330	BG673330 DRNBSF09
C 17	9	75.0	30	17	A2427759	AZ427759 1M0209P20
C 18	9	75.0	30	17	A2604126	AZ604126 1M0243O13
C 19	9	75.0	31	17	A2465005	AZ465005 1M0274J09
C 20	9	75.0	32	17	A2587757	AZ587757 1M0395P07
C 21	9	75.0	32	17	A2792853	AZ792853 2M0045C07
C 22	9	75.0	32	17	BH847691	BH847691 SALK_0558
C 23	9	75.0	34	9	A1537243	A1537243 EP01E01.X
C 24	9	75.0	35	17	A2581591	AZ581591 1M0370O23
C 25	9	75.0	36	17	A2828679	AZ828679 2M0105K18
C 26	9	75.0	37	9	AA625816	AA625816 zv87a04.f
C 27	9	75.0	37	13	B1063841	B1063841 B1063841
C 28	9	75.0	37	17	A2474017	AZ474017 1M0290A18
C 29	9	75.0	37	17	A2625706	AZ625706 1M0465O23
C 30	9	75.0	37	17	A2761912	AZ761912 1M0556D02
C 31	9	75.0	38	17	A2339873	AZ339873 1M0071I04
C 32	9	75.0	38	17	A2949952	AZ949952 2M0213J13
C 33	9	75.0	40	14	H51330	H51330 Y030b01.r1
C 34	9	75.0	40	17	A2597058	AZ597058 1M0410M08
C 35	9	75.0	40	17	A2627381	AZ627381 1M0469H09
C 36	9	75.0	41	17	A2484545	AZ484545 1M0311M04
C 37	9	75.0	42	14	T17558	T17558 mps v145 Th
C 38	9	75.0	42	17	BH640418	BH640418 1008035G0
C 39	9	75.0	43	9	AA981631	AA981631 ua24b12.r
C 40	9	75.0	43	14	H41505	H41505 yp68h12.81
C 41	9	75.0	43	17	BH849028	BH849028 SALK_0691
C 42	9	75.0	44	14	W23377	W23377 SWMCA702SK
C 43	9	75.0	44	17	A2761199	AZ761199 1M0555G21
C 44	9	75.0	45	17	A2423992	AZ423992 1M0203A16
C 45	9	75.0	45	17	A2657409	AZ657409 1M0533M04

#### ALIGNMENTS

RESULT 1  
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DEFINITION 603021011F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5191659 5',  
mRNA sequence.  
ACCESSION BI488502  
VERSION BI488502.1 GI:115327730  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 46)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.jnl.gov>  
Plate: LHAM11479 row: e column: 04  
High quality sequence stop: 46.  
Location/Qualifiers

FEATURES  
source

1. 46

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5191659"
/clone_1lb="NH_MGC_114"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-Sport6; Site: 1; Not;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yr. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NH_MGC library."
This is a NH_MGC library."

BASE COUNT      9 a      8 c      25 g      4 t
ORIGIN

Query Match      91.7%; Score 11; DB 13; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2 GTTCCCTCTCC 12
        |||||
        12 GTTCCCTCTCC 2

Db

RESULT 2
AL767395      46 bp      DNA      linear      GSS 18-JUN-2002
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-219A03-014202,
genomic survey sequence.
ACCESSION
AL767395
VERSION
AL767395.1 GI:21520514
KEYWORDS
GSS.
SOURCE
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosid 11; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.
and Weishaar, B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 46)
JOURNAL
REFERENCE
AUTHORS
Li, Y., Rosso, M., Strizhov, N. and Weishaar, B.
TITLE
Direct Submission
JOURNAL
COMMENT
Submitted (17-JUN-2002) Weishaar, B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone FSK7. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source
1..46
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-219A03-014202"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA

```

```

insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

BASE COUNT      7 a      19 c      2 g      18 t
ORIGIN

Query Match      91.7%; Score 11; DB 17; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2 GTTCCCTCTCC 12
        |||||
        29 GTTCCCTCTCC 39

Db

RESULT 3
A2942099/c
LOCUS
DEFINITION
A2942099      26 bp      DNA      linear      GSS 26-APR-2001
2M0202C09F Mouse 10kb plasmid UNGC2M library Mus musculus genomic
clone UNGC2M0202C09 F, DNA sequence.
ACCESSION
A2942099
VERSION
A2942099.1 GI:13805115
KEYWORDS
GSS.
SOURCE
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Dvali, B., Hamill, C.,
Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0202 row: C column: 09
Seq primer: GTTGTAAACGACGCGCACT
Clase: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNG2M0202C09"
/clone_1lb="Mouse 10kb plasmid UNGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistent, F-"
/notes="Vector: pMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory House DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrotynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adapter oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g11473211419b|AF129072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 0 c 16 g 0 t

Query Match 83.3%; Score 10; DB 17; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.7e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCTCTCC 12  
12 TTCCTCTCC 3

RESULT 4  
A2630179 27 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0483B10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
DEFINITION clone UUGCIM0483B10 R, DNA sequence.

ACCESSION A2630179.1 GI:11752369  
VERSION GSS.  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center

FEATURES  
source  
1. 27  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0483B10"  
/clone\_1lb="Mouse 10kb plasmid UUGCIM library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI14732114|GB|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 9 g 0 t

Query Match 83.3%; Score 10; DB 17; Length 27;  
Best Local Similarity 100.0%; Pred. No. 7.7e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCTCTCC 12  
4 TTCCTCTCC 13

RESULT 5  
N92455 28 bp mRNA linear EST 20-AUG-1996  
LOCUS zb63h01.s1 Soares fetal lung NBHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:308305.3' similar to gb:X06323\_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);, mRNA sequence.

ACCESSION N92455  
VERSION N92455.1 GI:1264764  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 28)

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiappelli,B., Chisoe,S., Dietrich,N., Dubugue,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucada,T., Lacy,M., Le,M., Le,N., Matlis,B., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasis,B., Underwood,K., Woldmann,P., Waterston,R., Wilson,R. and Merris,M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)

JOURNAL MEDLINE  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

FEATURES  
source  
1. 28  
/organism="Homo sapiens"  
/db\_xref="GDB:1251718"  
/db\_xref="taxon:9606"  
/clone="IMAGE:308305"  
/clone\_1lb="Soares fetal\_lung\_NBHL19W"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5'-GTGACCATCTGAGTGAGCGCCGACATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares

BASE COUNT fetal heart NbhH19W."  
ORIGIN 7 a 9 c 4 g 8 t

Query Match 83.3%; Score 10; DB 14; Length 28;  
Best Local Similarity 100.0%; Pred. No. 7.8e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTCTCTTTC 11  
| | | | |  
| | | | |  
Db 3 TTCTCTTTC 12

RESULT 6  
BH850686 33 bp DNA linear GSS 13-JUN-2002  
LOCUS  
DEFINITION Arabidopsis thaliana genomic clone SALK\_071692.32.90.x, DNA

ACCESSION  
VERSION BH850686.1 GI:21421557  
KEYWORDS  
SOURCE

ORGANISM  
thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 33)

REFERENCE  
AUTHORS Alonso,J.M., Leisae,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,  
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
CONTACT: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers

FEATURES  
source 1..33  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_071692.32.90.x"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocol used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 5 a 16 c 1 g 11 t  
ORIGIN

Query Match 83.3%; Score 10; DB 17; Length 33;  
Best Local Similarity 100.0%; Pred. No. 8.1e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCTCTTTC 12  
| | | | |  
| | | | |  
Db 19 TTCTCTTTC 28

RESULT 7  
AZ392980 37 bp DNA linear GSS 03-OCT-2000  
LOCUS  
DEFINITION IM0155P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION  
VERSION AZ392980  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus  
house mouse.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 37)

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Kelly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0155 row: P column: 13  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 37.  
Location/Qualifiers

FEATURES  
source 1..37  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0155P13"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g14732114[9b]AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 15 a 0 c 22 g 0 t  
ORIGIN

Query Match 83.3%; Score 10; DB 17; Length 37;  
Best Local Similarity 100.0%; Pred. No. 8.4e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCTCTTTC 12  
| | | | |  
| | | | |  
Db 16 TTCTCTTTC 7

RESULT 8  
AZ974736 38 bp DNA linear GSS 27-APR-2001  
LOCUS  
DEFINITION 2M0249A03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

```

ACCESSION   clone UUGC2M0249A03 R, DNA sequence.
VERSION     A2974736
KEYWORDS    A2974736.1 GI:13845963
SOURCE      house mouse.
ORGANISM    Mus musculus
            Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 38)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah
            Genome Center
            308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0249 row: A column: 03
            Seq primer: CACACAGCAACAGCTTAGACC
            Class: plasmid ends
            High quality sequence stop: 38.
            Location/Qualifiers
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                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0249A03"
                /clone_1lb="Mouse 10kb plasmid UUGC2M library"
                /sex="Female"
                /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                /note="Vector: PWD42n; Purified genomic DNA from M.
                musculus C57BL/6J (female) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 [g14732114[gblAF129072.1], a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
BASE COUNT   14 a      8 c      9 g      7 t
ORIGIN
Query Match      83.3%; Score 10; DB 17; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy      3 TTCCTCTTCC 12
        |||||
        |||||
        |||||
Db      19 TTCCTCTTCC 10

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```

ACCESSION      clone UGCG1M0195N23 F, DNA sequence.
VERSION        AZ419099
KEYWORDS       AZ419099.1 GI:10543112
SOURCE         GSS.
ORGANISM       house mouse.
                Mus musculus.
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
                ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
                84112, USA
                Tel.: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0195 Row: N Column: 23
                Seq primer: CGTTGTAAACGACGGCCAGT
                Class: plasmid ends
                High quality sequence stop: 43.
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SOURCE         Location/Qualifiers
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                /strain="C57BL/6J"
                /db_xref="taxon:10090"
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                /sex="Male"
                /lab_host="B. Coli strain XL10-Gold, TI-resistant, F-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 (g1[4732114]gb[AR129072.1], a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
BASE COUNT
ORIGIN         21 a
                0 c
                22 g
                0 t
Query Match      83.3%; Score 10; DB 17; Length 43;
Best Local Similarity 100.0%; Prid. No. 8.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 3 TTCTCTTCC 12
   |||||
   |||||
   |||||
Db 33 TTCTCTTCC 24

```

Fr1 Jun 27 07:42:34 2003

us-08-770-564a-4.oligo.rst

Page 6

```

ACCESSION      clone UGCG2M0109M04 R, DNA sequence.
VERSION        A2830358
GSS            A2830358.1 GI:11000266
KEYWORDS
SOURCE
ORGANISM       Mus musculus
Eukaryotes; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS       Dunn, D., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weiss, R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL
COMMENT       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax.: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Place: 0109 row: M column: 04
Seq primer: CACACAGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0109M04"
/clone_lib="Mouse 10kb plasmid UUGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/vector="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT
ORIGIN        7 a 10 c 8 g 18 t
Query Match 83.3%; Score 10; DB 17; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3 TTCCCTCTCC 12
|||||||
|||||||
Db 23 TTCCCTCTCC 32
RESULT 11
AA052407/c AA052407 46 bp mRNA linear EST 13-SEP-1996
DEFINITION mb70h06.r1 Soares mouse p3MMF15.5 Mus musculus cDNA clone

```

```

ACCESSION      IMAGE_334811_5', similar to SW:IN35_HUMAN P80217 INTERFERON-INDUCED
VERSION        AA052407
KEYWORDS       AA052407.1 GI:1543362
SOURCE         EST
ORGANISM       house mouse
               Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 46)
               Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
               Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
               Schellander, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
               Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
               Waterston, R.
TITLE          The Mashu-HHMI Mouse EST Project
JOURNAL        Unpublished (1996)
COMMENT        Contact: Maria M/Mouse EST Project
               Mashu-HHMI Mouse EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: mueseel@watson.wustl.edu
               This clone is available royalty-free through LNL ; contact the
               IMAGE Consortium (lnl@image.lnl.gov) for further information.
               MGI:216211
               Trace considered overall poor quality
               Putative full length read
               vector to vector length is
               Possible reversed clone: similarity on wrong strand
               Seg primer: -28M13 rev2 from Amer sham
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                   /dev_stage="19.5 dpc total fetus"
                   /lab_host="DH10s (ampicillin resistant)"
                   /note="Vector: pTV73D (Pharmacia) with a modified
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                   double-stranded cDNA was size selected, ligated to Eco RI
                   adaptors (Pharmacia), digested with Not I and cloned into
                   the Not I and Eco RI sites of a modified pTV73 vector
                   (Pharmacia). Library went through one round of
                   normalization to a Cot = 5. Library constructed by Benito
                   Soares and M. Palma Bonaldi. RNA was kindly provided by
                   Dr. Minoru Ko (Wayne State University)."
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```

SOURCE
ORGANISM      human.
REFERENCE      Homo sapiens
AUTHORS        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL        NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
               Contact: Robert Strausberg, Ph.D.
               Email: cgaps-remail.nih.gov
               unknown library type
               Trace considered overall poor quality
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               High quality sequence stop: 1.
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               /lab_host="DH10B"
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               [5'-AACTGAGAGATCGCGCGCATGCTTTTCTTTTCTTTT-3'],
               double-stranded cDNA was ligated to Eco RI adaptors
               (Pharmacia), digested with Not I and cloned into the Not I
               and Eco RI sites of the modified pTT3D vector. Library
               went through one round of normalization. Library
               constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TTCTCTTC 12
Db 17 TTCTCTTC 8

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ACCESSION   CAS08541, mRNA sequence.
VERSION     AU102702
KEYWORDS    AU102702.1 GI:13552223
SOURCE      EST.
ORGANISM    human.
REFERENCE    Homo sapiens
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE        Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL      1 (bases 1 to 50)
COMMENT      Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
               'H., Ota, T., Isega, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
               'Y., Nakamura, Y., Suyama, A. and Sugano, S.
               Diverse transcriptional initiation revealed by fine, large-scale
               mapping of mRNA start sites
               EMBO Rep. 2 (5), 388-393 (2001)
               21270072
               Contact: Yutaka Suzuki
               Department of Virology
               Institute of Medical Science, University of Tokyo
               4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
               Email: yusuzuki@ims.u-tokyo.ac.jp
               Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
               'S. Construction and characterization of a full length-enriched and
               a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
               Location/Qualifiers

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Db 12 GTTCTCTTC 3

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ACCESSION   1M0455B21R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
VERSION     clone UGCGIM0455B21 R, DNA sequence.
KEYWORDS    AZ636812
SOURCE      GSS.
ORGANISM    house mouse.
REFERENCE    Mus musculus
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL      1 (bases 1 to 19)
COMMENT      Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
               Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellily
               'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
               and Wright, D., Weis, R.
               Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
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               /note="Vector: PMD29v. Purified genomic DNA from M.
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               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 18.2151 Seconds  
(without alignments)  
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Title: US-08-770-564A-4  
Perfect score: 12  
Sequence: 1 CGTTCCTCTCC 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents NA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	12	100.0	30	2	US-08-770-565-2
5	11	91.7	20	1	US-08-031-143B-6
6	11	91.7	20	1	US-08-031-143B-33
7	11	91.7	20	2	US-08-833-377-14
8	11	91.7	20	5	PCT-US94-02891-6
9	11	91.7	20	5	PCT-US94-02891-33
10	10.4	86.7	15	1	US-08-363-240A-690
11	10.4	86.7	18	1	US-08-363-240A-1209
12	10.4	86.7	20	3	US-08-418-641-39
13	10.4	86.7	24	1	US-08-211-202-16
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16	10.4	86.7	24	2	US-08-350-260A-53
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21	10.4	86.7	42	1	US-08-487-037-8
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24	10.4	86.7	45	1	US-08-307-619-22
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28	10.4	86.7	45	4	US-08-669-656A-26	Sequence 26, Appl
29	10.4	86.7	47	4	US-09-641-638-892	Sequence 892, App
30	10	83.3	14	1	US-08-294-424-33	Sequence 33, Appl
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32	10	83.3	17	3	US-08-988-706-54	Sequence 54, Appl
33	10	83.3	17	4	US-08-584-040-2519	Sequence 2519, Ap
34	10	83.3	17	4	US-08-584-040-2520	Sequence 2520, Ap
35	10	83.3	17	4	US-08-584-040-2521	Sequence 2521, Ap
36	10	83.3	17	4	US-08-584-040-2522	Sequence 2522, Ap
37	10	83.3	18	4	US-09-306-595C-30	Sequence 30, Appl
38	10	83.3	20	2	US-08-534-479-1	Sequence 1, Appl
39	10	83.3	20	4	US-09-490-692-85	Sequence 85, Appl
40	10	83.3	20	4	US-09-258-377-30	Sequence 30, Appl
41	10	83.3	20	4	US-09-203-895-5	Sequence 5, Appl
42	10	83.3	21	4	US-08-949-344C-18	Sequence 18, Appl
43	10	83.3	22	1	US-07-820-412-8	Sequence 8, Appl
44	10	83.3	22	1	US-08-488-144-4	Sequence 4, Appl
45	10	83.3	22	1	US-08-611-155B-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-770-565-4  
; Sequence 4, Application US/08770565  
; Patent No. 5846723  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Puzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; TITLE OF INVENTION: Telomerase  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002300US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-770-565-4  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTCCTCTCC 12

Fri Jun 27 07:42:35 2003

us-08-770-564a-4.rn1

Page 2

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RESULT 2  
US-08-770-565-3  
Sequence 3, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
TITLE OF INVENTION: Telomerase  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-3

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RESULT 3  
US-08-833-377-7  
Sequence 7, Application US/08833377  
Patent No. 5968506  
GENERAL INFORMATION:  
APPLICANT: Weinrich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichtsteiner, Serge P.  
APPLICANT: Vassero, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,377  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
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LOCATION: 1..20  
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US-08-833-377-7

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RESULT 4  
US-08-770-565-2  
Sequence 2, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
TITLE OF INVENTION: Telomerase  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565

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DB 18 GTTCCCTCTCC 8  
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US-08-031-143B-33  
Sequence 33, Application US/08031143B  
Patent No. 5518880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
ATTORNEY/AGENT INFORMATION:  
NAME: MCBRIDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CURRENT APPLICATION DATA:  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
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HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: HUMAN

US-08-031-143B-6/c  
Sequence 6, Application US/08031143B  
Patent No. 5518880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
ATTORNEY/AGENT INFORMATION:  
NAME: MCBRIDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CURRENT APPLICATION DATA:  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: HUMAN

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DB 1 CGTTCCTCTCC 12  
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Sequence 6, Application US/08031143B  
Patent No. 5518880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
ATTORNEY/AGENT INFORMATION:  
NAME: MCBRIDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CURRENT APPLICATION DATA:  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: HUMAN

INDIVIDUAL ISOLATE: IL-2R  
US-08-031-143B-6  
Query Match  
Best Local Similarity 100.0%; Score 11; DB 1; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GTTCCCTCTCC 12  
DB 18 GTTCCCTCTCC 8  
RESULT 6  
US-08-031-143B-33  
Sequence 33, Application US/08031143B  
Patent No. 5518880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
ATTORNEY/AGENT INFORMATION:  
NAME: MCBRIDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CURRENT APPLICATION DATA:  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R

US-08-031-143B-33  
Sequence 33, Application US/08031143B  
Patent No. 5518880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
ATTORNEY/AGENT INFORMATION:  
NAME: MCBRIDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CURRENT APPLICATION DATA:  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R

Query Match  
Best Local Similarity 100.0%; Score 11; DB 1; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GTTCCCTCTCC 12  
DB 3 GTTCCCTCTCC 13  
RESULT 7  
US-08-833-377-14  
Sequence 14, Application US/08833377

```

Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinlich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtsteiner, Serge P.
APPLICANT: Vassero, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Scorella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base= OTHER
FEATURE:
NAME/KEY:
LOCATION: 1..20
OTHER INFORMATION: /note= "N = 5'-biotinylated cytidine"
US-08-833-377-14

Query Match          91.7%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTCCTCTCC 12
Db      2 GTTCCTCTCC 12

RESULT 8
PCT-US94-02891-6/c
Sequence 6, Application PC/TUS9402891
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

```

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TITLE OF INVENTION: XSCID
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & PINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/031,143
APPLICATION NUMBER: 12-MAR-1993
FILING DATE: 08/121,435
APPLICATION NUMBER: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TEXT: 421792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: YES
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-6

Query Match          91.7%; Score 11; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GTTCCTCTCC 12
Db      18 GTTCCTCTCC 8

RESULT 9
PCT-US94-02891-33
Sequence 33, Application PC/TUS9402891
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & PINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

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ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02891  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/031,143  
FILING DATE: 12-MAR-1993  
APPLICATION NUMBER: 08/121,435  
FILING DATE: 14-SEPT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FELTER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R  
PCT-US94-02891-33

Query Match 91.7%; Score 11; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCC 12  
DB 3 GTTCTCTTCC 13

RESULT 10  
US-08-363-240A-690  
Sequence 690, Application US/08363240A  
Patent No. 5705388  
GENERAL INFORMATION:  
APPLICANT: Couture, Larry  
APPLICANT: McSwiggen, James  
APPLICANT: Bisgaler, Charles  
APPLICANT: Pape, Michael  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
PREVENTION, INHIBITION OF  
PROGRESSION AND REGRESSION  
TITLE OF INVENTION: OF VASCULAR DISEASES  
NUMBER OF SEQUENCES: 1243  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,240A  
FILING DATE: December 23, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/096  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 690:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-363-240A-690

Query Match 86.7%; Score 10.4; DB 1; Length 15;  
Best Local Similarity 58.3%; Pred. No. 1.9e+03;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTCTCTTCC 12  
DB 4 CGTCTCTTCC 15

RESULT 11  
US-08-363-240A-1209  
Sequence 1209, Application US/08363240A  
Patent No. 5705388  
GENERAL INFORMATION:  
APPLICANT: Couture, Larry  
APPLICANT: McSwiggen, James  
APPLICANT: Bisgaler, Charles  
APPLICANT: Pape, Michael  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
PREVENTION, INHIBITION OF  
PROGRESSION AND REGRESSION  
TITLE OF INVENTION: OF VASCULAR DISEASES  
NUMBER OF SEQUENCES: 1243  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,240A  
FILING DATE: December 23, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/096  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1209:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-240A-1209

Query Match 86.7%; Score 10.4; DB 1; Length 18;  
Best Local Similarity 58.3%; Pred. No. 1.9e+03;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCC 12  
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DB 2 CGUCCGCUCC 13

RESULT 12  
US-08-418-641-39  
Sequence 39, Application US/09418641A  
Patent No. 6124133  
GENERAL INFORMATION:  
APPLICANT: Jennifer K. Taylor  
APPLICANT: Lex M. Cowbert  
TITLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION  
FILE REFERENCE: RTS-0105  
CURRENT APPLICATION NUMBER: US/09/418,641A  
CURRENT FILING DATE: 1999-10-15  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 39  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-418-641-39

Query Match 86.7%; Score 10.4; DB 3; Length 20;  
Best Local Similarity 91.7%; Pred. No. 1.9e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCC 12  
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DB 4 CGTTCCTCTCC 15

RESULT 13  
US-08-211-202-16/c  
Sequence 16, Application US/08211202  
Patent No. 5565332  
GENERAL INFORMATION:  
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus  
APPLICANT: BAIER, Michael  
APPLICANT: JESPEERS, Laurent Stephane Anne Therese  
APPLICANT: WINTER, Gregory Paul  
TITLE OF INVENTION: Production of chimeric antibodies - a  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &  
ADDRESSER: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,202  
FILING DATE: 23-SEP-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9120252.3  
FILING DATE: 23-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9120377.8  
FILING DATE: 25-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/31960  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-211-202-16

Query Match 86.7%; Score 10.4; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCC 12  
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DB 13 CGTTCCTCTCC 2

RESULT 14  
US-08-211-202-36/c  
Sequence 36, Application US/08211202  
Patent No. 5565332  
GENERAL INFORMATION:  
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus  
APPLICANT: BAIER, Michael  
APPLICANT: JESPEERS, Laurent Stephane Anne Therese  
APPLICANT: WINTER, Gregory Paul  
TITLE OF INVENTION: Production of chimeric antibodies - a  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &  
ADDRESSER: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,202  
FILING DATE: 23-SEP-1992



CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9120252.3  
FILING DATE: 23-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9120377.8  
FILING DATE: 25-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/31960  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-211-202-36

Query Match 86.7%; Score 10.4; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTTCC 12  
Db 13 CGTGCCTCTTCC 2

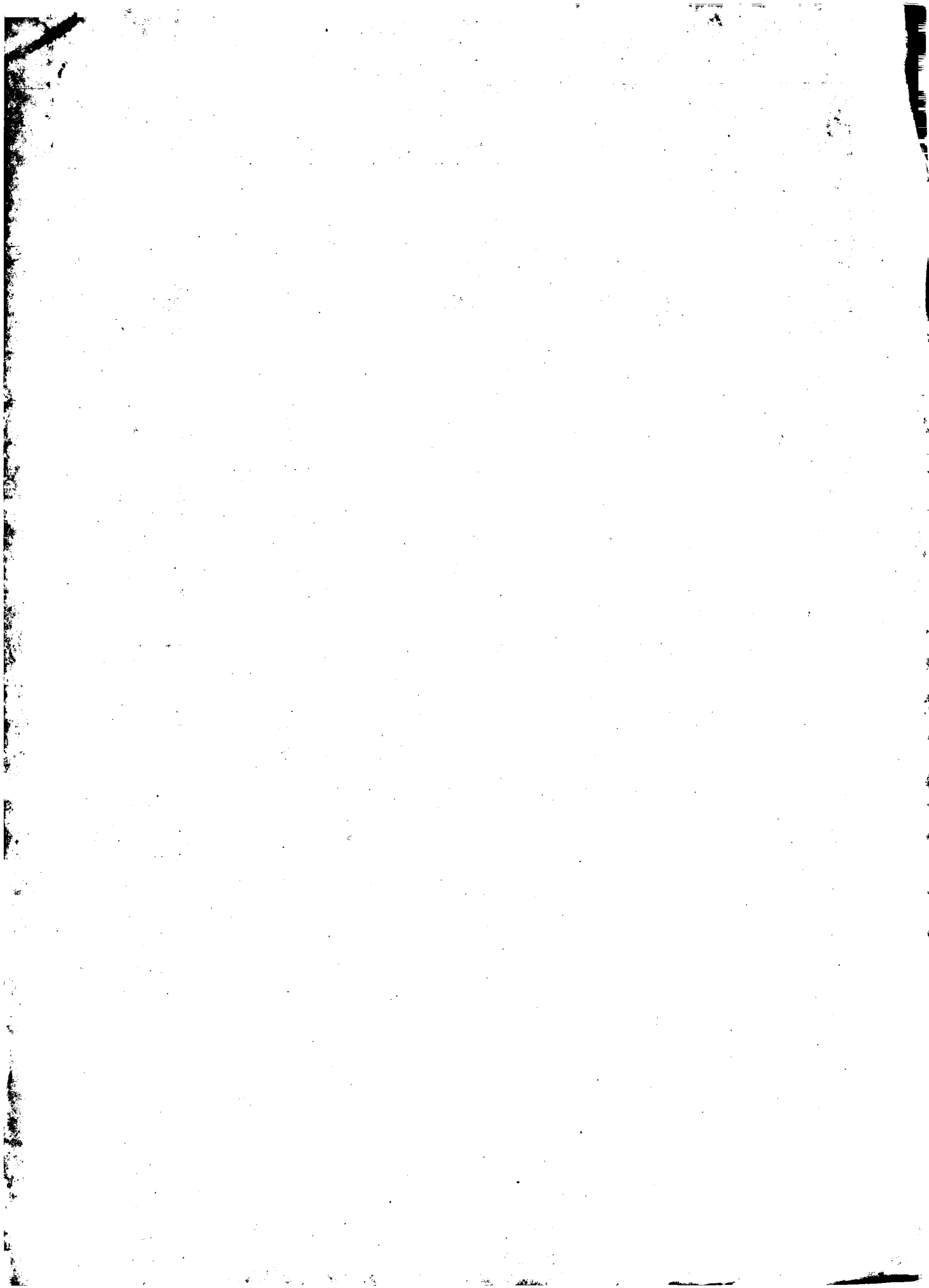
RESULT 15  
US-08-307-619-7/c  
Sequence 7, Application us/08307619  
Patent No. 5733743  
GENERAL INFORMATION:  
APPLICANT: Johnson, Kevin S  
APPLICANT: Winter, Gregory P  
APPLICANT: Griffiths, Andrew D  
APPLICANT: Smith, Andrew JH  
APPLICANT: Waterhouse, P  
TITLE OF INVENTION: Methods for producing members of specific  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: us/08/307,619  
FILING DATE: 16-SEP-1994  
CLASSIFICATION: 435  
CLASSIFICATION: G01N 33/531, G01N 33/68  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/32238  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-307-619-7

Query Match 86.7%; Score 10.4; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTTCC 12  
Db 13 CGTGCCTCTTCC 2

Search completed: June 25, 2003, 00:24:35  
Job time: 18.2151 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1018.23 Seconds  
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Title: US-08-770-564A-4  
Perfect score: 12  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Result No.	Score	Query		DB ID	Description
		Match	Length		
1	12	100.0	12	1 PCT-US97-23619-4	Sequence 4, Appl1
2	12	100.0	12	US-08-770-564A-4	Sequence 4, Appl1
3	12	100.0	20	1 PCT-US97-23619-3	Sequence 3, Appl1
4	12	100.0	20	US-08-770-564A-3	Sequence 3, Appl1
5	12	100.0	25	36 US-09-954-437-81691	Sequence 81691, A
6	12	100.0	25	36 US-09-956-584-18655	Sequence 18655, A
7	12	100.0	25	67 US-60-233-166-81691	Sequence 81691, A
8	12	100.0	25	67 US-60-233-620-45573	Sequence 45573, A
9	12	100.0	25	67 US-60-234-017-52883	Sequence 52883, A
10	12	100.0	35	79 US-60-353-987-396546	Sequence 396546, A
11	12	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appl1
12	12	100.0	30	US-08-770-564A-2	Sequence 2, Appl1
13	12	100.0	31	9 US-08-521-634-17	Sequence 17, Appl1
14	12	100.0	32	1 PCT-US02-25943-62884	Sequence 62884, A
15	12	100.0	32	42 US-10-227-565-62884	Sequence 62884, A
16	11	91.7	16	1 PCT-US02-25943-46617	Sequence 46617, A
17	11	91.7	16	42 US-10-227-565-46617	Sequence 46617, A
18	11	91.7	18	1 PCT-US02-25943-25195	Sequence 25195, A
19	11	91.7	18	1 PCT-US02-25943-62885	Sequence 62885, A
20	11	91.7	18	42 US-10-227-565-25195	Sequence 25195, A
21	11	91.7	18	42 US-10-227-565-62885	Sequence 62885, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

22 11 91.7 25 17 US-09-396-186F-95194 Sequence 95194, A  
23 11 91.7 25 17 US-09-396-186F-95195 Sequence 95195, A  
24 11 91.7 25 17 US-09-396-186F-95206 Sequence 95206, A  
25 11 91.7 25 17 US-09-396-186F-119937 Sequence 119937, A  
26 11 91.7 25 17 US-09-396-186G-95194 Sequence 95194, A  
27 11 91.7 25 17 US-09-396-186G-95195 Sequence 95195, A  
28 11 91.7 25 17 US-09-396-186G-95206 Sequence 95206, A  
29 11 91.7 25 17 US-09-396-186G-119937 Sequence 119937, A  
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31 11 91.7 25 26 US-09-660-220-124403 Sequence 124403, A  
32 11 91.7 25 26 US-09-660-220-124404 Sequence 124404, A  
33 11 91.7 25 26 US-09-660-220-124417 Sequence 124417, A  
34 11 91.7 25 36 US-09-954-427-15992 Sequence 15992, A  
35 11 91.7 25 36 US-09-954-427-56129 Sequence 56129, A  
36 11 91.7 25 36 US-09-954-427-56139 Sequence 56139, A  
37 11 91.7 25 36 US-09-954-427-56140 Sequence 56140, A  
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39 11 91.7 25 36 US-09-954-427-149920 Sequence 149920, A  
40 11 91.7 25 36 US-09-954-427-291192 Sequence 291192, A  
41 11 91.7 25 36 US-09-954-427-291202 Sequence 291202, A  
42 11 91.7 25 36 US-09-954-427-291352 Sequence 291352, A  
43 11 91.7 25 36 US-09-954-427-377727 Sequence 377727, A  
44 11 91.7 25 36 US-09-956-584-14807 Sequence 14807, A  
45 11 91.7 25 36 US-09-956-584-100805 Sequence 100805, A

## ALIGNMENTS

RESULT 1  
PCT-US97-23619-4  
Sequence 4, Application PC/TUS9723619  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Kealey, James T.  
APPLICANT: Kealey, James T.  
APPLICANT: Kealey, James T.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
NUMBER OF SEQUENCES: 25  
TITLE OF INVENTION: RNA Component of Telomerase  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: 1.12  
LOCATION: 1.12  
OTHER INFORMATION: /note="oligo 14d"  
PCT-US97-23619-4  
Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
US-08-770-564a-4  
Sequence 4, Application US/08770564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Kealey, James T.  
APPLICANT: Kealey, James T.  
APPLICANT: Kealey, James T.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
NUMBER OF SEQUENCES: 15  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564a-4  
Query Match 100.0%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence 3, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..20
OTHER INFORMATION: /note= "oligo 14ab"
PCT-US97-23619-3

Query Match          100.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCC 12
DB 1 CGTCTCTCTCC 12

RESULT 4
US-08-770-564A-3
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Prizan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
```

```
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-564A-3
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Query Match          100.0%; Score 12; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCC 12
DB 1 CGTCTCTCTCC 12
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RESULT 5
US-09-954-427-81691
Sequence 81691, Application US/09954427
GENERAL INFORMATION:
APPLICANT: Maltman
APPLICANT: Afymetric, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/09/954,427
CURRENT FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 81691
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank AA819663
US-09-954-427-81691
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Query Match          100.0%; Score 12; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCC 12
DB 5 CGTCTCTCTCC 16
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```
RESULT 6
US-09-956-584-18655/c
Sequence 18655, Application US/09956584
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; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIORITY FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18655
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-18655

Query Match          100.0%; Score 12; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTTCCTCTTCC 12
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Db 18 CGTTCCTCTTCC 7

RESULT 7
US-60-233-166-81691
; Sequence 81691, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AA819663
US-60-233-166-81691

Query Match          100.0%; Score 12; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTTCCTCTTCC 12
    |||||
Db 5 CGTTCCTCTTCC 16

RESULT 8
US-60-233-620-45573/c
; Sequence 45573, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
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; DATABASE ACCESSION NUMBER: Genbank AL034567
US-60-233-620-45573

Query Match          100.0%; Score 12; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTTCCTCTTCC 12
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Db 15 CGTTCCTCTTCC 4

RESULT 9
US-60-234-017-52883/c
; Sequence 52883, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltman, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank U41285
US-60-234-017-52883

Query Match          100.0%; Score 12; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTTCCTCTTCC 12
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Db 18 CGTTCCTCTTCC 7

RESULT 10
US-60-353-987-396546/c
; Sequence 396546, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 396546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-396546

Query Match          100.0%; Score 12; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTTCCTCTTCC 12
    |||||
Db 24 CGTTCCTCTTCC 13

RESULT 11
PCT-US97-23619-2
; Sequence 2, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
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APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
NUMBER OF SEQUENCES: 29  
TITLE OF INVENTION: RNA Component of Telomerase  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY:  
LOCATION: 1..30  
OTHER INFORMATION: /note= "oligo 14"  
PCT-US97-23619-2  
Query Match 100.0%; Score 12; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTCTCTCTCC 12  
DB 1 CGTCTCTCTCC 12  
RESULT 12  
US-08-770-564A-2  
Sequence 2, Application US/08770564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Prizant, Ron  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564A-2  
Query Match 100.0%; Score 12; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTCTCTCTCC 12  
DB 1 CGTCTCTCTCC 12  
RESULT 13  
US-08-521-634-17/C  
Sequence 17, Application US/08521634  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/521,634  
FILING DATE: 31-AUG-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,115  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:

Fri Jun 27 07:42:37 2003

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Page 6

APPLICATION NUMBER: US 08/272,102  
FILING DATE: 7-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy J.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 15389-000850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-521-634-17

Query Match 100.0%; Score 12; DB 9; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCC 12  
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DB 31 CGTTCCTCTCC 20

RESULT 14  
PCT-US02-25943-62884/C  
Sequence 62884, Application PC/TUS0225943  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: PCT/US02/25943  
CURRENT FILING DATE: 2002-08-27  
NUMBER OF SEQ ID NOS: 64156  
SOFTWARE: Proprietary  
SEQ ID NO 62884  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
FEATURE:  
LOCATION: (6132858) ... (6132888)  
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 67367  
PCT-US02-25943-62884

Query Match 100.0%; Score 12; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCC 12  
|||  
DB 22 CGTTCCTCTCC 11

RESULT 15  
US-10-227-565-62884/C  
Sequence 62884, Application US/10227565  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/227,565  
CURRENT FILING DATE: 2002-08-26  
NUMBER OF SEQ ID NOS: 64158  
SOFTWARE: Proprietary  
SEQ ID NO 62884  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
FEATURE:  
LOCATION: (6132858) ... (6132888)

OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 6736  
US-10-227-565-62884

Query Match 100.0%; Score 12; DB 42; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCC 12  
|||  
DB 22 CGTTCCTCTCC 11

Search completed: June 25, 2003, 06:20:21  
Job time : 1018.85 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 36.4781 Seconds  
(without alignments)  
482.732 Million cell updates/sec

Title: US-08-770-564A-4  
Perfect score: 12  
Sequence: 1 CGTTCCTCTCC 12

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues  
Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PTCT\_NEM\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEM\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEM\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PTCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEM\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEM\_PUB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEM\_PUB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEM\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	91.7	25	US-10-215-112-12736	Sequence 12736, A
C 2	11	91.7	25	US-10-098-263B-24096	Sequence 24096, A
C 3	11	91.7	25	US-10-098-263B-81647	Sequence 81647, A
C 4	11	91.7	25	US-10-098-263B-81648	Sequence 81648, A
C 5	11	91.7	25	US-10-098-263B-96226	Sequence 96226, A
C 6	11	91.7	25	US-10-098-263B-114611	Sequence 114611, A
C 7	10.4	86.7	17	US-09-818-875-899	Sequence 899, App
C 8	10.4	86.7	17	US-09-818-875-900	Sequence 900, App
C 9	10.4	86.7	20	US-09-854-883-302	Sequence 302, App
C 10	10.4	86.7	22	US-08-864-636A-1899	Sequence 1899, App
C 11	10.4	86.7	24	US-09-818-954A-4	Sequence 4, Appl
C 12	10.4	86.7	24	US-09-988-899-9	Sequence 9, Appl
C 13	10.4	86.7	25	US-09-943-388-16	Sequence 16, Appl
C 14	10.4	86.7	25	US-10-045-631A-12	Sequence 12, Appl
C 15	10.4	86.7	25	US-10-098-263B-9063	Sequence 9063, App
C 16	10.4	86.7	25	US-10-098-263B-9064	Sequence 9064, App
C 17	10.4	86.7	25	US-10-098-263B-21621	Sequence 21621, A
C 18	10.4	86.7	25	US-10-098-263B-22257	Sequence 22257, A
C 19	10.4	86.7	25	US-10-098-263B-23782	Sequence 23782, A

20	10.4	86.7	25	US-10-098-263B-25281	Sequence 25281, A
21	10.4	86.7	25	US-10-098-263B-48100	Sequence 48100, A
22	10.4	86.7	25	US-10-098-263B-57561	Sequence 57561, A
23	10.4	86.7	25	US-10-098-263B-81106	Sequence 81106, A
24	10.4	86.7	25	US-10-098-263B-84565	Sequence 84565, A
25	10.4	86.7	25	US-10-098-263B-89842	Sequence 89842, A
26	10.4	86.7	25	US-10-098-263B-95403	Sequence 95403, A
27	10.4	86.7	25	US-10-098-263B-117167	Sequence 117167, A
28	10.4	86.7	25	US-10-098-263B-117168	Sequence 117168, A
29	10.4	86.7	25	US-10-098-263B-120874	Sequence 120874, A
30	10.4	86.7	25	US-10-098-263B-120939	Sequence 120939, A
31	10.4	86.7	30	US-09-987-456-129	Sequence 129, App
32	10.4	86.7	31	US-10-052-942-80	Sequence 80, Appl
33	10.4	86.7	31	US-09-987-456-128	Sequence 128, App
34	10.4	83.3	17	US-10-163-552-930	Sequence 930, App
35	10.4	83.3	18	US-09-925-388-30	Sequence 30, Appl
36	10.4	83.3	18	US-09-969-373-3188	Sequence 3188, App
37	10.4	83.3	19	US-10-139-496-25	Sequence 1794, App
38	10.4	83.3	20	US-10-181-846-85	Sequence 25, Appl
39	10.4	83.3	20	US-09-953-047-40	Sequence 40, Appl
40	10.4	83.3	20	US-10-216-484-94	Sequence 94, Appl
41	10.4	83.3	20	US-10-216-484-98	Sequence 98, Appl
42	10.4	83.3	20	US-10-101-487-12	Sequence 12, Appl
43	10.4	83.3	24	US-10-101-487-13	Sequence 13, Appl
44	10.4	83.3	24	US-10-101-487-13	Sequence 13, Appl
45	10.4	83.3	24	US-09-037-657-4	Sequence 4, Appl

# ALIGNMENTS

RESULT 1  
US-10-215-112-12736/c  
Sequence 12736, Application US/10215112  
Publication No. US2003082596A1  
GENERAL INFORMATION:  
APPLICANT: Michael Miltman  
TITLE OF INVENTION: Method of Genetic Analysis of Probes:  
TITLE OF INVENTION: Test3  
FILE REFERENCE: 3119  
CURRENT APPLICATION NUMBER: US/10/215,112  
CURRENT FILING DATE: 2002-08-08  
NUMBER OF SEQ ID NOS: 14936  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12736  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-215-112-12736

Query Match 91.7%; Score 11; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 GTTCCCTCTCC 12  
18 GTTCCCTCTCC 8

RESULT 2  
US-10-098-263B-24096/c  
Sequence 24096, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIORITY APPLICATION NUMBER: 60/276,759  
PRIORITY FILING DATE: 2001-03-16

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/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO: 24096
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ US-10-098-263B-24096

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every Match	91.7%;	Score 11;	DB 9;	Length 25;
1st Local Similarity	100.0%;	Pred. No. 6.5e+03;		
Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	2	GTTCTCTTCC	12
Db	16	GTTCTCTTCC	6

RESULT 3  
US-10-098-263B-81647  
: Sequence 81647, Application US/10098263B  
: Publication No. US20030104410A1

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1  APPLICANT: Miltman, Michael
2  TITLE OF INVENTION: Human Microarray
3  FILE REFERENCE: 3118.1
4  CURRENT APPLICATION NUMBER: US/10/099,263B
5  CURRENT FILING DATE: 2003-01-08
6  PRIOR APPLICATION NUMBER: 60/276,759
7  PRIOR FILING DATE: 2001-03-16
8  NUMBER OF SEQ ID NOS: 131066
9  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
10 SEQ ID NO: 81647
11 LENGTH: 25
12 TYPE: DNA
13 ORGANISM: Homo sapien
14 IS-10-098-263B-81647

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Query Match 91.7%; Score 11; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	GTTCTCTTCC	12
Db	1	GTTCTCTTCC	11

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US-10-098-263B-81648
RESULT 4
Sequence 81648, Application US/10098263B
Publication No. US200301064410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 133066
SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1
SEQ ID NO 81648
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-81648

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Query Match	91.7%;	Score 11;	DB 9;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 6.5e+03;		
Matches 11; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

oy	2	GTTCCCTCTTCC	12
nb	1	GTTCCCTCTTCC	11

RESULT 5  
US-10-098-263B-96226  
; Sequence 96226, Application US/10098263B

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1 TITLE OF INVENTION: Human Microarray
2 FILE REFERENCE: 3118.1
3 CURRENT APPLICATION NUMBER: US/10/098,263B
4 CURRENT FILING DATE: 2003-01-08
5 PRIORITY DATE: 2002-03-16
6 PRIOR FILING DATE: 2001-03-16
7 NUMBER OF SEQ ID NOS: 13006
8
9 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1.1
10 SEQ ID NO: 96226

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-263B-96226

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Query Match      91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2	GTTCCTCTTC	12
Db	11	GTTCCTCTTC	21

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RESULT 6
US-10-098-263B-114611
: Sequence 114611, Application US/10098263B
: Publication No. US20030104410A1
: GENERAL INFORMATION:
: APPLICANT: Milman, Michael
: TITLE OF INVENTION: Human Microarray
: FILE REFERENCE: 3118.1
: CURRENT APPLICATION NUMBER: US/10/098,263B
: CURRENT FILING DATE: 2003-01-08
: PRIOR APPLICATION NUMBER: 60/276,759
: PRIOR FILING DATE: 2001-03-06
: NUMBER OF SEQ ID NOS: 131066
: SOFTWARE: Microarray Probe Sequence Listing
: Generator V 1.1.1
: SEQ ID NO 114611
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Homo sapien
: US-10-098-263B-114611

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```

Query Match      91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2	GTTCCCTCTTC	12
Db	6	GTTCCCTCTTC	16

RESULT 7  
 US-09-818-875-899/c  
 Sequence 899, Application US/09818875  
 Publication No. US20030051270A1  
 GENERAL INFORMATION:  
 APPLICANT: Kmiec, Eric B.  
 APPLICANT: Gamper, Michael B.  
 APPLICANT: Rice, Michael C.  
 TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
 TITLE OF INVENTION: Stranded Oligonucleotides  
 FILE REFERENCE: Napro-4  
 CURRENT APPLICATION NUMBER: US/09/818, 875  
 CURRENT FILING DATE: 2001-03-27

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; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 899
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-818-875-899

Query Match      86.7%; Score 10.4; DB 9; Length 17;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
DB      17 CGTTCCTCTTTC 6

RESULT 8
US-09-818-875-900
; Sequence 900, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 900
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-818-875-900

Query Match      86.7%; Score 10.4; DB 9; Length 17;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
DB      1 CGTTCCTCTTTC 12

RESULT 9
US-09-854-883-302/c
; Sequence 302, Application US/09854883
; Patent No. US2002005479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
```

```

; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 302
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-854-883-302

Query Match      86.7%; Score 10.4; DB 10; Length 20;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
DB      20 CGCTCCTCTTCC 9

RESULT 10
US-09-864-636A-1899/c
; Sequence 1899, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Alwai, Hachim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1899
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-864-636A-1899

Query Match      86.7%; Score 10.4; DB 9; Length 22;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
DB      12 CTTCTCTTCC 1

RESULT 11
US-09-818-954A-4
; Sequence 4, Application US/09818954A
; Patent No. US20020015981A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher
; APPLICANT: Cao, Jin
; APPLICANT: Danilenko, Dmitry
; APPLICANT: Gong, Jianhua
; APPLICANT: Hill, David
; TITLE OF INVENTION: Beta-like Glycoprotein Hormone Polypeptide and Heterodimer
; FILE REFERENCE: A-676B
; CURRENT APPLICATION NUMBER: US/09/818,954A
; CURRENT FILING DATE: 2001-03-27
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;; PRIOR APPLICATION NUMBER: 09/723,970  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/199,211  
;; PRIOR FILING DATE: 2000-04-24  
;; PRIOR APPLICATION NUMBER: 60/192,654  
;; PRIOR FILING DATE: 2000-03-28  
;; NUMBER OF SEQ ID NOS: 28  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO: 4  
;; LENGTH: 24  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-818-954A-4

Query Match 86.7%; Score 10.4; DB 10; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.4e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12  
Db 11 CATTCCTCTCC 22

RESULT 12  
US-09-968-899-9/c  
; Sequence 9, Application US/09988899  
; Patent No. US20020102613A1  
; GENERAL INFORMATION:  
; APPLICANT: HOOGENBOOM, HENDRICUS R.J.M.  
; TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE  
; FILE REFERENCE: DX/003 CON  
; CURRENT APPLICATION NUMBER: US/09/988,899  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: PCT/US00/13682  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: 99201558.6  
; PRIOR FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 9  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-968-899-9

Query Match 86.7%; Score 10.4; DB 10; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.4e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12  
Db 13 CGTTCCTCTCC 2

RESULT 13  
US-09-943-388-16  
; Sequence 16, Application US/09943388  
; Patent No. US20020160953A1  
; GENERAL INFORMATION:  
; APPLICANT: Holloway, James L.  
; APPLICANT: Webster, Philippa J.  
; APPLICANT: Thayer, Edward C.  
; TITLE OF INVENTION: Mammalian Glycoprotein Hormone-1  
; FILE REFERENCE: 00-34  
; CURRENT APPLICATION NUMBER: US/09/943,388  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 09/839,706  
; PRIOR APPLICATION NUMBER: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 60/199,498  
; PRIOR APPLICATION NUMBER: 2000-04-25  
; NUMBER OF SEQ ID NOS: 44

;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO: 16  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-943-388-16

Query Match 86.7%; Score 10.4; DB 9; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.4e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12  
Db 11 CATTCCTCTCC 22

RESULT 14  
US-10-045-631A-12  
; Sequence 12, Application US/10045631A  
; Publication No. US20030044900A1  
; GENERAL INFORMATION:  
; APPLICANT: Berand, Christophe  
; APPLICANT: Onishi, Cara  
; APPLICANT: Sakowicz, Roman  
; APPLICANT: Vaisberg, Eugene  
; APPLICANT: Wood, Ken  
; APPLICANT: Yu, Ming  
; APPLICANT: CytoKinetix, Inc.  
; TITLE OF INVENTION: HUMAN KINESINS AND METHODS OF PRODUCING AND PURIFYING  
; FILE REFERENCE: 020552-000410US  
; CURRENT APPLICATION NUMBER: US/10/045,631A  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: WO PCT/US00/10670  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 09/295,612  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 12  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: (Spanning 22-2274)  
US-10-045-631A-12

Query Match 86.7%; Score 10.4; DB 9; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.4e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12  
Db 2 CGTTCCTCTCC 13

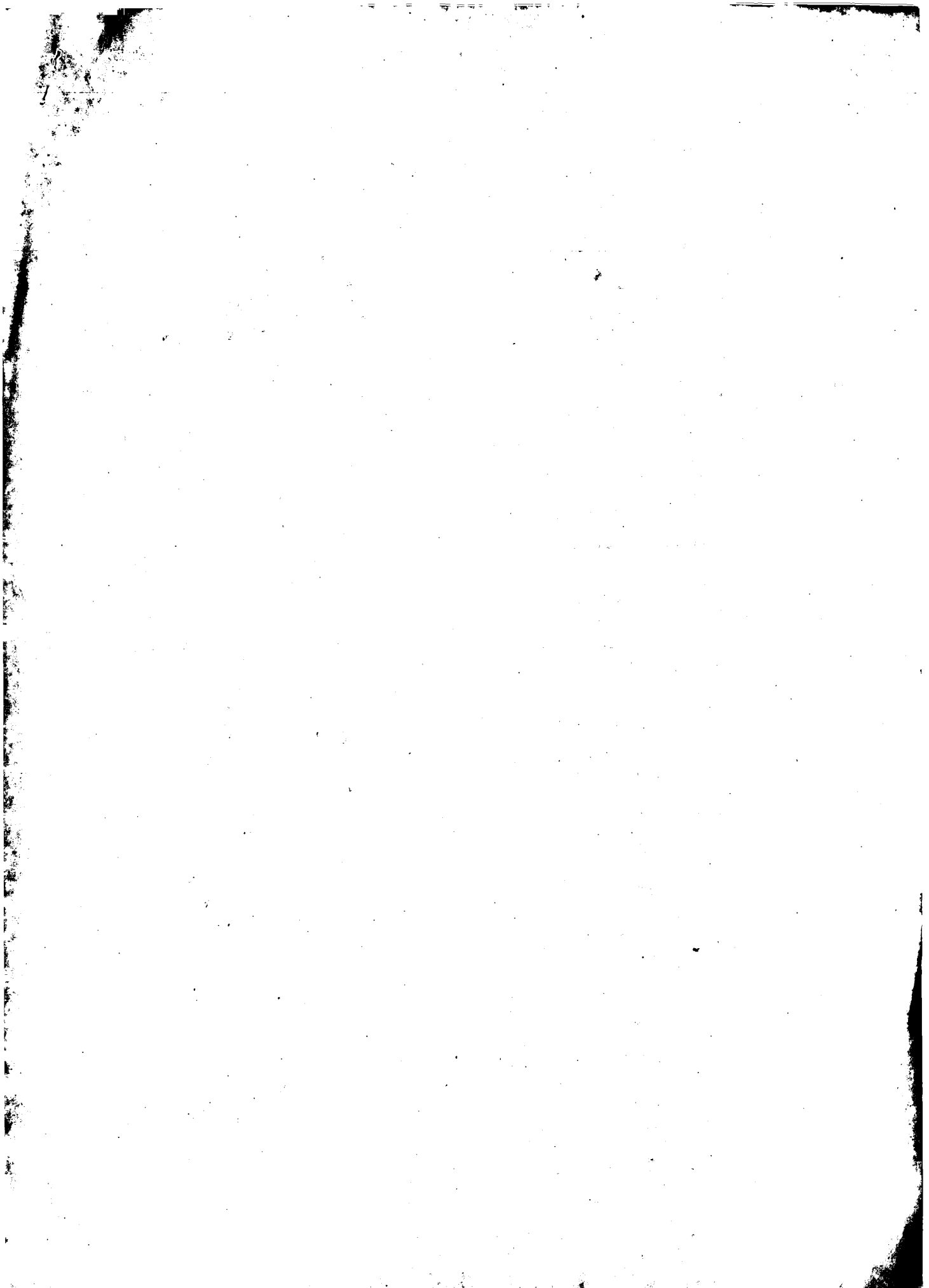
RESULT 15  
US-10-098-263B-9063  
; Sequence 9063, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Miltman, Michael  
; APPLICANT: Human Microarray  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118-1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO: 9063  
; LENGTH: 25

; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-9063

Query Match 86.7%; Score 10.4; DB 9; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.4e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTC 12  
|||  
Db 1 CGTTCCTCTTC 12

Search completed: June 25, 2003, 22:25:02  
Job time : 37.4781 secs



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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 60.7968 Seconds  
(without alignments)  
482.732 Million cell updates/sec

Title: US-08-770-564a-3

Perfect score: 20  
Sequence: 1 CGTTCCTCTCTGCGGCT 20

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEM\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	71.0	25	US-10-098-263B-114611	Sequence 114611, App1
2	14.2	71.0	39	US-09-832-355A-71	Sequence 71, App1
3	13.8	69.0	25	US-10-098-263B-23782	Sequence 23782, A
4	13.6	68.0	25	US-10-098-263B-69585	Sequence 69585, A
5	13.4	67.0	31	US-09-912-263-428	Sequence 428, App
6	13.2	66.0	23	US-09-439-429-17	Sequence 17, App1
7	13.2	66.0	25	US-10-098-263B-24011	Sequence 24011, A
8	13.2	66.0	25	US-10-098-263B-48100	Sequence 48100, A
9	13	65.0	31	US-09-801-274-1791	Sequence 1791, App
10	12.8	64.0	17	US-09-780-533A-58	Sequence 58, App1
11	12.8	64.0	17	US-09-533A-59	Sequence 59, App1
12	12.8	64.0	25	US-09-944-160-26	Sequence 26, App1
13	12.8	64.0	25	US-09-944-160-40	Sequence 40, App1
14	12.8	64.0	25	US-10-098-263B-49318	Sequence 49318, A
15	12.8	64.0	25	US-10-098-263B-116559	Sequence 116559, A
16	12.8	64.0	25	US-10-098-263B-116560	Sequence 116560, App1
17	12.8	64.0	28	US-09-225-201-40	Sequence 40, App1
18	12.8	64.0	38	US-09-780-533A-3290	Sequence 3290, App
19	12.8	64.0	38	US-09-930-423-1849	Sequence 1849, App

C 20	12.8	64.0	42	9	US-09-500-700-58	Sequence 59, App1
C 21	12.6	63.0	20	9	US-10-060-301-189	Sequence 189, App
C 22	12.6	63.0	25	9	US-10-098-263B-114612	Sequence 114612, App
C 23	12.6	63.0	25	10	US-09-866-108-5348	Sequence 5348, App
C 24	12.6	63.0	25	10	US-09-866-108-5349	Sequence 5349, App
C 25	12.6	63.0	25	10	US-09-866-108-5350	Sequence 5350, App
C 26	12.6	63.0	25	10	US-09-866-108-5351	Sequence 5351, App
C 27	12.6	63.0	25	10	US-09-866-108-5352	Sequence 5352, App
C 28	12.6	63.0	25	10	US-09-866-108-5353	Sequence 5353, App
C 29	12.6	63.0	25	10	US-09-866-108-5354	Sequence 5354, App
C 30	12.4	62.0	18	10	US-09-969-373-1923	Sequence 1923, App
C 31	12.4	62.0	25	9	US-10-215-112-326	Sequence 326, App
C 32	12.4	62.0	25	9	US-10-215-112-3587	Sequence 3587, App
C 33	12.4	62.0	25	9	US-10-098-263B-46242	Sequence 46242, A
C 34	12.4	62.0	25	9	US-10-098-263B-47500	Sequence 47500, A
C 35	12.4	62.0	38	9	US-09-780-533A-3556	Sequence 3556, App
C 36	12.4	62.0	38	9	US-09-780-533A-3688	Sequence 3688, App
C 37	12.4	62.0	38	9	US-09-848-754A-5600	Sequence 5600, App
C 38	12.4	62.0	38	9	US-09-780-164-1506	Sequence 1506, App
C 39	12.2	61.0	17	9	US-09-780-533A-954	Sequence 954, App
C 40	12.2	61.0	17	10	US-09-866-108-2417	Sequence 2417, App
C 41	12.2	61.0	20	10	US-09-854-883-127	Sequence 127, App
C 42	12.2	61.0	23	9	US-10-061-395-97	Sequence 97, App1
C 43	12.2	61.0	23	9	US-09-818-921-62	Sequence 62, App1
C 44	12.2	61.0	23	9	US-10-052-942-140	Sequence 140, App
C 45	12.2	61.0	23	10	US-09-987-456-108	Sequence 108, App

#### ALIGNMENTS

RESULT 1  
US-10-098-263B-114611  
Sequence 114611, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION: Michael  
APPLICANT: Miltman, Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098, 263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276, 759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 114611  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-114611

Query Match 71.0%; Score 14.2; DB 9; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 6 GTTCCCTCTCTGAGACT 24  
2 GTTCCCTCTCTGAGACT 20

RESULT 2  
US-09-832-355A-71/C  
Sequence 71, Application US/0982355A  
Publication No. US20030027751A1  
GENERAL INFORMATION: Imre  
APPLICANT: Kovacs, Imre  
FILE REFERENCE: 205654  
CURRENT APPLICATION NUMBER: US/09/832, 355A  
CURRENT FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 126  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 71  
LENGTH: 39  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: ( )  
OTHER INFORMATION: Synthetic  
US-09-832-355A-71

Query Match  
Best Local Similarity 71.0%; Score 14.2; DB 9; Length 39;  
84.2%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCTGCGGCT 20  
DB 32 GTTCTCTTCTCTGCGGCT 14

RESULT 3  
US-10-098-263B-23782/c  
Sequence 23782, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 23782  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-23782

Query Match  
Best Local Similarity 69.0%; Score 13.8; DB 9; Length 25;  
88.2%; Pred. No. 2.6e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCTGCGG 17  
DB 20 CGTCTCTTCTCTGCGG 4

RESULT 4  
US-10-098-263B-69585/c  
Sequence 69585, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 69585  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-69585

Query Match  
Best Local Similarity 68.0%; Score 13.6; DB 9; Length 25;  
80.0%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCTGCGGCT 20

DB 21 CGGTCTCTTCTCTGCGACT 2

RESULT 5  
US-09-912-263-428/c  
Sequence 428, Application US/09912263  
Publication No. US20030039973A1  
GENERAL INFORMATION:  
APPLICANT: Cargill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Lander, Eric S.  
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
FILE REFERENCE: 2825.2017-001  
CURRENT APPLICATION NUMBER: US/09/912,263  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: US 60/220,315  
PRIOR FILING DATE: 2000-07-24  
NUMBER OF SEQ ID NOS: 552  
SOFTWARE: PastSeq for Windows Version 4.0  
SEQ ID NO 428  
LENGTH: 31  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-912-263-428

Query Match  
Best Local Similarity 67.0%; Score 13.4; DB 9; Length 31;  
82.4%; Pred. No. 3.9e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTCCTCTTCTCTGCGCC 19  
DB 28 TGCCTTCTCTGCGACC 12

RESULT 6  
US-09-439-429-17/c  
Sequence 17, Application US/09439429  
Publication No. US2003008375A1  
GENERAL INFORMATION:  
APPLICANT: Power, Christopher  
APPLICANT: Mayne, Michael B.  
TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES REGULATING EXPRESSION  
FILE REFERENCE: 3045.00002  
CURRENT APPLICATION NUMBER: US/09/439,429  
CURRENT FILING DATE: 1999-11-15  
PRIOR APPLICATION NUMBER: 60/062,718  
PRIOR FILING DATE: 1997-10-22  
PRIOR APPLICATION NUMBER: 09/176,862  
PRIOR FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-439-429-17

Query Match  
Best Local Similarity 66.0%; Score 13.2; DB 9; Length 23;  
83.3%; Pred. No. 4.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCTGCGGC 18  
DB 18 CGCTCTTCTCTGCTGC 1

RESULT 7  
US-10-098-263B-24011  
Sequence 24011, Application US/10098263B



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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24011
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-098-263B-24011

Query Match      66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GTTCCTCTCTCTGCGGC 19
Db      8 GTTCCTCTCTCTCTGTC 25

RESULT 8
; US-10-098-263B-48100
; Sequence 48100, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-098-263B-48100

Query Match      66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGTTCCTCTCTCTGCGGC 18
Db      5 CGGTCTCTCTCTCTGTGAC 22

RESULT 9
; US-09-801-274-1791
; Sequence 1791, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1791
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-274-1791

Query Match      65.0%; Score 13; DB 10; Length 31;
Best Local Similarity 86.7%; Pred. No. 5.8e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GTTCCTCTCTCTGCG 16
Db      6 GGTCCTCTCTCTGTCG 20

RESULT 10
; US-09-780-533A-58
; Sequence 58, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Chowrita, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 58
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-780-533A-58

Query Match      64.0%; Score 12.8; DB 9; Length 17;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy      3 TTCCTCTCTCTGCGGC 18
Db      2 UUCGUCUUCUUCGUCG 17

RESULT 11
; US-09-780-533A-59
; Sequence 59, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Chowrita, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-780-533A-59

Query Match      64.0%; Score 12.8; DB 9; Length 17;
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Fr1 Jun 27 07:42:27 2003

us-08-770-564a-3.rnpb

Page 4

Best Local Similarity 50.0%; Pred: No. 7.7e+03;  
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

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        ::||::||::||
Db      1  UUGCUCUUCGCGUC 16

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RESULT 12
US-09-944-160-26
? Sequence 26, Application US/09944160
? Patent No. US20020174452A1
? GENERAL INFORMATION:
? APPLICANT: Lewis, No. US20020174452A1man
? APPLICANT: Davlin, Laurence
? APPLICANT: .. Huang, Ning
? TITLE OF INVENTION: Monocot Seeds with Increased Lignan
? TITLE OF INVENTION: Content
? FILE REFERENCE: WSUR117983
? CURRENT APPLICATION NUMBER: US/09/944,160
? CURRENT FILING DATE: 2001-08-30
? PRIOR APPLICATION NUMBER: US 60/230,632
? PRIOR FILING DATE: 2000-09-07
? NUMBER OF SEQ ID NOS: 49
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 25
? LENGTH: 25
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: primer
US-09-944-160-26

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Query Match	64.0%;	Score 12.8;	DB 9;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 7.4e+03;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Dy            3 TTCTTCTTCCTGCGGC 18  
               |||||  
Db          10 TTCCTCTCATGCTGC 25

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RESULT 13
US-09-944-160-40
? Sequence 40, Application US/09944160
? Patent No. US20020174452A1
? GENERAL INFORMATION:
? APPLICANT: Lewis, No. US20020174452A1man
? APPLICANT: Davlin, Leutene
? APPLICANT: .. Huang, Ning
? TITLE OF INVENTION: Monocot Seeds with Increased Lignan
? TITLE OF INVENTION: Content
? FILE REFERENCE: WSUR117983
? CURRENT APPLICATION NUMBER: US/09/944,160
? CURRENT FILING DATE: 2001-08-30
? PRIOR APPLICATION NUMBER: US 60/230,632
? PRIOR FILING DATE: 2000-09-07
? NUMBER OF SEQ ID NOS: 49
? SOFTWARE: Parseq for Windows Version 4.0
? SEQ ID NO 40
? LENGTH: 25
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: primer
? US-09-944-160-40

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Query Match	64.0%	Score 12.8;	DB 9;	Length 25;
Best Local Similarity	87.5%	Pred. No. 7.4e+03;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

3 TTCCTCTTCCTGCGC 18

Db 10 TTCCTCTTCATGCTGC 25

RESULT 14  
US-10-098-263B-49318/c  
; Sequence 49318, Application US/10098263B  
; Publication No. US20030104410A1

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1  APPLICANT: Mitleman, Michael
2  TITLE OF INVENTION: Human Microarray
3  FILE REFERENCE: 3118.1
4  CURRENT APPLICATION NUMBER: US/10/039,263B
5  CURRENT FILING DATE: 2003-01-08
6  PRIOR APPLICATION NUMBER: 60/276,759
7  PRIOR FILING DATE: 2001-03-16
8  NUMBER OF SEQ ID NOS: 131066
9  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
10 SEQ ID NO 49318
11
12 LENGTH: 25
13 TYPE: DNA
14 ORGANISM: Homo sapien
15
16 US-10-098-263B-49318

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Query Match	64.0%;	Score 12.8;	DB 9;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 7.4e+03;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

**Dy**

2 GTTCCTCTTCCGCG 17  
|||  
**Db** 18 GTGACTCTTCCGCG 3

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RESULT 15
US-10-098-263B-116559/c
; Sequence 116559, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michel
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/2726,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 13106
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 116559
;
; LENGTH: 25
;
; TYPE: DNA
;
; ORGANISM: Homo sapien
;
; US-10-098-263B-116559

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Query Match	64.0%;	Score 12.8;	DB 9;	length 25;
Best Local Similarity	87.5%;	Pred. No. 7.4e+03;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 CGTTCCTCTTCCTGCG 16  
||| ||| ||| |||  
DB 18 CGTTCCTCTTCCTGCG 3

Search completed: June 25, 2003, 22:25:01  
Job time : 61.7968 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1697.05 Seconds  
(without alignments)  
296.308 Million cell updates/sec

Title: US-08-770-564A-3  
Perfect score: 20  
Sequence: 1 CGTTCCTCTCTGCGGCTT 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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13: /cgn2\_6/prodata/2/pna/US089\_COMB.seq.\*  
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37: /cgn2\_6/prodata/2/pna/US099D\_COMB.seq.\*  
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42: /cgn2\_6/prodata/2/pna/US102A\_COMB.seq.\*  
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Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1 PCT-US97-23619-3	Sequence 3, Appl1
2	20	100.0	20	US-08-770-564A-3	Sequence 3, Appl1
3	20	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appl1
4	20	100.0	30	11 US-08-770-564A-2	Sequence 2, Appl1
5	20	100.0	31	9 US-08-521-634-17	Sequence 17, Appl1
6	15.8	79.0	20	41 US-10-174-020-71	Sequence 71, Appl1
7	15.8	79.0	20	41 US-10-174-020-118	Sequence 138, Appl1
8	15.2	76.0	24	1 PCT-US01-30828-5	Sequence 8, Appl1
9	15.2	76.0	24	1 PCT-US01-42431-18	Sequence 18, Appl1
10	14.4	72.0	25	36 US-09-956-584-18655	Sequence 18655, A
11	14.4	72.0	25	67 US-60-234-017-52883	Sequence 52883, A
12	14.4	72.0	29	13 US-08-913-665-14	Sequence 14, Appl1
13	14.4	72.0	42	26 US-09-671-346-8	Sequence 14, Appl1
14	14.2	71.0	25	79 US-60-353-987-421837	Sequence 421837, A
15	14.2	71.0	32	US-09-832-355A-71	Sequence 71, Appl1
16	14.2	71.0	47	3 US-07-972-453-31	Sequence 31, Appl1
17	14.2	71.0	47	3 US-07-972-453-38	Sequence 38, Appl1
18	14.2	71.0	49	3 US-07-972-453-34	Sequence 34, Appl1
19	14.2	71.0	49	3 US-07-972-453-40	Sequence 40, Appl1
20	14	70.0	25	17 US-09-396-196F-119937	Sequence 119937, A
21	14	70.0	25	17 US-09-396-196G-119937	Sequence 119937, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

22 13.8 69.0 20 1 PCT-US00-27954A-39 Sequence 39, Appl  
23 13.8 69.0 20 18 US-09-418-641-39 Sequence 39, Appl  
24 13.8 69.0 20 40 US-10-110-514-39 Sequence 39, Appl  
25 13.8 69.0 25 26 US-09-660-220-118104 Sequence 118104  
26 13.8 69.0 25 36 US-09-856-584-257212 Sequence 257212  
27 13.8 69.0 25 67 US-60-234-017-252876 Sequence 252876  
28 13.8 69.0 25 79 US-60-353-987-593121 Sequence 593121  
29 13.8 69.0 25 79 US-60-353-987-646261 Sequence 646261  
30 13.8 69.0 25 79 US-60-353-987-749521 Sequence 749521  
31 13.8 69.0 27 27 US-09-687-246A-2 Sequence 2, Appl  
32 13.8 69.0 27 27 US-09-687-246B-2 Sequence 2, Appl  
33 13.8 69.0 31 18 US-09-454-623-15 Sequence 15, Appl  
34 13.8 69.0 31 17 US-09-367-170-23 Sequence 23, Appl  
35 13.8 69.0 33 18 US-09-407-402-8 Sequence 44, Appl  
36 13.8 69.0 33 18 US-09-407-402-44 Sequence 44, Appl  
37 13.8 69.0 33 18 US-09-481-620-6 Sequence 6, Appl  
38 13.8 69.0 33 18 US-09-481-620A-6 Sequence 6, Appl  
39 13.8 69.0 33 32 US-09-852-370-38 Sequence 38, Appl  
40 13.8 69.0 33 32 US-09-852-370A-38 Sequence 38, Appl  
41 13.8 69.0 33 38 US-10-002-244-8 Sequence 8, Appl  
42 13.8 69.0 33 38 US-10-002-244-44 Sequence 44, Appl  
43 13.8 69.0 33 38 US-10-002-244A-8 Sequence 8, Appl  
44 13.8 69.0 33 38 US-10-002-244A-44 Sequence 44, Appl  
45 13.8 69.0 33 39 US-10-087-286-30 Sequence 30, Appl

## ALIGNMENTS

RESULT 1  
PCT-US97-23619-3  
Sequence 3, Application PC/TUS9723619  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Method for Detecting and Inhibiting the  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note="oligo 14ab"  
PCT-US97-23619-3

Query Match 100.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTTCTCGGCGCT 20  
Db 1 CGTTCCTTCTCGGCGCT 20

RESULT 2  
US-08-770-564A-3  
Sequence 3, Application US/0870564A  
GENERAL INFORMATION:  
APPLICANT: Kaley, James T.  
APPLICANT: Pruzan, Ron  
APPLICANT: Weinlich, Scott L.  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-770-564A-3

Query Match 100.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTTCTCGGCGCT 20  
Db 1 CGTTCCTTCTCGGCGCT 20

RESULT 3  
PCT-US97-23619-2

Sequence 2, Application PC/TUS9723619  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Scorelila, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY:  
LOCATION: 1..30  
OTHER INFORMATION: /note= "oligo 14"  
PCT-US97-23619-2  
Query Match 100.0%; Score 20; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCGCGGCT 20  
DB 1 CGTTCCTCTTCGCGGCT 20

RESULT 4  
US-08-770-564A-2  
Sequence 2, Application US/08770564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ron  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Scorelila, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564A-2

Query Match 100.0%; Score 20; DB 11; Length 30;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCGCGGCT 20  
DB 1 CGTTCCTCTTCGCGGCT 20

RESULT 5  
US-08-521-634-17/c  
Sequence 17, Application US/08521634  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/521,634  
FILING DATE: 31-AUG-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,115  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-521-634-17

Query Match          100.0%; Score 20; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20
DB 31 CGTTCCTCTCTCGGCGCT 12

RESULT 6
US-10-174-020-71
; Sequence 71, Application US/10174020
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EXP
; FILE REFERENCE: R1S-0369
; CURRENT APPLICATION NUMBER: US/10/174,020
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-174-020-71

Query Match          79.0%; Score 15.8; DB 41; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 19
DB 2 CGTTCCTCTCTCGGCGCT 20

RESULT 7
US-10-174-020-138/C
; Sequence 138, Application US/10174020
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EXP
; FILE REFERENCE: R1S-0369
; CURRENT APPLICATION NUMBER: US/10/174,020
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 138
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
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; FEATURE:
; US-10-174-020-138

Query Match          79.0%; Score 15.8; DB 41; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 19
DB 19 CGTTCCTCTCTCGGCGCT 1

RESULT 8
PCT-US01-30828-5/C
; Sequence 5, Application PC/TUS0130828
; GENERAL INFORMATION:
; APPLICANT: Keck Graduate Institute
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Galas, David J.
; APPLICANT: Garrison, Lori K.
; TITLE OF INVENTION: GENOTYPING BY LIQUID CHROMATOGRAPHIC ANALYSIS OF SHORT
; FILE REFERENCE: 480189.403PC
; CURRENT APPLICATION NUMBER: PCT/US01/30828
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/300,350
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primers
; PCT-US01-30828-5

Query Match          76.0%; Score 15.2; DB 1; Length 24;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20
DB 22 CGTTCCTCTCTCGGCGCT 3

RESULT 9
PCT-US01-42432-18/C
; Sequence 18, Application PC/TUS0142432
; GENERAL INFORMATION:
; APPLICANT: Keck Graduate Institute
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Galas, David J.
; APPLICANT: Garrison, Lori K.
; TITLE OF INVENTION: METHODS FOR PARALLEL MEASUREMENT OF GENETIC VARIATIONS
; FILE REFERENCE: 480189.402PC
; CURRENT APPLICATION NUMBER: PCT/US01/42432
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/269,244
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; PCT-US01-42432-18

Query Match          76.0%; Score 15.2; DB 1; Length 24;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CGTTCCTCTCTCGGCGCT 20  
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 Db 22 CGTTCCTCTCTCGGCGCT 3

RESULT 10  
 US-09-956-584-18655/c  
 ; Sequence 18655, Application US/09956584  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltman, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus  
 ; FILE REFERENCE: 3115.1  
 ; CURRENT APPLICATION NUMBER: US/09/956,584  
 ; CURRENT FILING DATE: 2001-09-19  
 ; PRIOR APPLICATION NUMBER: 60/234,017  
 ; PRIOR FILING DATE: 2000-09-20  
 ; NUMBER OF SEQ ID NOS: 605887  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO.18655  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-956-584-18655

Query Match 72.0%; Score 14.4; DB 36; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 3.1e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCG 16  
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 Db 18 CGTTCCTCTCTCGGCG 3

RESULT 11  
 US-60-234-017-52883/c  
 ; Sequence 52883, Application US/60234017  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltman, M  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
 ; FILE REFERENCE: 3115  
 ; CURRENT APPLICATION NUMBER: US/60/234,017  
 ; CURRENT FILING DATE: 2000-09-20  
 ; NUMBER OF SEQ ID NOS: 605887  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 52883  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank U41285  
 US-60-234-017-52883

Query Match 72.0%; Score 14.4; DB 67; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 3.1e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCG 16  
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 Db 18 CGTTCCTCTCTCGGCG 3

RESULT 12  
 US-08-913-665-14/c  
 ; Sequence 14, Application US/08913665  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Saiga, Akihiko  
 ; APPLICANT: Oriita, Satoshi  
 ; APPLICANT: Igarashi, Hisanaga  
 ; APPLICANT: Okumura, Kouichi  
 ; APPLICANT: Sakaguchi, Gaku

;; TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
 ;; TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN  
 ;; NUMBER OF SEQUENCES: 20  
 ;; CORRESPONDENCE ADDRESS:  
 ;; ADDRESSER: FISH & NEAVE  
 ;; STREET: 1251 Avenue of the Americas  
 ;; CITY: New York  
 ;; STATE: New York  
 ;; COUNTRY: USA  
 ;; ZIP: 10020

;; COMPUTER READABLE FORM:  
 ;; MEDIUM TYPE: Floppy disk  
 ;; COMPUTER: IBM PC compatible  
 ;; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ;; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ;; CURRENT APPLICATION DATA:  
 ;; APPLICATION NUMBER: US/08/913,665  
 ;; FILING DATE: 19-SEP-1997  
 ;; CLASSIFICATION: 536  
 ;; ATTORNEY/AGENT INFORMATION:  
 ;; NAME: Haley, James F.  
 ;; REGISTRATION NUMBER: 27,794  
 ;; REFERENCE/DOCKET NUMBER: SHGN-12  
 ;; TELECOMMUNICATION INFORMATION:  
 ;; TELEPHONE: 212-596-9000  
 ;; TELEFAX: 212-596-9090  
 ;; INFORMATION FOR SEQ ID NO: 14:  
 ;; SEQUENCE CHARACTERISTICS:  
 ;; LENGTH: 29 base pairs  
 ;; TYPE: nucleic acid  
 ;; STRANDEDNESS: single  
 ;; TOPOLOGY: linear  
 ;; MOLECULE TYPE: other nucleic acid  
 ;; DESCRIPTION: /desc = "synthetic DNA"  
 US-08-913-665-14

Query Match 72.0%; Score 14.4; DB 13; Length 29;  
 Best Local Similarity 93.8%; Pred. No. 3.2e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTCGGCGCC 19  
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 Db 21 TACTCTCTCTCGGCGCC 6

RESULT 13  
 US-09-671-346-8/c  
 ; Sequence 8, Application US/09671346  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wolf, David L.  
 ; APPLICANT: Sigma, David  
 ; TITLE OF INVENTION: Agents Affecting Thrombosis and Hemostasis  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: Morgan, Lewis & Bockius LLP  
 ; STREET: 1111 Pennsylvania Avenue, NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004

;; COMPUTER READABLE FORM:  
 ;; MEDIUM TYPE: Floppy disk  
 ;; COMPUTER: IBM PC compatible  
 ;; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ;; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ;; CURRENT APPLICATION DATA:  
 ;; APPLICATION NUMBER: US/09/671,346  
 ;; FILING DATE: 27-Sep-2000  
 ;; PRIOR APPLICATION DATA:  
 ;; APPLICATION NUMBER: US 07/578,646  
 ;; FILING DATE: 1990-09-04  
 ;; APPLICATION NUMBER: US 07/808,329  
 ;; FILING DATE: 1991-12-16

Fri Jun 27 07:42:28 2003

us-08-770-564a-3, from

Page 6

APPLICATION NUMBER: US 08/249,777  
 FILING DATE: 1994-05-26  
 APPLICATION NUMBER: US 08/266,003  
 FILING DATE: 1994-06-29  
 APPLICATION NUMBER: US 08/469,301  
 FILING DATE: 1995-06-06  
 APPLICATION NUMBER: US 09/016,403  
 FILING DATE: 1998-01-30  
 APPLICATION NUMBER: US 09/362,207  
 FILING DATE: 1999-07-28  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Michael S. Tuccan, Ph.D.  
 REGISTRATION NUMBER: 43,210  
 REFERENCE/DOCKET NUMBER: 44461-5002-15-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 739-3000  
 TELEFAX: (202) 739-3001  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 42 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 -IS-09-671-346-8

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      SEQ ID NO 71
      LENGTH: 39
      TYPE: DNA
      ORGANISM: Artificial sequence
      FEATURE:
      NAME/KEY: misc feature
      LOCATION: (1..7)
      OTHER INFORMATION: Synthetic
US-09-832-355A-71

Query Match          71.0%; Score 14.2; DB 32; Length 39;
Best Local Similarity 84.2%; Fred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GTTCCTCTTCTCTCGGCGCT 20
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Db      32 GTTCTCTTCTCTCGGCGCT 14

Search completed: June 25, 2003, 06:20:21
Job time : 1698.67 secs

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Best Local Similarity	93.8%	Pred. No.	3.3e+04	
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				Indels 0
				Gaps 0
QY	1 CGTCTCTTCTCGG	16		
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RESULT 14
US-60-353-987-421837/c
/ Sequence 421837, Application US/60353987
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
/ FILE REFERENCE: 3121
/ CURRENT APPLICATION NUMBER: US/60/353,987
/ CURRENT FILING DATE: 2002-02-01
/ NUMBER OF SEQ ID NOS: 997516
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO: 421837
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ US-60-353-987-421837

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Query Match	71.0%;	Score 14.2;	DB 79;	Length 25;
Best Local Similarity	84.2%;	Pred. No. 3.8e+04;		
Matches	16;	Conservative	0;	Indels 0;
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QY	1	CGTTCCTCTTCTGCGGCC	19	
b	20	CGTACTCTCTGCGGCC	2	

RESULT 15  
 US-09-832-355A-71/c  
 Sequence 71, Application US/09833355A  
 GENERAL INFORMATION:  
 APPLICANT: Kovacs, Imre  
 APPLICANT: Keeslar, Paul  
 TITLE OF INVENTION: VEGF FUSION PROTEINS  
 FILE REFERENCE: 205654  
 CURRENT APPLICATION NUMBER: US/09/832,355A  
 CURRENT FILING DATE: 2001-04-10  
 NUMBER OF SEQ ID NOS: 126  
 SOFTWARE: PatentIn version 3.0

Search completed: June 25, 2003, 06:20:21  
Job time : 1698.67 secs

	Query Match	71.0%	Score 14.2	DB 32.	Length 32;
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	Matches	16;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
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Db	32 GTTCTCTTCTCCGCCCT	14			

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: SEQ ID NO 71
: LENGTH: 39
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1..7)
: OTHER INFORMATION: Synthetic
: OS-09-832-355A-71

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 30.3586 Seconds  
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Title: US-08-770-564A-3

Perfect score: 20  
Sequence: 1 CGTTCCTCTCTCGCGGCT 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents NA.\*  
2: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
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5: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	20	100.0	20	2	US-08-833-377-7
3	20	100.0	20	2	US-08-770-565-2
4	19	95.0	20	2	US-08-833-377-14
5	14.4	72.0	29	3	US-09-121-321-14
6	14.4	72.0	29	4	US-08-933-803A-14
7	14.4	72.0	42	1	US-08-487-037-8
8	13.8	69.0	20	3	US-09-418-641-39
9	13.8	69.0	31	2	US-08-576-626A-15
10	13.8	69.0	33	4	US-08-672-213-8
11	13.8	69.0	33	4	US-08-973-131-38
12	13.8	69.0	33	4	US-08-973-131-38
13	13.4	67.0	20	2	US-08-534-479-1
14	13.2	66.0	20	3	US-09-009-913-173
15	13.2	66.0	23	3	US-09-176-862-17
16	13.2	66.0	45	1	US-08-211-202-11
17	13.2	66.0	45	1	US-08-211-202-11
18	13.2	66.0	45	1	US-08-211-202-15
19	13.2	66.0	45	1	US-08-307-619-22
20	13.2	66.0	45	2	US-08-350-260A-68
21	13	65.0	45	3	US-09-050-783-22
22	12.8	64.0	20	2	US-08-487-037-9
23	12.8	64.0	20	5	PCT-US95-02943-18
24	12.8	64.0	21	1	US-08-206-790A-18
25	12.8	64.0	21	2	US-08-691-123-8
26	12.8	64.0	21	3	US-09-107-075-8
27	12.8	64.0	21	3	US-08-866-544-1

C 28	12.8	64.0	28	2	US-08-859-398-40	Sequence 40, Appl
C 29	12.8	64.0	28	4	US-09-225-928-40	Sequence 40, Appl
C 30	12.8	64.0	42	3	US-08-863-813A-58	Sequence 58, Appl
C 31	12.6	63.0	30	4	US-08-348-548-48	Sequence 48, Appl
C 32	12.6	63.0	30	5	PCT-US95-15716-48	Sequence 48, Appl
C 33	12.6	63.0	37	1	US-08-431-080-10	Sequence 10, Appl
C 34	12.6	63.0	37	2	US-08-938-534-10	Sequence 10, Appl
C 35	12.6	63.0	37	4	US-09-345-294-10	Sequence 10, Appl
C 36	12.6	63.0	49	4	US-09-538-709-935	Sequence 935, App
C 37	12.6	63.0	49	4	US-09-538-709-935	Sequence 935, App
C 38	12.4	62.0	20	1	US-08-031-143B-6	Sequence 6, Appl
C 39	12.4	62.0	20	1	US-08-031-143B-33	Sequence 6, Appl
C 40	12.4	62.0	20	5	PCT-US94-02891-6	Sequence 6, Appl
C 41	12.4	62.0	20	5	PCT-US94-02891-33	Sequence 33, Appl
C 42	12.2	61.0	20	4	US-09-487-368A-127	Sequence 127, App
C 43	12.2	61.0	20	4	US-09-851-896-86	Sequence 86, Appl
C 44	12.2	61.0	24	3	US-08-936-632B-16	Sequence 16, Appl
C 45	12.2	61.0	33	1	US-08-078-683A-22	Sequence 22, Appl

## ALIGNMENTS

RESULT 1  
US-08-770-565-3  
Sequence 3, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION/DOCKET NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-3  
Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.95;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 CGTTCCTCTCTCGCGGCT 20

Db 1 CGTTCCTCTCTCGGCGCT 20

RESULT 2  
US-08-833-377-7  
Sequence 7, Application US/08833377  
Patent No. 5968506  
GENERAL INFORMATION:  
APPLICANT: Weinrich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichtsteiner, Serge P.  
APPLICANT: Vassero, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,377  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note= "Oligo 14ab"  
US-08-833-377-7  
Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.95;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20  
Db 1 CGTTCCTCTCTCGGCGCT 20

RESULT 3  
US-08-770-565-2  
Sequence 2, Application US/0870565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
TITLE OF INVENTION: Telomerase  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-2  
Query Match 100.0%; Score 20; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.95;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20  
Db 1 CGTTCCTCTCTCGGCGCT 20

RESULT 4  
US-08-833-377-14  
Sequence 14, Application US/08833377  
Patent No. 5968506  
GENERAL INFORMATION:  
APPLICANT: Weinrich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichtsteiner, Serge P.  
APPLICANT: Vassero, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,377

FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "N = 5' biotinylated cytidine"  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note= "biotinylated Oligo 14ab"  
US-08-833-377-14

Query Match 95.0%; Score 19; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTTCTCGGCGCT 20  
DB 2 GTTCCTTCTCGGCGCT 20

RESULT 5  
US-09-121-321-14/c  
Sequence 14, Application US/09121321  
Patent No. 6090783  
GENERAL INFORMATION:  
APPLICANT: Saiga, Akihiko  
APPLICANT: Orita, Satoshi  
APPLICANT: Igarashi, Hisanaga  
APPLICANT: Sakaguchi, Gaku  
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/121,321  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/933,803  
FILING DATE: 19-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.

REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-12CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-09-121-321-14

Query Match 72.0%; Score 14.4; DB 3; Length 29;  
Best Local Similarity 93.8%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCTCTCTCGGCGCC 19  
DB 21 TACTCTTCTCGGCGCC 6

RESULT 6  
US-08-933-803A-14/c  
Sequence 14, Application US/08933803A  
Patent No. 6218522  
GENERAL INFORMATION:  
APPLICANT: Saiga, Akihiko  
APPLICANT: Orita, Satoshi  
APPLICANT: Igarashi, Hisanaga  
APPLICANT: Sakaguchi, Gaku  
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,803A  
FILING DATE: 19-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-12CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-08-933-803A-14

Query Match 72.0%; Score 14.4; DB 4; Length 29;  
Best Local Similarity 93.8%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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us-08-770-564a-3.rn1

Page 4

QY 4 TCGTCTCTCTCGGCGC 19  
DB 21 TACTCTCTCTCGGCGC 6

US-08-487-037-8/c  
Sequence 8, Application US/08487037  
Patent No. 5795863

GENERAL INFORMATION:  
APPLICANT: Wolf, David L.  
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,037  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0002.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-037-8

Query Match 72.0%; Score 14.4; DB 1; Length 42;  
Best Local Similarity 93.8%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCTCGGCG 16  
DB 25 CGATCTCTCTCTCGGCG 10

US-09-418-641-39  
Sequence 39, Application US/09418641A  
Patent No. 6124133  
GENERAL INFORMATION:  
APPLICANT: Jennifer K. Taylor  
TITLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION  
FILE REFERENCE: RTS-0105  
CURRENT APPLICATION NUMBER: US/09/418,641A  
CURRENT FILING DATE: 1999-10-15  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 39  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide

US-09-418-641-39  
Query Match 69.0%; Score 13.8; DB 3; Length 20;  
Best Local Similarity 88.2%; Pred. No. 5.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCTCGGCG 17  
DB 4 CGCTCTCTCTCTCGGCG 20

US-08-576-626A-15/c  
Sequence 15, Application US/08576626A  
Patent No. 598194  
GENERAL INFORMATION:  
APPLICANT: Summers, R.G.  
APPLICANT: Katz, L.  
APPLICANT: Donadio, S.  
APPLICANT: Staver, M.J.  
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR  
TITLE OF INVENTION: BIOSYNTHESIS GENES  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FaastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/576,626A  
FILING DATE: 21-DEC-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dianne Casuto  
REGISTRATION NUMBER: P-40,943  
REFERENCE/DOCKET NUMBER: 5857.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (847) 938-3137  
TELEFAX: (847) 938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-576-626A-15

Query Match 69.0%; Score 13.8; DB 2; Length 31;  
Best Local Similarity 88.2%; Pred. No. 6.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCGTCTCTCTCGGCGCT 20  
DB 23 TCTCTCTCTCTCGGCGCT 7

US-08-672-213-8/c  
Sequence 8, Application US/08672213  
Patent No. 6306649  
GENERAL INFORMATION:  
APPLICANT: GILMAN, Michael Z.

APPLICANT: NATESAN, Sridaran  
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION  
FACTORS IN GENE THERAPY  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ARIAD Gene Therapeutics, Inc.  
STREET: 26 Landedowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139-4234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,213  
FILING DATE: 27-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,553  
FILING DATE: 27-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,614  
FILING DATE: 29-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BERSTEIN, David L.  
REGISTRATION NUMBER: 31,235  
REFERENCE/DOCKET NUMBER: ARIAD 346B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-494-0400  
TELEFAX: 617-494-0208  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-672-213-8

Query Match 69.0%; Score 13.8; DB 4; Length 33;  
Best Local Similarity 88.2%; Pred. No. 6.2e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTCTCTTCTGCGGCC 19  
Db 23 TTCTCTCTCTGCGGCC 7

RESULT 11  
US-08-672-213-49/c  
Sequence 49, Application US/08672213  
Patent No. 6306649  
GENERAL INFORMATION:  
APPLICANT: GILMAN, Michael Z.  
APPLICANT: NATESAN, Sridaran  
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION  
FACTORS IN GENE THERAPY  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ARIAD Gene Therapeutics, Inc.  
STREET: 26 Landedowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139-4234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,213  
FILING DATE: 27-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,553  
FILING DATE: 27-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,614  
FILING DATE: 29-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BERSTEIN, David L.  
REGISTRATION NUMBER: 31,235  
REFERENCE/DOCKET NUMBER: ARIAD 346B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-494-0400  
TELEFAX: 617-494-0208  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-672-213-49

Query Match 69.0%; Score 13.8; DB 4; Length 33;  
Best Local Similarity 88.2%; Pred. No. 6.2e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTCTCTTCTGCGGCC 19  
Db 23 TTCTCTCTCTGCGGCC 7

RESULT 12  
US-08-973-131-38/c  
Sequence 38, Application US/08973131  
Patent No. 6326166  
GENERAL INFORMATION:  
APPLICANT: Pomerantz, Joel L.  
APPLICANT: Sabo, Carl O.  
TITLE OF INVENTION: Chimeric DNA-binding proteins  
FILE REFERENCE: APV-022.02  
CURRENT APPLICATION NUMBER: US/08/973,131  
EARLIER FILING DATE: 1998-03-16  
EARLIER APPLICATION NUMBER: PCT/US95/16982  
EARLIER FILING DATE: 1995-12-29  
EARLIER APPLICATION NUMBER: 08/366,083  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 38  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-973-131-38

Query Match 69.0%; Score 13.8; DB 4; Length 33;  
Best Local Similarity 88.2%; Pred. No. 6.2e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTCTCTTCTGCGGCC 19  
Db 23 TTCTCTCTCTGCGGCC 7

RESULT 13  
US-08-534-479-1  
Sequence 1, Application US/08534479

Patent No. 5851769  
GENERAL INFORMATION:  
APPLICANT: GRAY, JOE W.  
TITLE OF INVENTION: QUANTITATIVE FIBER MAPPING  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,479  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MACKNIGHT, KAMRIN T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: LBL-01754  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-534-479-1  
Query Match 67.0%; Score 13.4; DB 2; Length 20;  
Best Local Similarity 93.3%; Pred. No. 8.9e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 TTCCTCTTCTCGCG 17  
Db 1 TTCCTCTTCTCGCAG 15  
RESULT 14  
US-09-009-913-173/c  
Sequence 173, Application US/09009913  
GENERAL INFORMATION:  
APPLICANT: AXYS Pharmaceuticals, Inc.  
TITLE OF INVENTION: Asthma Related Genes  
NUMBER OF SEQUENCES: 339  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Ave, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,913  
FILING DATE: 21-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J.  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEQ-4P  
TELEPHONE: 650-327-3231  
TELEFAX: 650-327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 173:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-009-913-173

Query Match 66.0%; Score 13.2; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTCCTCTTCTCGCGCT 20  
Db 20 TTCGTCTTCGAGGCGCT 3

RESULT 15  
US-09-176-862-17/c  
Sequence 17, Application US/09176862B  
Patent No. 6046319  
GENERAL INFORMATION:  
APPLICANT: Power, Christopher  
TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES REGULATING EXPRESSION  
FILE REFERENCE: 3045,00002  
CURRENT APPLICATION NUMBER: US/09/176,862B  
CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: 60/062,718  
EARLIER FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-176-862-17

Query Match 66.0%; Score 13.2; DB 3; Length 23;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTCGCGCG 18  
Db 18 CGCTCTTCTTCTCGTGC 1

Search completed: June 25, 2003, 00:24:35  
UOD time : 51.586 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1031.16 Seconds  
(without alignments)  
314.123 Million cell updates/sec

Title: US-08-770-564A-3

Perfect score: 20  
Sequence: 1 CGTTCCTCTCTCGCGGCT 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hlc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_hlc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: gb\_gss: \*  
18: em\_gss\_hum: \*  
19: em\_gss\_inv: \*  
20: em\_gss\_pln: \*  
21: em\_gss\_vit: \*  
22: em\_gss\_fun: \*  
23: em\_gss\_mam: \*  
24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
27: em\_gss\_rnd: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	60.0	38	17	AZ974736 2M0249A03
C 2	12	60.0	43	17	AZ830358 2M0109M04
C 3	12	60.0	46	17	AL767395 Arabidops
C 4	11	55.0	26	17	AZ942099 2M0202C09
C 5	11	55.0	33	17	BH850686 SALX_0716
C 6	11	55.0	37	17	AZ392980 1M0155P13

Result No.	Score	Query Match	Length	ID	Description
C 7	11	55.0	40	17	AZ627381 1M0469H09
C 8	11	55.0	43	17	AZ419099 1M0195N23
C 9	11	55.0	45	17	AZ423992 1M0203A16
C 10	11	55.0	46	13	B1488502
C 11	11	55.0	50	9	AU102629
C 12	11	55.0	50	13	B1685073
C 13	10	50.0	27	17	AZ630179 1M0483B10
C 14	10	50.0	28	14	N92455
C 15	10	50.0	29	17	AZ794049 2M0047H08
C 16	10	50.0	32	17	AZ587757 1M0395F07
C 17	10	50.0	32	17	AZ792853 2M0045C07
C 18	10	50.0	32	17	BH847691 SALX_0558
C 19	10	50.0	35	17	AZ581591 1M0370O23
C 20	10	50.0	37	17	AZ625706 1M0456O23
C 21	10	50.0	37	17	AZ761912 1M0555G21
C 22	10	50.0	41	17	AZ608460 1M0432J07
C 23	10	50.0	41	17	BH625029 1007102B0
C 24	10	50.0	42	17	BH640418 1008035G0
C 25	10	50.0	43	14	H41505
C 26	10	50.0	43	14	T77849
C 27	10	50.0	44	17	AZ657109 1M0555G21
C 28	10	50.0	45	17	AZ657109 1M0555G21
C 29	10	50.0	45	17	AZ843544 2M0142O22
C 30	10	50.0	45	17	AL754108 Arabidops
C 31	10	50.0	46	9	AA052407 mb70h06.x
C 32	10	50.0	46	9	A1003193 an12a01.s
C 33	10	50.0	46	14	R87862
C 34	10	50.0	47	14	H80650
C 35	10	50.0	47	17	AZ784478 2M0027K02
C 36	10	50.0	47	17	AZ845343 2M0145B07
C 37	10	50.0	48	17	AZ443723 1M0238D11
C 38	10	50.0	48	17	BH840628 KG05923-5
C 39	10	50.0	49	9	AA902962 ok44b09.s
C 40	10	50.0	50	9	A1252059 qv39f04.x
C 41	10	50.0	50	9	AU102702 AU102702
C 42	10	50.0	50	9	AU104073 AU104073
C 43	10	50.0	50	9	AU104281 AU104281
C 44	10	50.0	50	9	AU104282 AU104282
C 45	10	50.0	50	9	AU104283 AU104283

## ALIGNMENTS

RESULT 1  
LOCUS AZ974736/c 38 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0249A03R Mouse 10kb plasmid UGC2M library Mus musculus genomic  
ACCESSION UGC2M0249A03 R, DNA sequence.  
VERSION AZ974736  
KEYWORDS AZ974736.1 GI:13645963  
SOURCE GSS.  
ORGANISM house mouse.  
MUS musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.  
REFERENCE 1 (bases 1 to 38)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00

Plate: 0249 row: A column: 03  
 Seq primer: CACACAGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 38.  
 Location/Qualifiers  
 1. 38

FEATURES  
 source  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0249A03"  
 /clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN  
 14 a 8 c 9 g 7 t

Query Match 60.0%; Score 12; DB 17; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCTG 14  
 19 TTCTCTTCTCTG 8

RESULT 2  
 AZ830358 43 bp DNA linear GSS 20-FEB-2001  
 LOCUS 2M0109M04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0109M04 R, DNA sequence.  
 ACCESSION AZ830358  
 VERSION AZ830358.1 GI:13000266  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 43)  
 Dunn, P., Ayvaz, A., Barber, M., Becorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmood, M., Meenen, B., Petersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiser, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 CONTACT Contact: Robert B. Weiss  
 UNIVERSITY University of Utah Genome Center  
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 TEL: 801 585 5606  
 FAX: 801 585 7177  
 EMAIL: dunn@genetics.utah.edu  
 INSERT LENGTH: 10000 Std Error: 0.00

Plate: 0109 row: M column: 04  
 Seq primer: CACACAGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 43.  
 Location/Qualifiers  
 1. 43

FEATURES  
 source  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0109M04"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN  
 7 a 10 c 8 g 18 t

Query Match 60.0%; Score 12; DB 17; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCTG 14  
 23 TTCTCTTCTCTG 34

RESULT 3  
 AL767395 46 bp DNA linear GSS 18-JUN-2002  
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-219A03-014202,  
 DEFINITION genomic survey sequence.  
 ACCESSION AL767395  
 VERSION AL767395.1 GI:21520514  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosoids II; Brassicales; Brassicaceae; Arabidopsis.  
 1  
 Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Seadler, H. and Weishaar, B.  
 A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines  
 Unpublished  
 2  
 Rosso, M., Strizhov, N., Li, Y., Reis, B., Dekker, K. and Weishaar, B.  
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics  
 Unpublished  
 3 (bases 1 to 46)  
 Strizhov, N., Rosso, M., and Weishaar, B.  
 Direct Submission  
 Submitted (17-JUN-2002) Weishaar B., Max-Planck-Institut fuer



## COMMENT

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone f5k7. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

## FEATURES

## SOURCE

Location/Qualifiers

1..46

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-219A03-014202"

/clone\_1lb="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 7 a 19 c 2 g 18 t  
ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 12; DB 17; Length 46;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCT 13  
|||||  
Db 29 GTTCTCTTCTCT 40

RESULT 4  
AZ942099/c

LOCUS

DEFINITION 26 bp DNA linear GSS 26-APR-2001

clone UUGC2M020C09 F, DNA sequence.

## ACCESSION

AZ942099.1 GI:13805115

## VERSION

GSS.

## KEYWORDS

house mouse.

## SOURCE

Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

## JOURNAL

## COMMENT

University of Utah

Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0202 row: C column: 09

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid insert

High quality sequence stop: 26.

## FEATURES

## SOURCE

1..26

/organism="Mus musculus"

/strain="C57BL/6J"

BASE COUNT 10 a 0 c 16 g 0 t  
ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 11; DB 17; Length 26;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCT 13  
|||||  
Db 12 TTCTCTTCTCT 2

RESULT 5  
BH850686

LOCUS

DEFINITION 33 bp DNA linear GSS 13-JUN-2002

SAUK\_071692.32.90 x Arabidopsis thaliana TDNA insertion lines

## ACCESSION

BH850686.1 GI:21421557

## VERSION

GSS.

## KEYWORDS

thale cress.

## SOURCE

Arabidopsis thaliana

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 33)  
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..33

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SAUK\_071692.32.90.x"

/clone.lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tDNA\\_protocols.html](http://signal.salk.edu/tDNA_protocols.html)"

BASE COUNT 5 a 16 c 1 g 11 t  
 ORIGIN  
 Query Match 55.0%; Score 11; DB 17; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 TTCTCTTCT 13  
 Db 19 TTCTCTTCT 29

RESULT 6  
 LOCUS A2392980 37 bp. DNA linear GSS 03-OCT-2000  
 DEFINITION 1M0155P13R Mouse 10kb plasmid UUGCM library Mus musculus genomic  
 accession A2392980  
 version A2392980  
 keywords A2392980.1 GI:10508052  
 source GSS.  
 organism house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 37)  
 Authors Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 unpublished (2000)

JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plates: 0155 row: P column: 13  
 Seq primer: CACGACGAAACGCGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 37.  
 Location/Qualifiers

#### FEATURES

1. 37  
 source  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCM0155P13"  
 /clone.lib="Mouse 10kb plasmid UUGCM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /note="Vector: FMD42ny; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 15 a 0 c 22 g 0 t  
 ORIGIN  
 Query Match 55.0%; Score 11; DB 17; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 TTCTCTTCT 13  
 Db 16 TTCTCTTCT 6

RESULT 7  
 LOCUS A2627381 40 bp. DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0469H09R Mouse 10kb plasmid UUGCM library Mus musculus genomic  
 accession A2627381  
 version A2627381  
 keywords A2627381.1 GI:11749571  
 source GSS.  
 organism house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 40)  
 Authors Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 unpublished (2000)

JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plates: 0469 row: H column: 09  
 Seq primer: CGTGTAAACGACGCGCGT  
 Class: plasmid ends  
 High quality sequence stop: 40.  
 Location/Qualifiers

#### FEATURES

1. 40  
 source  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCM0469H09"  
 /clone.lib="Mouse 10kb plasmid UUGCM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /note="Vector: FMD42ny; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 16 c 3 g 13 t  
ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 40;  
Best Local Similarity 100.0%; Pred. No. 6.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 TTCTCTTCTG 14  
|||||  
Db 9 TTCTCTTCTG 19

RESULT 8 43 bp DNA linear GSS 03-OCT-2000  
AZ419099/c  
LOCUS  
DEFINITION IM0195N23P Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0195N23 F, DNA sequence.  
ACCESSION  
AZ419099  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
1 (bases 1 to 43)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0195 row: N column: 23  
Seq primer: CGTTGTAAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 43.

TITLE  
JOURNAL  
COMMENT  
FEATURES  
SOURCE

Location/Qualifiers  
1. 43  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0195N23"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 21 a 0 c 22 g 0 t  
ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 43;  
Best Local Similarity 100.0%; Pred. No. 6.9e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TTCTCTTCT 13  
|||||  
Db 33 TTCTCTTCT 23

RESULT 9 45 bp DNA linear GSS 03-OCT-2000  
AZ423992  
LOCUS  
DEFINITION IM0203A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0203A16 F, DNA sequence.  
ACCESSION  
AZ423992  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
1 (bases 1 to 45)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0203 row: A column: 16  
Seq primer: CGTTGTAAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 45.

TITLE  
JOURNAL  
COMMENT  
FEATURES  
SOURCE

Location/Qualifiers  
1. 45  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0203A16"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 11 c 6 g 20 t  
 Query Match 55.0%; Score 11; DB 17; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 4 TCCTCTCTCTG 14  
 18 TCCTCTCTCTG 28

RESULT 10  
 BI488502/c 46 bp mRNA linear EST 28-AUG-2001  
 LOCUS 603021011F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5191659 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI488502  
 VERSION BI488502.1 GI:15327730  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 46)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strauberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L14M1479 row: 6 column: 04  
 High quality sequence prep: 46.  
 Location/Qualifiers

FEATURES  
 source 1..46  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5191659"  
 /clone\_1ib="NIH\_MGC\_114"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMV-Sport6; Site 1: NotI;  
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6  
 male brains, age range 23-27 yo. Library is oligo-dT  
 primed and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.5 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Graber  
 (Invtrogen). Research Genetics tracking code 019. Note:  
 this is a NIH\_MGC Library."  
 BASE COUNT 9 a 8 c 25 g 4 t  
 ORIGIN

BASE COUNT 9 a 8 c 25 g 4 t  
 ORIGIN

Query Match 55.0%; Score 11; DB 13; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTCTC 12  
 DB 12 GTTCTCTCTC 2

RESULT 11  
 AU102629/c 50 bp mRNA linear EST 30-AUG-2001  
 LOCUS AU102629 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 DEFINITION CAS04232, mRNA sequence.  
 ACCESSION AU102629  
 VERSION AU102629.1 GI:13552150  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hara  
 H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
 Y., Nakamura, Y., Suyama, A., and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)  
 21270072  
 CONTACT: Yutaka Suzuki  
 Institute of Medical Science, University of Tokyo  
 Department of Virology  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A., and Sugano  
 S. Construction and characterization of a full length-enriched and  
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
 Location/Qualifiers

FEATURES  
 source 1..50  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CAS04232"  
 /clone\_1ib="Sugano Homo sapiens cDNA library"  
 /note="Differential display comparison of untreated and  
 dimethylmitomate treated U937 cells"  
 BASE COUNT 13 a 10 c 18 g 9 t  
 ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTG 14  
 DB 19 TCCTCTCTCTG 9

RESULT 12  
 BI685073 50 bp mRNA linear EST 18-SEP-2001  
 LOCUS BI685073  
 DEFINITION 603310058F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5345950 5',  
 mRNA sequence.  
 ACCESSION BI685073  
 VERSION BI685073.1 GI:15647701  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 50)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strauberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Jeffrey Green M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov  
Plate: LHAM1879 row: c column: 15  
High quality sequence stop: 50.  
Location/Qualifiers

# FEATURES

1..50

source  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5345990"  
/clone\_lib="NCI CGAP Mam6"  
/sex="Female, virgin"  
/tissue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: PCMV-SPORE6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 3 a 20 c 17 g 10 t

ORIGIN

Query Match 55.0%; Score 11; DB 13; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TCTGCGGCT 20  
|||||  
Db 6 TCTGCGGCT 16

## RESULT 13

AZ630179 27 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0483B10R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION clone UGCG1M0483B10 R, DNA sequence.  
ACCESSION AZ630179  
VERSION AZ630179.1 GI:11752369  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0483 row: B column: 10  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers

# FEATURES

1..27

source  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG1M0483B10"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/sex="Male"  
/lab\_host="E. Coli XL10-Gold, TI-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[GB|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 9 t

ORIGIN

Query Match 50.0%; Score 10; DB 17; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCC 12  
|||||  
Db 4 TTCTCTTCC 13

## RESULT 14

N92455 28 bp mRNA linear EST 20-AUG-1996  
LOCUS 263301.81 Soares fetal\_lung\_NbHL19w Homo sapiens cDNA clone  
DEFINITION IMAGE:308305 3', similar to gb:X06322.cdsl MITOCHONDRIAL 60S  
ACCESSION N92455  
VERSION N92455.1 GI:1264764  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 28)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B.,  
Chissee, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,  
'M., Hultman, M., Kucada, T., Lacy, M., Le, M., De, N., Mardis, E., Moore,  
'B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,  
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,  
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
97044478  
Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LMLT; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 866 Std Error: 0.00  
Seq primer: mob.RBGA+RT  
High quality sequence stop: 1.  
Location/Qualifiers

# FEATURES

1..28

source  
/organism="Homo sapiens"  
/db\_xref="GDB:1251718"  
/db\_xref="taxon:9606"  
/clone="IMAGE:308305"  
/clone\_lib="Soares\_fetal\_lung\_NbHL19w"  
/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer  
 [5'-TGTACCAATCTGAAGGAGCGCGCAATTTTCTTTTCTT-3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldi. This library was constructed  
 from the same fetus as the fetal heart library, Soares  
 fetal heart NBH119W."

## BASE COUNT

7 a 9 c 4 g 8 t

## BASE COUNT

5 a 11 c 7 g 6 t

Query Match 50.0%; Score 10; DB 14; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 50.0%; Score 10; DB 17; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTC 11  
 |||||  
 DB 3 GTTCCTCTTC 12

QY 11 CCTGCGGCGCT 20  
 |||||  
 DB 27 CCTGCGGCGCT 18

## RESULT 15

A2794049 29 bp DNA linear GSS 16-FEB-2001  
 LOCUS A2794049/c 290047H08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0047H08 R, DNA sequence.

Search completed: June 23, 2003, 10:10:15  
 Job time : 1032.31 secs

ACCESSION A2794049  
 VERSION A2794049.1 GI:12939621

KEYWORDS GSS.  
 SOURCE house mouse.

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 29)

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
 and Wright,D., Weiss,R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: dunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00

Plate: 0047 row: H column: 08  
 Seq primer: CACACGAAACACCTATGACC

Class: plasmid ends  
 High quality sequence step: 29.

## FEATURES

## SOURCE

1..29

Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0047H08"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMW42 (G14732114[9b]AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 877.928 Seconds  
(without alignments)  
158.668 Million cell updates/sec

Title: US-08-770-564a-3

Perfect score: 20  
Sequence: 1 CGTTCCTCTCTGCGGCTT 20

Scoring table:  
OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

Pending Patents\_NA\_New:\*

- 1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	70.0	19	1 PCT-US03-04088-26	Sequence 26, App1
C 2	14	70.0	19	1 PCT-US03-04088-290	Sequence 290, App1
C 3	13	65.0	20	6 US-09-905-688-11	Sequence 11, App1
C 4	13	65.0	20	9 US-10-310-188-34029	Sequence 34029, A
C 5	13	65.0	21	4 US-08-825-746-11	Sequence 11, App1
C 6	13	65.0	25	7 US-09-954-455A-45573	Sequence 45573, A
C 7	13	65.0	25	9 US-10-355-577-198249	Sequence 198249, A
C 8	13	65.0	25	9 US-10-355-577-223567	Sequence 223567, A
C 9	13	65.0	25	9 US-10-355-577-498091	Sequence 498091, A
C 10	13	65.0	25	12 US-60-417-190-13946	Sequence 13946, A
C 11	13	65.0	25	12 US-60-417-190-13947	Sequence 13947, A
C 12	13	65.0	25	12 US-60-417-190-48932	Sequence 48932, A
C 13	13	65.0	25	12 US-60-417-190-48933	Sequence 48933, A
C 14	13	65.0	25	12 US-60-417-190-48939	Sequence 48939, A
C 15	13	65.0	25	12 US-60-417-190-48940	Sequence 48940, A
C 16	13	65.0	25	12 US-60-427-808-172999	Sequence 172999, A
C 17	13	65.0	25	12 US-60-427-808-218754	Sequence 218754, A
C 18	13	65.0	25	12 US-60-427-808-275829	Sequence 275829, A
C 19	13	65.0	25	12 US-60-427-808-469548	Sequence 469548, A
C 20	13	65.0	25	12 US-60-427-808-564830	Sequence 564830, A

C 21	13	65.0	25	12	US-60-427-836-440978	Sequence 440978, A
C 22	13	65.0	25	12	US-60-427-836-549003	Sequence 549003, A
C 23	13	65.0	25	12	US-60-427-836-599225	Sequence 599225, A
C 24	13	65.0	25	12	US-60-427-836-683575	Sequence 683575, A
C 25	13	65.0	25	13	US-60-470-475-51737	Sequence 51737, A
C 26	13	65.0	25	13	US-60-470-475-51738	Sequence 51738, A
C 27	13	65.0	25	13	US-60-470-475-55703	Sequence 55703, A
C 28	13	65.0	25	13	US-60-470-475-57853	Sequence 57853, A
C 29	13	65.0	25	13	US-60-470-475-61267	Sequence 61267, A
C 30	13	65.0	25	13	US-60-470-475-61272	Sequence 61272, A
C 31	13	65.0	25	13	US-60-470-475-73706	Sequence 73706, A
C 32	13	65.0	25	13	US-60-470-475-98981	Sequence 98981, A
C 33	13	65.0	25	9	US-10-294-719-499	Sequence 499, App
C 34	13	65.0	50	5	US-09-749-8808-7801	Sequence 7801, App
C 35	13	65.0	50	9	US-10-325-899-3869	Sequence 3869, App
C 36	12	60.0	20	9	US-10-303-778-15311	Sequence 15311, A
C 37	12	60.0	20	9	US-10-310-188-28440	Sequence 28440, A
C 38	12	60.0	20	10	US-10-289-762-3651	Sequence 3651, App
C 39	12	60.0	25	7	US-09-953-570-131778	Sequence 131778, A
C 40	12	60.0	25	7	US-09-954-445A-13116	Sequence 13116, App
C 41	12	60.0	25	7	US-09-954-445A-21805	Sequence 21805, A
C 42	12	60.0	25	7	US-09-954-445A-49318	Sequence 49318, A
C 43	12	60.0	25	9	US-10-098-263B-114611	Sequence 114611, A
C 44	12	60.0	25	9	US-10-098-263B-114611	Sequence 80134, A
C 45	12	60.0	25	9	US-10-355-577-80134	Sequence 80134, A

#### ALIGNMENTS

RESULT 1  
PCT-US03-04088-26/c  
Sequence 26, Application PC/TUS0304088  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene  
FILE REFERENCE: 02-708-A (400/080)  
CURRENT APPLICATION NUMBER: PCT/US03/04088  
PRIOR FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: US 60/396,600  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 26  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense  
OTHER INFORMATION: region  
PCT-US03-04088-26

Query Match 70.0%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TCTTCTGCGGCT 20  
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Db 19 TCTTCTGCGGCT 6

## RESULT 2

PCT-US03-04088-290  
; Sequence 290, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwigen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; PRIORITY FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 290  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense  
PCT-US03-04088-290

Query Match 70.0%; Score 14; DB 1; Length 19;  
Best Local Similarity 64.3%; Pred. No. 1.7e+03;  
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 7 TCTTCTGCGGCT 20  
| | | | | | | | | |  
Db 1 UCUUCUGGCGCT 14

## RESULT 3

US-09-905-688-11  
; Sequence 11, Application US/09905688  
; GENERAL INFORMATION:  
; APPLICANT: CZERNAK, BOGDAN  
; TITLE OF INVENTION: METHODS OF DETECTING AND DIAGNOSING BLADDER CANCER AND  
; FILE REFERENCE: UTSC:663US  
; CURRENT APPLICATION NUMBER: US/09/905,688  
; PRIORITY FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-905-688-11

Query Match 65.0%; Score 13; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCTCTTCTGTC 15  
| | | | | | | | | |  
Db 1 TTCTCTTCTGTC 13

## RESULT 4

US-10-310-188-34029/c  
; Sequence 34029, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: Rosetademonics  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN  
; FILE REFERENCE: 47487  
; CURRENT APPLICATION NUMBER: US/10/310,188  
; PRIORITY FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 34029  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-34029

Query Match 65.0%; Score 13; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCTCTTCTGTC 15  
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Db 19 TTCTCTTCTGTC 7

## RESULT 5

US-08-825-746-11  
; Sequence 11, Application US/08825746  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Baker, Suzanne  
; APPLICANT: Fearon, Eric  
; TITLE OF INVENTION: Methods for Restoring Wild-Type p53 Gene Function  
; FILE REFERENCE: 001107.05677  
; CURRENT APPLICATION NUMBER: US/08/825,746  
; PRIORITY FILING DATE: 1997-04-03  
; PRIOR APPLICATION NUMBER: 08/035,366  
; PRIOR FILING DATE: 1993-03-22  
; PRIOR APPLICATION NUMBER: 07/860,758  
; PRIOR FILING DATE: 1992-03-21  
; PRIOR APPLICATION NUMBER: 07/715,182  
; PRIOR FILING DATE: 1991-06-14  
; PRIOR APPLICATION NUMBER: 07/928,661  
; PRIOR FILING DATE: 1992-08-17  
; PRIOR APPLICATION NUMBER: 07/446,584  
; PRIOR FILING DATE: 1989-12-06  
; PRIOR APPLICATION NUMBER: 07/350,566  
; PRIORITY FILING DATE: 1989-03-29  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-08-825-746-11

Query Match 65.0%; Score 13; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 3 TTCTCTTCTGTC 15  
 |||||  
 1 TTCTCTTCTGTC 13

RESULT 6  
 US-09-954-445A-45573/c

; Sequence 45573, Application US/09954445A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana  
 ; FILE REFERENCE: 3116.1  
 ; CURRENT APPLICATION NUMBER: US/09/954,445A  
 ; CURRENT FILING DATE: 2000-09-17  
 ; PRIOR APPLICATION NUMBER: 60/233,620  
 ; PRIOR FILING DATE: 2000-09-18  
 ; NUMBER OF SEQ ID NOS: 131820  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 45573  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-09-954-445A-45573

Query Match 65.0%; Score 13; DB 7; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTCTTCTCT 13  
 |||||  
 15 GTTCTCTTCTCT 3

RESULT 7  
 US-10-355-577-198249

; Sequence 198249, Application US/10355577  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
 ; FILE REFERENCE: 3121  
 ; CURRENT APPLICATION NUMBER: US/10/355,577  
 ; CURRENT FILING DATE: 2003-01-31  
 ; NUMBER OF SEQ ID NOS: 997516  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 198249  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-355-577-198249

Query Match 65.0%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTCTCTTCTG 14  
 |||||  
 9 GTTCTCTTCTG 21

RESULT 8  
 US-10-355-577-223567/c

; Sequence 223567, Application US/10355577  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
 ; FILE REFERENCE: 3121  
 ; CURRENT APPLICATION NUMBER: US/10/355,577  
 ; CURRENT FILING DATE: 2003-01-31  
 ; NUMBER OF SEQ ID NOS: 997516  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 223567  
 ; LENGTH: 25  
 ; TYPE: DNA

; ORGANISM: Homo sapien  
 US-10-355-577-223567

Query Match 65.0%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CCTCTCTGCGG 17  
 |||||  
 25 CCTCTCTGCGG 13

RESULT 9  
 US-10-355-577-498091

; Sequence 498091, Application US/10355577  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
 ; FILE REFERENCE: 3121  
 ; CURRENT APPLICATION NUMBER: US/10/355,577  
 ; CURRENT FILING DATE: 2003-01-31  
 ; NUMBER OF SEQ ID NOS: 997516  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 498091  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-355-577-498091

Query Match 65.0%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTCTCTTCTG 14  
 |||||  
 3 GTTCTCTTCTG 15

RESULT 10  
 US-60-417-190-13946

; Sequence 13946, Application US/60417190  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Giulia Kennedy  
 ; APPLICANT: Hajime Matsuzaki  
 ; APPLICANT: Mei-Mei Shen  
 ; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans  
 ; FILE REFERENCE: 3522  
 ; CURRENT APPLICATION NUMBER: US/60/417,190  
 ; CURRENT FILING DATE: 2002-10-02  
 ; NUMBER OF SEQ ID NOS: 122930  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 13946  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-60-417-190-13946

Query Match 65.0%; Score 13; DB 12; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TTCTCTTCTGCG 16  
 |||||  
 2 TTCTCTTCTGCG 14

RESULT 11  
 US-60-417-190-13947

; Sequence 13947, Application US/60417190  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Giulia Kennedy  
 ; APPLICANT: Hajime Matsuzaki  
 ; APPLICANT: Mei-Mei Shen

```
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 13947
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-13947
```

```
Query Match          65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 TTCCTCTTCTGCG 16
         |||||
Db       1 TTCCTCTTCTGCG 13
```

```
RESULT 12
US-60-417-190-48932
/ Sequence 48932, Application US/60417190
/ GENERAL INFORMATION:
/ APPLICANT: Giulia Kennedy
/ APPLICANT: Hajime Matsuzaki
/ APPLICANT: Mei-Mei Shen
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 48932
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-48932
```

```
Query Match          65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 TTCCTCTTCTGCG 15
         |||||
Db       13 TTCCTCTTCTGCG 25
```

```
RESULT 13
US-60-417-190-48933
/ Sequence 48933, Application US/60417190
/ GENERAL INFORMATION:
/ APPLICANT: Giulia Kennedy
/ APPLICANT: Hajime Matsuzaki
/ APPLICANT: Mei-Mei Shen
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 48933
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-48933
```

```
Query Match          65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 TTCCTCTTCTGCG 15
```

```
Db       12 TTCCTCTTCTGCG 24
         |||||
```

```
RESULT 14
US-60-417-190-48939
/ Sequence 48939, Application US/60417190
/ GENERAL INFORMATION:
/ APPLICANT: Giulia Kennedy
/ APPLICANT: Hajime Matsuzaki
/ APPLICANT: Mei-Mei Shen
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 48939
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-48939
```

```
Query Match          65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 TTCCTCTTCTGCG 15
         |||||
Db       13 TTCCTCTTCTGCG 25
```

```
RESULT 15
US-60-417-190-48940
/ Sequence 48940, Application US/60417190
/ GENERAL INFORMATION:
/ APPLICANT: Giulia Kennedy
/ APPLICANT: Hajime Matsuzaki
/ APPLICANT: Mei-Mei Shen
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 48940
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-48940
```

```
Query Match          65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 TTCCTCTTCTGCG 15
         |||||
Db       12 TTCCTCTTCTGCG 24
```

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Search completed: June 23, 2003, 19:12:10
Job time : 877.926 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1677.45 Seconds  
(without alignments)  
299.770 Million cell updates/sec

Title: US-08-770-564A-3

Perfect score: 20  
Sequence: 1 CGTTCCTTCTCTGCGGCT 20

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
2: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
3: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
8: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
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10: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
11: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
12: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
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14: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
15: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
16: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
17: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
18: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
19: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
20: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
21: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
22: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
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25: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
26: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
27: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
28: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
29: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
30: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
31: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
32: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
33: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
34: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
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38: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
39: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
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41: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*  
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43: /cgn2\_6/ptodata/2/pna/US0950 COMB.seq:\*

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1 PCT-US97-23619-3	Sequence 3, Appl1
2	20	100.0	20	1 PCT-US97-23619-3	Sequence 3, Appl1
3	20	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appl1
4	20	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appl1
5	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
6	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
7	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
8	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
9	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
10	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
11	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
12	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
13	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
14	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
15	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
16	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
17	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
18	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
19	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
20	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
21	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
22	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
23	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
24	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
25	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
26	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
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31	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
32	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
33	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
34	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
35	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
36	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
37	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
38	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
39	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
40	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
41	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
42	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1
43	20	100.0	31	9 US-08-770-564A-2	Sequence 17, Appl1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

C. 22-13 65.0 50 40 US-10-131-827-3869 Sequence 3869, Ap  
C. 23-13 65.0 50 40 US-10-131-831-3869 Sequence 3869, Ap  
C. 24-12 60.0 12 1 PCT-US97-23619-4 Sequence 4, Appl  
C. 25-12 60.0 12 11 US-08-770-564A-4 Sequence 4, Appl  
C. 26-12 60.0 15 1 PCT-US01-06051-14 Sequence 1021, Ap  
C. 27-12 60.0 15 1 PCT-US02-25942-1021 Sequence 1021, Ap  
C. 28-12 60.0 15 1 PCT-US02-25942-1585 Sequence 1585, Ap  
C. 29-12 60.0 15 42 US-10-227-567-1021 Sequence 1021, Ap  
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C. 32-12 60.0 20 17 US-09-366-483B-21 Sequence 21, Appl  
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C. 35-12 60.0 20 19 US-09-514-000-14739 Sequence 14739, A  
C. 36-12 60.0 20 40 US-10-139-496-25 Sequence 25, Appl  
C. 37-12 60.0 24 6 US-08-231-975-2 Sequence 2, Appl  
C. 38-12 60.0 25 17 US-09-396-196F-22718 Sequence 22718, A  
C. 39-12 60.0 25 17 US-09-396-196F-34054 Sequence 34054, A  
C. 40-12 60.0 25 17 US-09-396-196F-95194 Sequence 95194, A  
C. 41-12 60.0 25 17 US-09-396-196F-95195 Sequence 95195, A  
C. 42-12 60.0 25 17 US-09-396-196F-95206 Sequence 95206, A  
C. 43-12 60.0 25 17 US-09-396-186G-22718 Sequence 22718, A  
C. 44-12 60.0 25 17 US-09-396-186G-34054 Sequence 34054, A  
C. 45-12 60.0 25 17 US-09-396-186G-95194 Sequence 95194, A

## ALIGNMENTS

## RESULT 1

PCT-US97-23619-3

Sequence 3, Application PC/TUS9723619

## GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: Methods for Detecting and Inhibiting the

TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/23619

FILING DATE: Not yet assigned

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/770,564

FILING DATE: 20-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/770,565

FILING DATE: 20-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 15389-27PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note= "oligo 14ab"  
PCT-US97-23619-3

## Query Match

Best Local Similarity 100.0%; Score 20; DB 1; Length 20;

Matches 20; Conservatively 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCTCTTCTCGGCGCT 20  
Db 1 CGTTCTCTTCTCGGCGCT 20

## RESULT 2

Sequence 3, Application US/08770564A

## GENERAL INFORMATION:

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ron

TITLE OF INVENTION: Inhibitory Polynucleotides Directed

TITLE OF INVENTION: Against the RNA Component of Telomerase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,564A

FILING DATE: 20-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002200US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-770-564A-3

Query Match .100.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 8.5; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservatively 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCTCTTCTCGGCGCT 20  
Db 1 CGTTCTCTTCTCGGCGCT 20

## RESULT 3

PCT-US97-23619-2

```
Sequence 2, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..30
OTHER INFORMATION: /note="oligo 14"
PCT-US97-23619-2

Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20
DB 1 CGTTCCTCTCTCGGCGCT 20

RESULT 4
US-08-770-564A-2
Sequence 2, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
```

```
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-2
```

```
Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20
DB 1 CGTTCCTCTCTCGGCGCT 20
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RESULT 5
US-08-521-634-17/c
Sequence 17, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 7-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy J.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 15389-000850  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-521-634-17

Query Match 100.0%; Score 20; DB 9; Length 31;  
Best Local Similarity 100.0%; Pred. No. 8.2; 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0;

QY 1 CGTTCCTCTCTCGGCGCT 20  
DB 31 CGTTCCTCTCTCGGCGCT 12

RESULT 6  
US-09-396-196F-119937/C  
Sequence 119937, Application US/09396196F  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196F  
PRIOR FILING DATE: 2001-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 119937  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196F-119937

Query Match 70.0%; Score 14; DB 17; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03; 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;

QY 2 GTTCTCTTCTGCGC 15  
DB 25 GTTCTCTTCTGCGC 12

RESULT 7  
US-09-396-196G-119937/C  
Sequence 119937, Application US/09396196G  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 119937  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-119937

PRIOR APPLICATION NUMBER: 60/100,678  
FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 119937  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-119937

Query Match 70.0%; Score 14; DB 17; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03; 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;

QY 2 GTTCTCTTCTGCGC 15  
DB 25 GTTCTCTTCTGCGC 12

RESULT 8  
US-09-956-584-18655/C  
Sequence 18655, Application US/09956584  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus  
FILE REFERENCE: 3115.1  
CURRENT APPLICATION NUMBER: US/09/956,584  
PRIOR FILING DATE: 2001-09-19  
PRIOR APPLICATION NUMBER: 60/234,017  
NUMBER OF SEQ ID NOS: 605887  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 18655  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-956-584-18655

Query Match 70.0%; Score 14; DB 36; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03; 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;

QY 1 CGTTCCTCTCTG 14  
DB 18 CGTTCCTCTCTG 5

RESULT 9  
US-60-234-017-52883/C  
Sequence 52883, Application US/60234017  
GENERAL INFORMATION:  
APPLICANT: Miltman, M  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
FILE REFERENCE: 3115  
CURRENT APPLICATION NUMBER: US/60/234,017  
PRIOR FILING DATE: 2000-09-20  
NUMBER OF SEQ ID NOS: 605887  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52883  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: GenBank U41285  
US-60-234-017-52883

Query Match 70.0%; Score 14; DB 67; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03; 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;

QY 1 CGTTCCTCTCTG 14

Db 18 CGTCTCTCTCTG 5

# RESULT 10

US-08-913-665-14/C  
 ; Sequence 14, Application US/08913665  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Saiga, Akihiko  
 ; APPLICANT: Orita, Satoshi  
 ; APPLICANT: Igarashi, Hisanaga  
 ; APPLICANT: Okumura, Kouichi  
 ; APPLICANT: Sakaguchi, Gaku  
 ; TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
 ; TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: FISH & NEAVE  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10020  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/913,665  
 ; FILING DATE: 19-SEP-1997  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haley, James F.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: SHN-12  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-596-9090  
 ; TELEFAX: 212-596-9000  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 29 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; DESCRIPTION: /desc = "synthetic DNA"  
 ; US-08-913-665-14

Query Match 70.0%; Score 14; DB 13; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTCTTCTGCGCC 19  
 Db 19 CTCTTCTGCGCC 6

RESULT 11  
 PCT-US02-18427-11  
 ; Sequence 11, Application PC/TUS0218427  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CZERNIAK, BOGDAN  
 ; APPLICANT: JOHNSTON, DENNIS  
 ; TITLE OF INVENTION: METHODS OF DETECTING, DIAGNOSING AND TREATING CANCER  
 ; TITLE OF INVENTION: AND IDENTIFYING NEOPLASTIC PROGRESSION  
 ; FILE REFERENCE: UTFC:712-WO  
 ; CURRENT APPLICATION NUMBER: PCT/US02/18427  
 ; CURRENT FILING DATE: 2002-06-11  
 ; PRIOR APPLICATION NUMBER: 60/297,813  
 ; PRIOR FILING DATE: 2001-06-12  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Primer  
 ; PCT-US02-18427-11

Query Match 65.0%; Score 13; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCTCTTCTGCGC 15  
 Db 1 TTCTCTTCTGCGC 13

RESULT 12  
 US-10-167-241-11  
 ; Sequence 11, Application US/10167241  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CZERNIAK, BOGDAN  
 ; APPLICANT: JOHNSTON, DENNIS  
 ; TITLE OF INVENTION: METHODS OF DETECTING, DIAGNOSING AND TREATING CANCER  
 ; TITLE OF INVENTION: AND IDENTIFYING NEOPLASTIC PROGRESSION  
 ; FILE REFERENCE: UTSC:712US  
 ; CURRENT APPLICATION NUMBER: US/10/167,241  
 ; CURRENT FILING DATE: 2002-06-11  
 ; PRIOR APPLICATION NUMBER: 60/297,813  
 ; PRIOR FILING DATE: 2001-06-12  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 11  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Primer  
 ; US-10-167-241-11

Query Match 65.0%; Score 13; DB 41; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCTCTTCTGCGC 15  
 Db 1 TTCTCTTCTGCGC 13

RESULT 13  
 US-10-157-058-11  
 ; Sequence 11, Application US/10157058  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vogelstein, Bert  
 ; APPLICANT: Baker, Suzanne  
 ; APPLICANT: Fearon, Eric R.  
 ; APPLICANT: Nigro, Janice M.  
 ; TITLE OF INVENTION: Methods for Restoring Wild-Type p53 Gene Function  
 ; FILE REFERENCE: 001107.00257  
 ; CURRENT APPLICATION NUMBER: US/10/157,058  
 ; CURRENT FILING DATE: 2002-08-28  
 ; PRIOR APPLICATION NUMBER: 08/825,746  
 ; PRIOR FILING DATE: 1997-04-03  
 ; PRIOR APPLICATION NUMBER: 08/035,366  
 ; PRIOR FILING DATE: 1993-03-22  
 ; PRIOR APPLICATION NUMBER: 07/928,661  
 ; PRIOR FILING DATE: 1992-08-17  
 ; PRIOR APPLICATION NUMBER: 07/860,758  
 ; PRIOR FILING DATE: 1992-03-31  
 ; PRIOR APPLICATION NUMBER: 07/715,182  
 ; PRIOR FILING DATE: 1991-06-14

PRIOR APPLICATION NUMBER: 07/446,584  
 PRIOR FILING DATE: 1989-12-06  
 PRIOR APPLICATION NUMBER: 07/330,566  
 PRIOR FILING DATE: 1989-03-29  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 11  
 LENGTH: 21  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-157-058-11

Query Match 65.0%; Score 13; DB 41; Length 21;  
 Best Local Similarity 100.0%; Pred.No. 2.1e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCTCTTCTCTG 15  
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 Db 1 TTCTCTTCTCTG 13

RESULT 14  
 US-60-233-620-45573/C  
 Sequence 45573, Application US/60233620  
 GENERAL INFORMATION:  
 APPLICANT: Miltenberg, Inc.  
 TITLE OF INVENTION: Methods of Genetic Analysis of  
 FILE REFERENCE: 3116  
 CURRENT APPLICATION NUMBER: US/60/233,620  
 CURRENT FILING DATE: 2000-10-24  
 NUMBER OF SEQ ID NOS: 131820  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 45573  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Arabidopsis thaliana  
 PUBLICATION INFORMATION:  
 DATABASE ACCESSION NUMBER: GenBank AL034567  
 US-60-233-620-45573

Query Match 65.0%; Score 13; DB 67; Length 25;  
 Best Local Similarity 100.0%; Pred.No. 2.1e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCTCTTCTCT 13  
 |||||  
 Db 15 CGTCTCTTCTCT 3

RESULT 15  
 US-60-353-987-198249  
 Sequence 198249, Application US/60353987  
 GENERAL INFORMATION:  
 APPLICANT: Miltenberg, Michael  
 TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
 FILE REFERENCE: 3121  
 CURRENT APPLICATION NUMBER: US/60/353,987  
 CURRENT FILING DATE: 2002-02-01  
 NUMBER OF SEQ ID NOS: 997518  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO: 198249  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 US-60-353-987-198249

Query Match 65.0%; Score 13; DB 79; Length 25;  
 Best Local Similarity 100.0%; Pred.No. 2.1e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTCTCTTCTCTG 14

Db 9 GTCTCTTCTCTG 21  
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 Job time: 1678.53 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 160.717 Seconds  
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Title: US-08-770-564A-3

Perfect score: 20  
Sequence: 1 CGTTCCTTCTCTGCGGCT 20

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:\*

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- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEM\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEM\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEM\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	12	60.0	20 9 US-10-139-496-25	Sequence 25, Appl
C 2	12	60.0	25 9 US-09-754-853A-686	Sequence 686, Ap
C 3	12	60.0	25 9 US-10-098-263B-49318	Sequence 49318, A
C 4	12	60.0	25 9 US-10-098-263B-114611	Sequence 114611, A
C 5	11	55.0	12 9 US-09-938-744-2	Sequence 2, Appl
C 6	11	55.0	18 10 US-09-969-373-1923	Sequence 1923, Ap
C 7	11	55.0	19 9 US-09-879-389B-4	Sequence 4, Appl
C 8	11	55.0	19 9 US-09-902-563-38	Sequence 38, Appl
C 9	11	55.0	19 9 US-09-902-563-41	Sequence 38, Appl
C 10	11	55.0	19 9 US-10-096-255-38	Sequence 38, Appl
C 11	11	55.0	19 9 US-10-096-255-41	Sequence 38, Appl
C 12	11	55.0	19 10 US-09-947-770-26	Sequence 41, Appl
C 13	11	55.0	20 9 US-09-919-197-23	Sequence 23, Appl
C 14	11	55.0	24 9 US-10-101-487-12	Sequence 12, Appl
C 15	11	55.0	24 9 US-10-101-487-13	Sequence 13, Appl
C 16	11	55.0	24 10 US-09-818-954A-4	Sequence 4, Appl
C 17	11	55.0	25 9 US-09-943-388-16	Sequence 16, Appl
C 18	11	55.0	25 9 US-09-990-940-48	Sequence 48, Appl
C 19	11	55.0	25 9 US-10-215-112-2042	Sequence 2042, Ap

20	11	55.0	25 9 US-10-215-112-10695	Sequence 10695, A
C 21	11	55.0	25 9 US-10-215-112-12736	Sequence 12736, A
C 22	11	55.0	25 9 US-10-098-263B-9249	Sequence 9249, Ap
C 23	11	55.0	25 9 US-10-098-263B-17568	Sequence 17568, A
C 24	11	55.0	25 9 US-10-098-263B-24096	Sequence 24096, A
C 25	11	55.0	25 9 US-10-098-263B-48043	Sequence 48043, A
C 26	11	55.0	25 9 US-10-098-263B-48044	Sequence 48044, A
C 27	11	55.0	25 9 US-10-098-263B-48100	Sequence 48100, A
C 28	11	55.0	25 9 US-10-098-263B-50057	Sequence 50057, A
C 29	11	55.0	25 9 US-10-098-263B-50058	Sequence 50058, A
C 30	11	55.0	25 9 US-10-098-263B-56723	Sequence 56723, A
C 31	11	55.0	25 9 US-10-098-263B-56724	Sequence 56724, A
C 32	11	55.0	25 9 US-10-098-263B-67054	Sequence 67054, A
C 33	11	55.0	25 9 US-10-098-263B-81647	Sequence 81647, A
C 34	11	55.0	25 9 US-10-098-263B-81648	Sequence 81648, A
C 35	11	55.0	25 9 US-10-098-263B-96226	Sequence 96226, A
C 36	11	55.0	27 10 US-09-898-541-26	Sequence 26, Appl
C 37	11	55.0	29 9 US-10-210-327A-9	Sequence 9, Appl
C 38	11	55.0	37 12 US-10-014-927-14	Sequence 14, Appl
C 39	11	55.0	38 9 US-09-930-423-1068	Sequence 1068, Ap
C 40	11	55.0	38 9 US-10-104-943-86	Sequence 86, Appl
C 41	11	55.0	45 9 US-09-938-744-1	Sequence 1, Appl
C 42	11	55.0	45 9 US-10-013-803A-10	Sequence 10, Appl
C 43	11	55.0	45 10 US-09-482-520-2	Sequence 2, Appl
C 44	11	55.0	45 10 US-09-773-882-8	Sequence 8, Appl
C 45	11	55.0	46 9 US-10-085-108-5	Sequence 5, Appl

#### ALIGNMENTS

RESULT 1  
US-10-139-496-25/C  
Sequence 25, Application US/10139496  
Publication No. US2003082646A1  
GENERAL INFORMATION:  
APPLICANT: Carey, Thomas E.  
APPLICANT: Gray, Jennifer P.  
TITLE OF INVENTION: Anticneic Targets of Autoimmune Sensorineural Hearing Loss (AISHL)  
FILE REFERENCE: UM-6982  
CURRENT FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: US/10/139,496  
PRIOR FILING DATE: 1998-12-29  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 25  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-139-496-25

Query Match 60.0%; Score 12; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 17 TTCTCTTCTCTG 6

RESULT 2  
US-09-754-853A-686/C  
Sequence 686, Application US/09754853A  
Publication No. US20030005491A1  
GENERAL INFORMATION:  
APPLICANT: Hauge, Brian M.  
APPLICANT: Parnell, Laurence D.  
APPLICANT: Parsons, Jeremy D.

```

; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 686
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 318013_region_A3_151839_17_Reverse_Primer_Seq
US-09-754-853A-686

Query Match          60.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  TTCCCTCTCCG 14
DB      12 TTCCCTCTCCG 1

RESULT 3
US-10-098-263B-49318/c
; Sequence 49318, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49318
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-49318

Query Match          60.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  CTCTCTCTCGG 17
DB      14 CTCTCTCTCGG 3

RESULT 4
US-10-098-263B-114611
; Sequence 114611, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 114611
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-10-098-263B-114611
Query Match          60.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  GTTCCCTCTCCT 13
DB      6  GTTCCCTCTCCT 17

RESULT 5
US-09-938-744-2/c
; Sequence 2, Application US/09938744
; Patent No. US20020172954A1
; GENERAL INFORMATION:
; APPLICANT: Mao, Yumin
; APPLICANT: Xie, Yi
; TITLE OF INVENTION: METHOD FOR LARGE SCALE CDNA CLONING AND
; FILE REFERENCE: A34606-PCT-USA-A 072975.0111
; CURRENT APPLICATION NUMBER: US/09/938,744
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/CN00/00036
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: CN 99102450.8
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-938-744-2

Query Match          55.0%; Score 11; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9  TTCCTGCGGCC 19
DB      11 TTCCTGCGGCC 1

RESULT 6
US-09-969-373-1923/c
; Sequence 1923, Application US/09969373
; Patent No. US20020135852A1
; GENERAL INFORMATION:
; APPLICANT: Eifert, Roger J.
; APPLICANT: Haug, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1923
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1923

Query Match          55.0%; Score 11; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 CCTCTTCTG 15  
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Db 14 CCTCTTCTG 4

RESULT 7  
US-09-879-389B-4/c  
; Sequence 4, Application US/09879389B  
; Publication No. US20030032165A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20030032165A1ocymes A/S  
; APPLICANT: Wu, Wemping  
; APPLICANT: Ostergaard, Peter Rahbek  
; APPLICANT: Kauppinen, Markus Sakari  
; TITLE OF INVENTION: ASPARTIC ACID PROTEASES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 6123.200-US  
; CURRENT APPLICATION NUMBER: US/09/879,389B  
; CURRENT FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-879-389B-4

Query Match 55.0%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TTCCGCGGCGCC 19  
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Db 11 TTCCGCGGCGCC 1

RESULT 8  
US-09-902-563-38/c  
; Sequence 38, Application US/09902563  
; Publication No. US20030099654A1  
; GENERAL INFORMATION:  
; APPLICANT: Levy, Gary  
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation  
; FILE REFERENCE: 9579-37  
; CURRENT APPLICATION NUMBER: US/09/902,563  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 09/442,143  
; PRIOR FILING DATE: 1999-11-15  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-902-563-38

Query Match 55.0%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTG 14  
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Db 17 TCCTCTTCTG 7

RESULT 9  
US-09-902-563-41  
; Sequence 41, Application US/09902563  
; Publication No. US20030099654A1

; GENERAL INFORMATION:  
; APPLICANT: Levy, Gary  
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation  
; FILE REFERENCE: 9579-37  
; CURRENT APPLICATION NUMBER: US/09/902,563  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 09/442,143  
; PRIOR FILING DATE: 1999-11-15  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-902-563-41

Query Match 55.0%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTG 14  
|||  
Db 8 TCCTCTTCTG 18

RESULT 10  
US-10-096-255-38/c  
; Sequence 38, Application US/10096255  
; Publication No. US20030103974A1  
; GENERAL INFORMATION:  
; APPLICANT: Levy, Gary  
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation  
; FILE REFERENCE: 9579-52  
; CURRENT APPLICATION NUMBER: US/10/096,255  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/046,537  
; PRIOR FILING DATE: 1997-05-17  
; PRIOR APPLICATION NUMBER: US 60/061,684  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-096-255-38

Query Match 55.0%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTG 14  
|||  
Db 17 TCCTCTTCTG 7

RESULT 11  
US-10-096-255-41  
; Sequence 41, Application US/10096255  
; Publication No. US20030103974A1  
; GENERAL INFORMATION:  
; APPLICANT: Levy, Gary  
; APPLICANT: Clark, David A.  
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation  
; FILE REFERENCE: 9579-52  
; CURRENT APPLICATION NUMBER: US/10/096,255  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/046,537

PRIOR FILING DATE: 1997-05-17  
PRIOR APPLICATION NUMBER: US 60/061,684  
PRIOR FILING DATE: 1997-10-10  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 41

LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-10-036-255-41

Query Match 55.0%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred.No. 5.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCCTCTTCTG 14  
Db 8 TCCTCTTCTG 18

RESULT 12  
US-09-947-770-26  
Sequence 26, Application US/09947770  
Patent No. US20020068715A1  
GENERAL INFORMATION:  
APPLICANT: Steinman, Lawrence  
APPLICANT: Ruiz, Pedro  
TITLE OF INVENTION: DNA Vaccination for Treatment of  
FILE REFERENCE: STAN123CIP  
CURRENT APPLICATION NUMBER: US/09/947,770  
PRIOR FILING DATE: 2001-09-05  
PRIOR APPLICATION NUMBER: PCT/US00/06233  
PRIOR FILING DATE: 2000-03-10  
PRIOR APPLICATION NUMBER: US 09/267,590  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: IFN-gamma primer  
US-09-947-770-26

Query Match 55.0%; Score 11; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred.No. 5.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TCCTGCGGCT 20  
Db 1 TCCTGCGGCT 11

RESULT 13  
US-09-919-197-23/c  
Sequence 23, Application US/09919197  
Publication No. US20030083484A1  
GENERAL INFORMATION:  
APPLICANT: Rosanne M. Crooke  
APPLICANT: Mark J. Graham  
TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION  
FILE REFERENCE: ISPH-0593  
CURRENT APPLICATION NUMBER: US/09/919,197  
PRIOR FILING DATE: 2001-07-31  
NUMBER OF SEQ ID NOS: 89  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 23  
LENGTH: 20

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-919-197-23

Query Match 55.0%; Score 11; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred.No. 5.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCTCTTCTGC 15  
Db 20 CCTCTTCTGC 10

RESULT 14  
US-10-101-487-12/c  
Sequence 12, Application US/10101487  
Patent No. US20020169125A1  
GENERAL INFORMATION:  
APPLICANT: LEUNG, DAVID W.  
APPLICANT: BERGMAN, PHILIP A.  
APPLICANT: LOFOUST, ALAN  
APPLICANT: PIETZ, GREGORY E.  
APPLICANT: TOMPKINS, CHRISTOPHER K.  
APPLICANT: MAGONER JR., DAVID W.  
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES  
FILE REFERENCE: 077319/0329  
CURRENT APPLICATION NUMBER: US/10/101,487  
PRIOR FILING DATE: 2002-03-20  
PRIOR APPLICATION NUMBER: 60/277,705  
PRIOR FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-101-487-12

Query Match 55.0%; Score 11; DB 9; Length 24;  
Best Local Similarity 100.0%; Pred.No. 5.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCTCTTCTCT 13  
Db 22 TTCTCTTCTCT 12

RESULT 15  
US-10-101-487-13  
Sequence 13, Application US/10101487  
Patent No. US20020169125A1  
GENERAL INFORMATION:  
APPLICANT: LEUNG, DAVID W.  
APPLICANT: BERGMAN, PHILIP A.  
APPLICANT: LOFOUST, ALAN  
APPLICANT: PIETZ, GREGORY E.  
APPLICANT: TOMPKINS, CHRISTOPHER K.  
APPLICANT: MAGONER JR., DAVID W.  
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES  
FILE REFERENCE: 077319/0329  
CURRENT APPLICATION NUMBER: US/10/101,487  
PRIOR FILING DATE: 2002-03-20  
PRIOR APPLICATION NUMBER: 60/277,705  
PRIOR FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 13
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-101-487-13

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Query Match      55.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      3 TTCTCTTCTTCT 13
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Db      7 TTCTCTTCTTCT 17

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Search completed: June 23, 2003, 20:01:28  
 Job time : 160.717 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 31.3147 Seconds  
(without alignments)  
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Title: US-08-770-564A-3

Perfect score: 20

Sequence: 1 CGTTCCTCTCTCGCGCCT 20

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:  
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3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
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5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	ID	Description
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2	20	100.0	20 2 US-08-833-377-7	Sequence 7, Appli
3	20	100.0	20 2 US-08-770-565-2	Sequence 2, Appli
4	19	95.0	20 2 US-08-833-377-14	Sequence 14, Appli
5	14	70.0	29 3 US-09-121-321-14	Sequence 14, Appli
6	14	70.0	29 4 US-08-933-803A-14	Sequence 14, Appli
7	13	65.0	20 2 US-08-534-479-1	Sequence 1, Appli
8	13	65.0	31 2 US-08-576-626A-15	Sequence 15, Appli
9	13	65.0	42 1 US-08-487-037-8	Sequence 8, Appli
10	12	60.0	45 1 US-08-487-037-9	Sequence 9, Appli
11	12	60.0	12 2 US-08-770-565-4	Sequence 4, Appli
12	12	60.0	20 1 US-08-031-143B-6	Sequence 6, Appli
13	12	60.0	20 1 US-08-031-143B-3	Sequence 3, Appli
14	12	60.0	20 5 PCT-US94-02891-6	Sequence 6, Appli
15	12	60.0	20 5 PCT-US94-02891-33	Sequence 33, Appli
16	12	60.0	33 4 US-08-090-369-15	Sequence 15, Appli
17	12	60.0	33 4 US-09-482-971-15	Sequence 15, Appli
18	11	55.0	11 1 US-08-126-594-5	Sequence 5, Appli
19	11	55.0	11 1 US-08-465-811A-5	Sequence 5, Appli
20	11	55.0	11 2 US-08-619-542B-5	Sequence 5, Appli
21	11	55.0	11 2 US-08-619-542B-48	Sequence 48, Appli
22	11	55.0	12 1 US-08-126-594-6	Sequence 6, Appli
23	11	55.0	12 1 US-08-465-811A-6	Sequence 6, Appli
24	11	55.0	12 2 US-08-294-424-33	Sequence 33, Appli
25	11	55.0	14 1 US-08-251-645-21	Sequence 21, Appli
26	11	55.0	18 4 US-09-442-143A-38	Sequence 38, Appli
27	11	55.0	19 4 US-09-442-143A-38	Sequence 38, Appli

28	11	55.0	19 4 US-09-442-143A-41	Sequence 41, Appli
29	11	55.0	20 1 US-08-068-945A-8	Sequence 8, Appli
30	11	55.0	20 1 US-08-442-806-8	Sequence 8, Appli
31	11	55.0	20 2 US-08-206-790A-18	Sequence 18, Appli
32	11	55.0	20 3 US-08-589-939-40	Sequence 40, Appli
33	11	55.0	20 4 US-09-258-377-30	Sequence 30, Appli
34	11	55.0	20 4 US-09-851-896-86	Sequence 86, Appli
35	11	55.0	20 5 PCT-US95-02943-18	Sequence 18, Appli
36	11	55.0	21 6 5177193-10	Patent No. 5177193
37	11	55.0	22 1 US-07-820-412-8	Sequence 8, Appli
38	11	55.0	22 1 US-08-611-155B-1	Sequence 1, Appli
39	11	55.0	22 1 US-08-611-155B-2	Sequence 2, Appli
40	11	55.0	22 1 US-08-611-155B-3	Sequence 3, Appli
41	11	55.0	22 1 US-08-611-155B-4	Sequence 4, Appli
42	11	55.0	22 1 US-08-611-155B-5	Sequence 5, Appli
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45	11	55.0	22 2 US-08-916-120A-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-770-565-3  
Sequence 3, Application US/08770565  
Patent No. 5846723

GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-3

Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTCCTCTCTCGCGCCT 20

Db 1 CGTTCCTCTTCTCGGGCCT 20

RESULT 2  
US-08-833-377-7  
Sequence 7, Application US/08833377  
Patent No. 5968506  
GENERAL INFORMATION:  
APPLICANT: Weinrich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichterstein, Serge P.  
APPLICANT: Vassero, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833.377  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510.736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note="Oligo 14ab"  
US-08-833-377-7  
Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.061; 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CGTTCCTCTTCTCGGGCCT 20  
Db 1 CGTTCCTCTTCTCGGGCCT 20  
RESULT 3  
US-08-770-565-2  
Sequence 2, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
Telomerase  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770.565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-2  
Query Match 100.0%; Score 20; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.06; 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CGTTCCTCTTCTCGGGCCT 20  
Db 1 CGTTCCTCTTCTCGGGCCT 20  
RESULT 4  
US-08-833-377-14  
Sequence 14, Application US/08833377  
Patent No. 5968506  
GENERAL INFORMATION:  
APPLICANT: Weinrich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichterstein, Serge P.  
APPLICANT: Vassero, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833.377



FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1  
OTHER INFORMATION: /mod\_base= OTHER  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note= "N = 5' biotinylated cytidine"  
US-08-833-377-14

Query Match 95.0%; Score 19; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCTCTCTCGCGCCT 20  
Db 2 GTTCCTCTCTCGCGCCT 20

RESULT 5  
US-09-121-321-14/C  
Sequence 14, Application US/09121321  
Patent No. 6090783  
GENERAL INFORMATION:  
APPLICANT: Saiga, Akihiko  
APPLICANT: Orita, Satoshi  
APPLICANT: Igarashi, Hisanaga  
APPLICANT: Okumura, Kouichi  
APPLICANT: Sakaguchi, Gaku  
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/121.321  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/933,803  
FILING DATE: 19-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.

REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-12CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-09-121-321-14

Query Match 70.0%; Score 14; DB 3; Length 29;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTCTTCTCGCGCC 19  
Db 19 CTCTTCTCGCGCC 6

RESULT 6  
US-08-933-803A-14/C  
Sequence 14, Application US/08933803A  
Patent No. 6218522  
GENERAL INFORMATION:  
APPLICANT: Saiga, Akihiko  
APPLICANT: Orita, Satoshi  
APPLICANT: Igarashi, Hisanaga  
APPLICANT: Okumura, Kouichi  
APPLICANT: Sakaguchi, Gaku  
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,803A  
FILING DATE: 19-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-12CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-08-933-803A-14

Query Match 70.0%; Score 14; DB 4; Length 29;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Jun 27 07:42:22 2003

us-08-770-564a-3.01lgo.rml

Page 4

QY 6 CTCTCTCGGCGCC 19  
DB 19 CTCTCTCGGCGCC 6

RESULT 7  
US-08-534-479-1  
Sequence 1, Application US/08534479

GENERAL INFORMATION:  
APPLICANT: GREY, HEINZ-URICH G.  
TITLE OF INVENTION: QUANTITATIVE FIBER MAPPING  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,479  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MACKNIGHT, KAREN T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: LBL-01754  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 97-8338  
TELEFAX: (415) 705-8410  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-534-479-1

Query Match 65.0%; Score 13; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0

QY 3 TTCCCTTCTCTGC 15  
DB 1 TTCCCTTCTCTGC 13

RESULT 8  
US-08-576-626a-15/c  
Sequence 15, Application US/08576626a

GENERAL INFORMATION:  
PATENT NO. 5996194  
APPLICANT: SUMMERS, R.G.  
APPLICANT: KATZ, L.S.  
APPLICANT: DONADIO, S.J.  
APPLICANT: SCAVER, W.J.  
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESS: 100 Abbott Park Road  
CITY: ABBOTT PARK  
STATE: ILLINOIS

COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS Version 2.0  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/576,626A  
FILING DATE: 21 435  
CLASSIFICATION: 210  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: DIERME CASULO  
REGISTRATION NUMBER: P-40,943  
REFERENCE/DOCKET NUMBER: 5857-US-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (847) 938-3137  
TELEFAX: (847) 938-2623  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-576-626a-15

Query Match 65.0%; Score 13; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0

QY 8 CTCTCTCGGCGCT 20  
DB 19 CTCTCTCGGCGCT 7

RESULT 9  
US-08-487-037-8/c  
Sequence 8, Application US/08487037

GENERAL INFORMATION:  
PATENT NO. 5793653  
APPLICANT: WOLF, DAVID L.  
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESS: MORRISON & FORSTER  
ADDRESS: 2000 Pennsylvania Avenue, NW  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,037  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 3143  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REBECCAH G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0002.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-037-8

Query Match 65.0%; Score 13; DB 1; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTGCG 16  
|||||  
DB 22 TCCTCTCTCTGCG 10

RESULT 10  
US-08-487-037-9/C  
Sequence 9, Application US/08487037  
Patent No. 5795863

GENERAL INFORMATION:  
APPLICANT: Wolf, David L.  
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS  
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,037

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.

REGISTRATION NUMBER: 30,988

REFERENCE/DOCKET NUMBER: 2803-0002.02

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-487-037-9

Query Match 65.0%; Score 13; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTGCG 16  
|||||  
DB 22 TCCTCTCTCTGCG 10

RESULT 11  
US-08-770-565-4

Sequence 4, Application US/08770565  
Patent No. 5846723

GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo

APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
TITLE OF INVENTION: Telomerase  
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002300US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-565-4

Query Match 60.0%; Score 12; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12  
|||||  
DB 1 CGTTCCTCTTCC 12

RESULT 12  
US-08-031-143B-6/C

Sequence 6, Application US/08031143B  
Patent No. 5518880

GENERAL INFORMATION:

APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;

APPLICANT: MCBRIDE, O. WESLEY

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND

TITLE OF INVENTION: TREATMENT OF XSCID

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVE.

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORD PERFECT # 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/031,143B

FILING DATE: 12-MAR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILLIAM S. FEILER

REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R  
US-08-031-143B-6

Query Match 60.0%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCT 13  
|||  
Db 18 GTTCTCTTCTCT 7

RESULT 13  
US-08-031-143B-33  
Sequence 33, Application US/08031143B  
Patent No. 5518880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
APPLICANT: MCBRIDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,143B  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R  
US-08-031-143B-33

Query Match 60.0%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCT 13  
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Db 3 GTTCTCTTCTCT 14

RESULT 14  
PCT-US94-02891-6/c  
Sequence 6, Application PC/TUS9402891  
GENERAL INFORMATION:  
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN  
SERVICES  
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL  
INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF  
XSCID  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02891  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/031,143  
FILING DATE: 12-MAR-1993  
APPLICATION NUMBER: 08/121,435  
FILING DATE: 14-SEPT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: OLIGONUCLEOTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R  
PCT-US94-02891-6

Query Match 60.0%; Score 12; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 31.3147 secs

Qy 2 GTTCTCTTCT 13  
 |||||  
 Db 18 GTTCTCTTCT 7

RESULT 15  
 PCT-US94-02891-33

; Sequence 33, Application PC/TUS9402891

; GENERAL INFORMATION:

; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS

; APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN

; APPLICANT: SERVICES

; APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL

; APPLICANT: INSTITUTES OF HEALTH, BOX 077, BETHESDA, MARYLAND 20892 USA

; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

; TITLE OF INVENTION: XSCID

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVE.

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORD PERFECT # 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/02891

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/031,143

; FILING DATE: 12-MAR-1993

; APPLICATION NUMBER: 08/121,435

; FILING DATE: 14-SEPT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAM S. FEILER

; REGISTRATION NUMBER: 26,728

; REFERENCE/DOCKET NUMBER: 2026-4061

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-4800

; TELEFAX: 212-751-6849

; TELEK: 421792

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: UNKNOWN

; MOLECULE TYPE:

; DESCRIPTION: OLIGONUCLEOTIDE

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: HUMAN

; INDIVIDUAL ISOLATE: IL-2R

; PCT-US94-02891-33

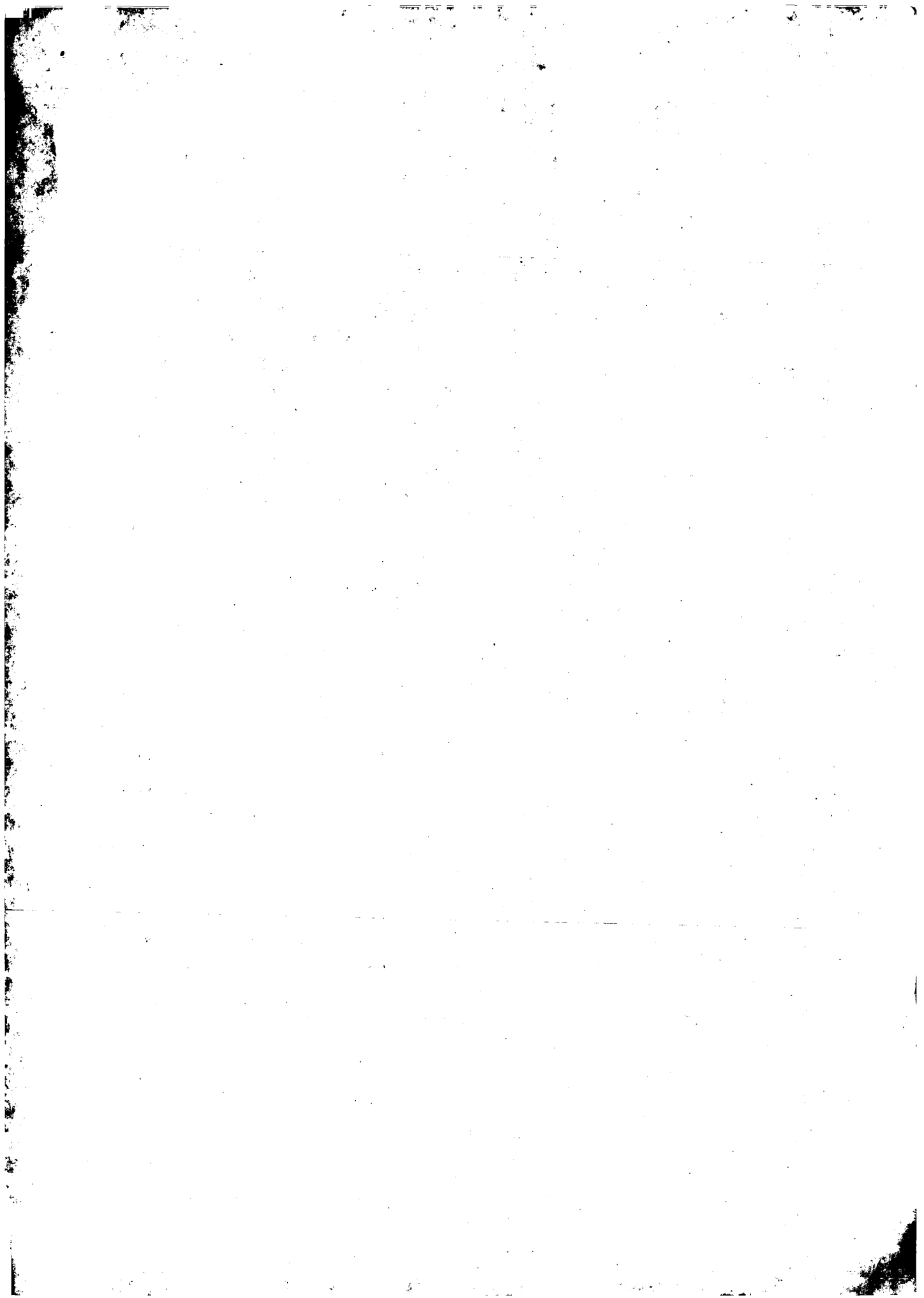
Query Match 60.0%; Score 12; DB 5; Length 20;

Best Local Similarity 100.0%; Pred.No. 5.9e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCTCTTCT 13  
 |||||  
 Db 3 GTTCTCTTCT 14

Search completed: June 23, 2003, 10:17:03



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 132.908 seconds  
(without alignments)  
338.880 Million cell updates/sec

Title: US-08-770-564a-3

Perfect score: 20

Sequence: 1 CGTCCCTCTCTCGCGCCT 20

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size: 0

2166140

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database: N\_Geneseq\_101002.\*

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	100.0	20	19	AAV71226
3	20	100.0	20	19	AAV41170
4	20	100.0	20	20	AAZ23632
5	20	100.0	20	20	AAZ23636
6	20	100.0	20	22	AAZ09477
7	20	100.0	20	22	AAZ09480
8	20	100.0	30	19	AAV41169
9	14	70.0	29	17	AAZ42916
	13	65.0	21	17	AAZ36484

10	13	65.0	21	21	AAZ72585	Upstream PCR prime
11	13	65.0	21	22	AAZ47842	Human p53 PCR prim
12	13	65.0	31	18	AAZ72696	Sugar biosynthesis
13	13	65.0	50	22	AAZ34593	Human SNP oligonuc
14	12	60.0	12	19	AAV41171	RNA component of h
15	12	60.0	20	15	AAQ71941	Human IL-2R gamma
16	12	60.0	20	15	AAQ71914	Human IL-2R gamma
17	12	60.0	20	19	AAV45148	Human saptiens P-TEN
18	12	60.0	20	20	AAZ94325	PCR primer used to
19	12	60.0	21	22	AAZ62356	RBP2 polymorphism
20	12	60.0	24	15	AAQ57316	Enzymatic RNA mole
21	12	60.0	25	22	AAI62055	Soybean 318013 reg
22	12	60.0	27	22	AAZ87709	Human glutathione
23	12	60.0	31	21	AAZ79024	Human genomic DNA
24	12	60.0	33	14	AAQ49474	Primer "a332" to a
25	12	60.0	37	24	ABA01509	EryCIII PCR primer
26	12	60.0	40	17	AAZ70784	Stenotic carotid a
27	12	60.0	40	17	AAZ70788	Stenotic carotid a
28	12	60.0	40	17	AAZ70789	Stenotic carotid a
29	11	55.0	14	13	AAZ02598	Predicted HPV-18 e
30	11	55.0	15	22	AAZ04286	ASO primer #2 for
31	11	55.0	15	22	AAZ04288	ASO primer #4 for
32	11	55.0	19	24	AAZ27185	Pseudozyma species
33	11	55.0	20	15	AAQ54225	BSSL/CEL Exon 10/1
34	11	55.0	20	16	AAQ09139	DNA antisense prim
35	11	55.0	20	20	AAZ23347	Bacillus amyloliqu
36	11	55.0	20	20	AAZ95176	PCR primer used to
37	11	55.0	20	21	AAZ68884	Dog genomic marker
38	11	55.0	20	21	AAZ07908	He-Unc-53/2 specif
39	11	55.0	20	21	AAZ88913	Human wolfram ex
40	11	55.0	20	22	AAZ09927	Short consensus am
41	11	55.0	20	24	AAZ40301	Human catpase 6 an
42	11	55.0	20	24	ABA01570	HLA class I micros
43	11	55.0	21	21	AAZ75837	Human biallelic ma
44	11	55.0	21	21	AAZ76054	Human biallelic ma
45	11	55.0	21	21	AAZ11686	Human GABA-B recep

## ALIGNMENTS

RESULT 1	
AAV71226	
ID	AAV71226 standard; DNA; 20 BP.
AC	AAV71226;
XX	
DT	15-FEB-1999 (first entry)
XX	
DE	Antisense oligonucleotide 14ab for human telomerase RNA component.
XX	
KW	Human; telomerase RNA component; anticancer therapy; purification;
KW	assay; vaccine; cancer; antisense oligonucleotide; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1
FT	/*tag= a
XX	/note= "biotinylated"
XX	
PN	W09845450-A1.
XX	
PD	15-OCT-1998.
XX	
PF	04-APR-1997; 97WO-US06012.
XX	
PR	04-APR-1997; 97WO-US06012.
XX	
PA	(GERO-) GERON CORP.
XX	
PI	Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA;

PI Vassero AP, Weinrich SL;  
XX  
DR WPI; 1998-594485/50.  
XX  
PT Purification of telomerase on affinity material - useful for, e.g.  
PT diagnosis and treatment of cancer  
XX  
PS Claim 6; Page 61; 76pp; English.

XX The present sequence represents an antisense oligonucleotide  
CC directed against the human telomerase RNA component gene sequences.  
CC The oligonucleotide can be used as an affinity agent in the methods of  
CC the invention, which are used to purify human telomerase. The methods  
CC involve the use of several sequential steps, including the use of two  
CC matrices that bind molecules bearing negative charges, a matrix that  
CC binds molecules bearing positive charges, an affinity purification step  
CC and a size separation. Telomerase is a particular target of anticancer  
CC therapies, and is useful in assays for characterizing (pre)cancerous  
CC cells. Telomerase can also be used to screen for specific modulators,  
CC for biochemical analysis of its activity, and in preparation of  
CC antibodies. Fragments of telomerase, or nucleic acid encoding them,  
CC are used in vaccines, and for treating over expression of telomerase,  
CC particularly in cancer.

SQ Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCTCTCGGCGCT 20  
DB 1 CGTTCCTCTCTCTCGGCGCT 20

RESULT 2  
AAV41170  
ID AAV41170 standard; DNA; 20 BP.  
XX  
AC AAV41170;

DT 08-OCT-1998 (first entry)

DE RNA component of human telomerase (hTR) antisense oligo 14ab.

XX RNA component; human telomerase; antisense oligonucleotide; infection;  
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;  
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;  
KW immune system down-regulation; anti-inflammatory therapy; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9828442-A1.

PD 02-JUL-1998.

PP 19-DEC-1997; 97WO-US23619.

XX 20-DEC-1996; 96US-0770565.

PR 20-DEC-1996; 96US-0770564.

XX (GERO-) GERON CORP.

PI Kealey JT, Kim NM, Pruzan R, Weinrich SL, Wu F;

DR WPI; 1998-377670/32.

XX New polynucleotide(s) anti-sense to human telomerase - used for  
PT detecting or inhibiting human telomerase, e.g. for treating cancers,  
PT contraception, immuno-suppression or treating infection  
XX Claim 11; Page 65; 80pp; English.

XX Sequences shown in AAV41169 to AAV41181 represent antisense  
CC oligonucleotides to the RNA component of human telomerase (hTR). These  
CC antisense oligonucleotides specifically hybridise to a nucleotide  
CC sequence within an accessible region of the hTR, but that does not  
CC hybridise to a sequence within the template region of hTR. These  
CC oligonucleotides may specifically be used for detection of an RNA  
CC component of human telomerase in a sample. This is useful for diagnosing  
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),  
CC and providing prognosis for a cancer patient. The inhibitory  
CC oligonucleotides can inhibit the telomerase activity level in a cell by  
CC interfering with transcription of the RNA component, decreasing the  
CC half-life of the telomerase RNA component transcript, inhibiting the  
CC polymerase activity of telomerase. These antisense oligonucleotides can  
CC be used for inhibiting telomerase activity in both cultured cells and in  
CC cells in vivo. They can be used in therapeutics for treating or  
CC preventing cancer, for contraception or sterilisation, for  
CC immunosuppression, and for selectively down-regulating specific branches  
CC of the immune system, e.g. a specific subset of T-cells, in  
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,  
CC parasites or fungi.

SQ Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCTCTCGGCGCT 20  
DB 1 CGTTCCTCTCTCTCGGCGCT 20

RESULT 3  
AAZ23632  
ID AAZ23632 standard; DNA; 20 BP.  
XX  
AC AAZ23632;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide 14ab.

XX Telomerase; human; immune response; cancer; vaccine; treatment;

KW disease; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX US5968506-A.

PD 19-OCT-1999.

PP 04-APR-1997; 97US-0833377.

XX 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;

PI Vassero AP;

DR WPI; 1999-590379/50.

XX Compositions comprising human telomerase, useful for treating diseases  
PT associated with overexpression of telomerase e.g. cancer -

XX Disclosure; Column 45-46; 34pp; English.

XX This invention describes a novel composition comprising human telomerase  
CC having at least 2000-fold (preferably at least 6000-fold) increased  
CC relative purity compared with crude extract of cells from



CC adenovirus-transformed kidney cell line. The composition is useful for  
CC eliciting an immune response in animals and may therefore be used as a  
CC vaccine for treating diseases associated with the overexpression of  
CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used  
CC in the isolation of human clone 28-1 which contains a fragment of the  
CC human telomerase described in the method of the invention.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTCGGCGCT 20  
DB 1 CGTTCCTCTTCTCGGCGCT 20

RESULT 4  
AA223636  
ID AA223636 standard; DNA; 20 BP.

AC AA223636;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide oligo 14ab.

KW Telomerase; human; immune response; cancer; vaccine; treatment;  
KW disease; primer; ss.

OS Synthetic.  
OS Homo sapiens.

FT Key Location/Qualifiers  
FT modified\_base 1  
FT /\*tag= a  
FT /note= "5'-biotinylated cytidine"

PN US5968506-A.

PD 19-OCT-1999.

PF 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;  
PI Vaaserot AP;

DR WPI; 1999-590379/50.

PT Compositions comprising human telomerase, useful for treating diseases  
PT associated with overexpression of telomerase e.g. cancer -

PS Disclosure; Column 49-50; 34pp; English.

XX This invention describes a novel composition comprising human telomerase  
CC having at least 2000-fold (preferably at least 6000-fold) increased  
CC relative purity compared with crude extract of cells from  
CC adenovirus-transformed kidney cell line. The composition is useful for  
CC eliciting an immune response in animals and may therefore be used as a  
CC vaccine for treating diseases associated with the overexpression of  
CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used  
CC in the isolation of human clone 28-1 which contains a fragment of the  
CC human telomerase described in the method of the invention.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTCCTCTTCTCGGCGCT 20  
DB 1 CGTTCCTCTTCTCGGCGCT 20

RESULT 5  
AAS09477  
ID AAS09477 standard; DNA; 20 BP.

AC AAS09477;

DT 24-OCT-2001 (first entry)

DE Antisense oligonucleotide for human telomerase, Oligo 14ab #1.

KW Human; Telomerase; vaccine; antibody; cancer; EF2H;  
KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

OS Homo sapiens.

PN US6261556-B1.

PD 17-JUL-2001.

PF 18-OCT-1999; 99US-0420056.

PR 04-APR-1997; 97US-0833377.  
PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vaaserot AP, Pruzan RA;  
PI Kealey JT;

DR WPI; 2001-450477/48.

PT Purified human telomerase, useful for inducing immune response in  
PT animals, comprises several thousand folds increased purity compared  
PT with cytoplasmic crude cell preparations -

PS Disclosure; Column 2; 29pp; English.

XX The sequence represents an antisense oligonucleotide used in  
CC the purification of human telomerase. The invention relates  
CC to a purified human telomerase core enzyme protein comprising  
CC 2000-fold increased purity compared with a crude extract of cells from  
CC adenovirus-transformed kidney cell line (293 cells) and when associated  
CC with telomerase RNA component has DNA polymerase activity and a molecular  
CC weight of 200-2000 kilo Daltons (kDa). The purified telomerase is useful  
CC for inducing a humoral or cell-mediated immune response in an animal.  
CC Purified telomerase or immunogenic fragments are useful as vaccines for  
CC treating diseases associated with over-expression of telomerase, such as  
CC cancer and for producing antibodies that recognize telomerase, which are  
CC useful as affinity agents in isolating the proteins and for detecting the  
CC presence of proteins in a sample, such as cell or tissue. Identification  
CC of telomerase aids in diagnosis of cancer or pre-cancerous states.  
CC Telomerase and/or telomerase associated proteins are also useful for  
CC screening compounds to identify agents that alter the association of  
CC telomerase-associated proteins, such as nucleolin or EF2H with  
CC telomerase.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTCGGCGCT 20  
DB 1 CGTTCCTCTTCTCGGCGCT 20

```
RESULT 6
ID AAS09480
AC AAS09480 standard; DNA; 20 BP.
XX
AC AAS09480;
XX
DT 24-OCT-2001 (first entry)
XX
DE Antisense oligonucleotide for human telomerase, Oligo 14ab #2.
XX
KW Human; Telomerase; vaccine; antibody; cancer; EP2H;
KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= C
FT /note= "C is biotinylated"
XX
PN US6261556-B1.
XX
PD 17-JUL-2001.
XX
PP 18-OCT-1999; 99US-0420056.
XX
PR 04-APR-1997; 97US-0833377.
XX
PR 04-AUG-1995; 95US-0510736.
XX
PA (GERO-) GERON CORP.
XX
PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vaasero AP, Pruzan RA;
PI Kealey JT;
PI WPI; 2001-450477/48.
XX
DR Purified human telomerase, useful for inducing immune response in
PT animals, comprises several thousand folds increased purity compared
PT with cytoplasmic crude cell preparations -
XX
PS Disclosure; Column 18; 29pp; English.
XX
CC The sequence represents a biotinylated antisense oligonucleotide
CC used in the purification of human telomerase. The invention
CC relates to a purified human telomerase core enzyme protein comprising
CC 2000-fold increased purity compared with a crude extract of cells from
CC adenovirus-transformed kidney cell line (293 cells) and when associated
CC with telomerase RNA component has DNA polymerase activity and a molecular
CC weight of 200-2000 kilo Daltons (kDa). The purified telomerase is useful
CC for inducing a humoral or cell-mediated immune response in an animal.
CC Purified telomerase or immunogenic fragments are useful as vaccines for
CC treating diseases associated with over-expression of telomerase, such as
CC cancer and for producing antibodies that recognize telomerase, which are
CC useful as affinity agents in isolating the proteins and for detecting the
CC presence of proteins in a sample, such as cell or tissue. Identification
CC of telomerase aids in diagnosis of cancer or pre-cancerous states.
CC Telomerase and/or telomerase associated proteins are also useful for
CC screening compounds to identify agents that alter the association of
CC telomerase-associated proteins, such as nucleolin or EP2H with
CC telomerase.
XX
SQ Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.45; 0; Indels 0;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
OY 1 CGTTCCTCTCTCTCGGCGCT 20
DB 1 CGTTCCTCTCTCTCGGCGCT 20
```

```
RESULT 7
ID AAV41169
AC AAV41169 standard; DNA; 30 BP.
XX
AC AAV41169;
XX
DT 08-OCT-1998 (first entry)
XX
DE RNA component of human telomerase (hTR) antisense oligo 14.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
XX
FH Homo sapiens.
XX
FT WO9828442-A1.
XX
PN 02-JUL-1998.
XX
PP 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
XX
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
PI WPI; 1998-377670/32.
XX
DR New polynucleotide(s) anti-sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Claim 11; Page 65; 80pp; English.
XX
CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC assembly of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 30 BP; 4 A; 10 C; 8 G; 8 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.44; 0; Indels 0;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
OY 1 CGTTCCTCTCTCTCGGCGCT 20
DB 1 CGTTCCTCTCTCTCGGCGCT 20
```

```

RESULT 8
AAAT42916/c
ID   AAT42916 standard; DNA; 29 BP.
XX
XX
AC   AAT42916;
XX
XX
DT   16-JUN-1997 (first entry)
XX
DE   Primer 8201RN, amplifies TSP-1 and gene regulation sequences.
XX
XX
KW   gene expression; regulation; plasmid; viral infection;
KW   human T-cell leukaemia; HIV; antiviral agent; detection; cancer;
KW   gene therapy; TSP; ss.
XX
XX
OS   Synthetic.
XX
XX
PN   WO9630522-A1.
XX
XX
PD   03-OCT-1996.
XX
XX
PF   19-MAR-1996; 96WO-JP00719.
XX
XX
PR   27-APR-1995; 95JP-0104299.
XX
XX
PR   24-MAR-1995; 95JP-0065559.
XX
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
XX
PI   Igaraishi H, Okumura K, Orita S, Saiga A, Sakaguchi G;
XX
XX
DR   WPI; 1996-455367/45.
XX
XX
PT   DNA molecule with gene expression regulation activity - for use in
PT   e.g. treatment of human T-cell leukemia and HIV, as antiviral agent
PT   and for detecting cancer
XX
XX
PS   Example 1; Page 48; 77pp; Japanese.
XX
XX
CC   The sequences given in AAT42904-16 are primers which were used in the
CC   construction of the plasmid of the invention. The plasmid contains a
CC   DNA sequence encoding the protein TSP-1 in conjunction with a DNA
CC   molecule with gene expression regulation activity. The plasmid is
CC   used for regulation of gene expression, and treatment of viral
CC   infection pref. human T-cell leukemia and HIV. The plasmid also encodes
CC   a protein which is used as an antiviral agent, and also in a method for
CC   detecting cancer. The DNA molecule and protein have potential uses in
CC   gene therapy, and the plasmid may also have potential use in the
CC   treatment of TSP.
XX
XX
SQ   Sequence 29 BP; 8 A; 5 C; 10 G; 6 T; 0 other;
XX

Query Match      70.0%; Score 14; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   6 CTCTTCTGCGGCC 19
    |||||
DB   19 CTCTTCTGCGGCC 6

RESULT 9
AAT36484
ID   AAT36484 standard; DNA; 21 BP.
XX
XX
AC   AAT36484;
XX
XX
DT   09-OCT-1996 (first entry)
XX
XX
DE   Upstream PCR primer for p53 gene region contg. Val 143 Ala mutation.
XX
XX
KW   Primer; PCR; polymerase chain reaction; amplification; human;
KW   p53 gene; tumour; cancer; Cx3; mutation; Val 143 Ala; assay;
KW   HhaI cleavage site; detection; gel electrophoresis; diagnosis;
KW   radioactive probe hybridisation; nude mouse xenograft; ss.

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XX
XX
OS   Synthetic.
XX
XX
PN   US5527676-A.
XX
XX
PD   18-JUN-1996.
XX
XX
PF   29-MAR-1989; 89US-0330566.
XX
XX
PR   06-DEC-1989; 89US-0446584.
XX
XX
PR   29-MAR-1989; 89US-0330566.
XX
XX
PR   17-AUG-1992; 92US-0928661.
XX
XX
PR   22-MAR-1993; 93US-0047041.
XX
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
XX
PI   Baker SJ, Fearon ER, Nigro JM, Vogelstein B;
XX
XX
DR   WPI; 1996-299851/30.
XX
XX
PT   Nucleic acid assay for cancer detection - based on comparing
PT   neoplastic p53 gene with wild-type p53 gene
XX
XX
PS   Example 4; Column 10; 38pp; English.
XX
XX
CC   The primer pair AAT36484/85 was used for the PCR amplification of a
CC   111 bp fragment of the human p53 gene, which may contain the tumour
CC   nude mouse xenograft (Cx3) mutation. Val 143 Ala, where the wild
CC   type codon 143 GTG is substd. with GCG. This mutation also
CC   introduces a new HhaI site (GCGC at nucleotides 427-430), so that
CC   HhaI cleavage of a PCR prod. amplified from a mutant template
CC   produces 68 and 43 nucleotide subfragments, which can be detected
CC   by gel electrophoresis separation, followed by radioactive probe
CC   hybridisation. This assay can be used to diagnose the presence of
CC   the Val 143 Ala mutation, and therefore the Cx3 tumour.
XX
XX
SQ   Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;
XX

Query Match      65.0%; Score 13; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   3 TTCTCTTCTGCG 15
    |||||
DB   1 TTCTCTTCTGCG 13

RESULT 10
AAA72585
ID   AAA72585 standard; DNA; 21 BP.
XX
XX
AC   AAA72585;
XX
XX
DT   27-NOV-2000 (first entry)
XX
XX
DE   Upstream PCR primer for mutant p53 gene fragment amplification.
XX
XX
KW   Human; p53; chromosome 17p; neoplastic tissue detection; lung; breast;
KW   brain; colorectal; bladder; mesenchyme; prostate; stomach; cancer;
KW   tumour; leukemia; osteosarcoma; PCR primer; ss.
XX
XX
OS   Homo sapiens.
XX
XX
PN   US6090566-A.
XX
XX
PD   18-JUL-2000.
XX
XX
PF   02-JUN-1995; 95US-0459676.
XX
XX
PR   22-MAR-1993; 93US-0047041.
XX
XX
PR   06-DEC-1989; 89US-0446584.
XX
XX
PR   17-AUG-1992; 92US-0928661.
XX
XX
PR   29-MAR-1989; 89US-0330566.

```

XX (UJJO ) UNIV JOHNS HOPKINS.  
 PA Nigro JM, Fearon ER, Baker SJ, Vogelstein B;  
 PI WPI; 2000-531419/48.  
 DR  
 XX Determining neoplastic tissue by detecting alteration in sequence of  
 PT neoplastic p53 proteins and wild type p53, comparing antibody binding  
 PT to p53 proteins or testing antigen complexing ability of p53 proteins  
 PT

Example 4; Column 10; 19pp; English.

CC A method for determining whether a human tissue is neoplastic comprises  
 CC detecting an alteration in the amino acid sequence of the p53 proteins in  
 CC a neoplastic tissue and wild type tissue by comparing binding of a  
 CC monoclonal antibody to the two p53 proteins and detecting loss of binding  
 CC in the mutant compared to the wild type protein. Alternatively a mutation  
 CC may be detected by testing the ability of the p53 proteins to bind an  
 CC antigen. Several genetic alterations occur during colorectal tumour  
 CC formation, the most common of which are deletions of the short arm of  
 CC chromosome 17. Allelic deletions of chromosome 17p particularly in the  
 CC p53 gene occur in a wide variety of cancers. The method of the invention  
 CC is useful for the diagnosis of neoplastic tissues such as lung, breast,  
 CC brain, colorectal, bladder, mesenchyme, prostate or stomach tumours and  
 CC also in the diagnosis of leukemias and osteosarcomas.  
 CC The present sequence represents a PCR primer used to amplify a fragment  
 CC of the human p53 gene from a tumour which has an allelic deletion of  
 CC chromosome 17p, yet still expresses p53. The primer is used to determine  
 CC that the tumour carries a point mutation at codon 143 of the p53 gene.

Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;

Query Match 65.0%; Score 13; DB 21; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCTGC 15  
 |||||  
 DB 1 TTCTCTTCTCTGC 13

RESULT 11  
 AAH47842  
 ID AAH47842 standard; DNA; 21 BP.

AC AAH47842;

DT 21-SEP-2001 (first entry)

DE Human p53 PCR primer 1.

Human; p53; PCR primer; immunological detection; ss.

Homo sapiens.

JP2001128685-A.

15-MAY-2001.

05-NOV-1999; 99JP-0315678.

05-NOV-1999; 99JP-0315678.

(IATR ) IATRON LAB INC.

WPI; 2001-373029/39.

A method for detection of variation of human p53 gene.

Claim 2; Page 10; 12pp; Japanese.

CC The present sequence is that of a PCR primer for detection of variation  
 CC in the human p53 gene useful to the invention. The invention relates to  
 CC detection of variation in the human p53 gene with an antibody which  
 CC specifically react with human p53 protein by steps of: immunological  
 CC detection of a sample with immunological staining; separation of stained  
 CC and un-stained cells; extraction of genome DNA from stained cells;  
 CC PCR amplification of a p53 DNA fragment which may contain an area of  
 CC variation of human p53 gene from the genome DNA obtained in the  
 CC preceding extraction step; and analysis of the reaction product.

Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;

Query Match 65.0%; Score 13; DB 21; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCTGC 15  
 |||||  
 DB 1 TTCTCTTCTCTGC 13

RESULT 12  
 AAT72696/C  
 ID AAT72696 standard; DNA; 31 BP.

AC AAT72696;

DT 18-SEP-1997 (first entry)

Sugar biosynthesis gene eryBII PCR primer.

Polyketide; glycosylation; eryBII; L-mycarose; antimicrobial;

antibiotic; antifungal; fungicide; anticancer; cytosstatic;

antimicrobial; Saccharopolyspora erythraea; primer; PCR;

polymerase chain reaction; PXB6; oleandomycin; ss.

Synthetic.

WO9723630-A2.

03-JUL-1997.

23-DEC-1996; 96WO-US20238.

21-DEC-1995; 95US-0576626.

(ABBO ) ABBOTT LAB.

Donadio S, Katz L, Staver MJ, Summers RG;

WPI; 1997-351066/32.

New genes involved in sugar biosynthesis and attachment - used to  
 generate polyketide antimicrobials etc. with altered pattern of  
 glycosylation

Example 3; Page 25; 85pp; English.

2 PCR primers (AAT72696-97) were used to amplify a 1.0 kb DNA  
 segment comprising nucleotides 2385-3410 of a Saccharopolyspora  
 erythraea gene segment (AAT72684), covering the eryBII gene that  
 encodes an enzyme (AAW19736) involved in L-mycarose biosynthesis.  
 The amplified DNA was utilised in the construction of plasmid pK6A  
 and hence of plasmid pXB6, which was used to transform Streptomyces  
 antibioticus ATCC 11891, resulting in prodn. of the novel  
 polyketide 3-des-oleandroyl-3-mycaroyl oleandomycin.

Sequence 31 BP; 10 A; 8 C; 11 G; 2 T; 0 other;

Query Match 65.0%; Score 13; DB 18; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	8	CTTCCTGCGGCT	20
Db	19	CTTCCTGCGGCT	7

## RESULT 13

AL34593/C  
ID AL34593 standard; DNA; 50 BP.

AC AAL34593;

DT 24-JAN-2002 (first entry)

Human SNP oligonucleotide #7801.

KM immunosuppressive; immunostimulatory; antinflammatory; cytostatic;  
 KM neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KM amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor  
 KM complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KM interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KM multifactorial disease; autoimmune disease; infection;  
 KM nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001

28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.  
PR 27-DEC-2000; 00US-0173419.

XX  
XX  
/CITY ) COUNTRY CODE

XX  
XX

XX WBT: 2001-455010/50  
DB

**XXIX**

PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer autophagy diseases and defects

PS Claim 1; Page 3646; 4143pp; English  
....

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesin, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

**Sequence 50 BP; 17 A; 12 C; 15 G; 6 T; 0 other;**

Query Match	65.0%	Score 13:	DB:22;	Length 50;
Best Local Similarity	100.0%	Pred. No.	1.3e+03;	
Matches 13; Conservative	0;	Mismatches	0;	Gaps 0

QY	7	TCTTCCTGCGGC	19
Db	21	TCTTCCTGCGGC	9

RESULT 14  
AAV41171

ID	AAV41171 standard; 12 BP.
yy	

AC AA41171

DT 08-OCT-1998 (first entry)

DE RNA component of human telomerase (hTR) antisense oligo 14d.

KM RNA component; human telomerase; antihense oligonucleotide; infection  
 KM neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;  
 KM contraception; sterilisation; immunosuppression; therapeutic; hTR;  
 KM immune system down-regulation; anti-inflammatory therapy; ss.

Synthetic.

XX  
PN W000020443-21

03-ПТ-1000

XX  
DE 19-DEC-1997

XX 30-DEC-1996, 06115-0770EE  
DB

PR 20-DEC-1996; 96US-0770564.  
VY

PA (GERO-) GERON CORP.  
VY

PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F, XY

DR WPI; 1998-377670/32.  
YY

PT New polynucleotide (8  
DT dotting or inhibition

PT New polynucleotide (s) anti:sense to human telomerase - used for  
PS depleting or inhibiting human telomerase, e.g. for treating  
XX cancer, immunosuppression or treating infection

Claim 11; Page 65; 80pp; English.

Sequences shown in AAV41169 to AAV41171

CC Sequences shown in AAV41169 to AAV41181 represent antisense  
CC oligonucleotides to the RNA component of human telomerase (hTR). These  
CC antisense oligonucleotides specifically hybridize to a nucleotide  
CC sequence within an accessible region of the hTR, but that does not  
CC hybridize to a sequence within the template region of hTR. These  
CC oligonucleotides may specifically be used for detection of an RNA  
CC component of human telomerase in a sample. This is useful for diagnosing  
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),  
CC and providing prognosis for a cancer patient. The inhibitory  
CC oligonucleotides can inhibit the telomerase activity level in a cell by  
CC interfering with transcription of the RNA component, decreasing the  
CC half-life of the telomerase RNA component transcript, inhibiting assembly  
CC of the RNA component into the telomerase holoenzyme, or inhibiting the  
CC polymerase activity of telomerase. These antisense oligonucleotides can  
CC be used for inhibiting telomerase activity in both cultured cells and in  
CC cells *in vivo*. They can be used in therapeutics for treating or  
CC preventing cancer, for contraception or sterilisation, for  
CC immunosuppression, and for selectively down-regulating specific branches  
CC of the immune system, e.g. a specific subset of T-cells, in  
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,  
CC parasites or fungi.

SQ Sequence 12 BP; 0 A; 6 C; 1 G; 5 T; 0 other;

Query Match	60.0%;	Score 12;	DB 19;	length 12;
Best Local Similarity	100.0%;	Pred. No.	4.3e+03;	
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CGTTCCTCTTCC	12
Db	1	CGTTCCTCTTCC	12

```

RESULT 15
AAQ71941
ID AAQ71941 standard; DNA; 20 BP.
XX
XX
AC AAQ71941;
XX
XX
DT 03-MAY-1995 (first entry)
XX
XX
DE Human IL-2R gamma gene exon 3 Nsense primer.
XX
XX
KW IL2-R gamma gene; X-linked severe combined immunodeficiency;
XX
XX
XSCID; interleukin; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "Biotin covalently bound to cytosine"
XX
XX
PN WO9420641-A.
XX
XX
PD 15-SEP-1994.
XX
XX
PF 10-MAR-1994; 94WO-US02891.
XX
XX
PR 12-MAR-1993; 93US-0031143.
XX
XX
PR 14-SEP-1993; 93US-0121435.
XX
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX
PI Leonard WJ, McBride WO, Noguchi M;
XX
XX
DR WPI; 1994-303046/37.
XX
XX
PT Diagnosis of X-linked severe combined immunodeficiency (XSCID) -
PT comprises detecting mutated IL-2R gamma gene, also vectors and
PT transgenic animals containing the mutated gene
XX
XX
PS Claim 12; Page 88; 98pp; English.
XX
XX
CC AAQ71941 to AAQ71975 are primers for the human IL-2R gamma gene, these
CC were used to amplify DNA from mutated and normal IL-2R gamma genes.
CC The mutated gene DNA was obtained either from female carriers or
CC male sufferers of X-linked severe combined immunodeficiency (XSCID).
CC The amplified DNA from normal and affected individuals was then
CC compared using a variety of methods including northern blotting and
CC dot and slot hybridisation. From this a claimed method for the
CC diagnosis of XSCID carriers and sufferers was developed.
XX
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 other;
XX

Query Match 60.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCT 13
   |||||
   |||||
Db 3 GTTCTCTTCT 14

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 Job time : 134.216 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 232.59 Seconds

(without alignments)  
2502.502 Million cell updates/sec

Title: US-08-770-564A-3

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Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

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11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_da:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mtl:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_hcg\_hum:\*

31: em\_hcg\_inv:\*

32: em\_hcg\_other:\*

33: em\_hcg\_mus:\*

34: em\_hcg\_pln:\*

35: em\_hcg\_rtd:\*

36: em\_hcg\_mam:\*

37: em\_hcg\_vrt:\*

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39: em\_hugo\_hum:\*

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41: em\_hugo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	20	100.0	20	6	AR063827
3	20	100.0	20	6	AR079894
4	20	100.0	20	6	AR063826
5	19	95.0	20	6	A84597
6	19	95.0	20	6	AR079898
7	14	70.0	29	6	AR146661
8	13	65.0	20	6	AR067594
9	13	65.0	31	6	AR092735
10	13	65.0	42	6	AR024197
11	13	65.0	45	6	AR024198
12	12	60.0	12	6	AR063828
13	12	60.0	19	6	A35686
14	12	60.0	20	6	I21035
15	12	60.0	20	6	I21062
16	12	60.0	25	6	AX196979
17	12	60.0	31	6	BD002728
18	12	60.0	33	6	AR162875
19	12	60.0	33	6	AR194025
20	12	60.0	37	6	AX283664
21	12	60.0	42	6	AX166899
22	11	55.0	11	6	AR051288
23	11	55.0	11	6	AR051324
24	11	55.0	11	6	I16936
25	11	55.0	11	6	I45730
26	11	55.0	12	6	AR051289
27	11	55.0	12	6	I16937
28	11	55.0	14	6	I45731
29	11	55.0	14	6	AR036791
30	11	55.0	18	6	AR166765
31	11	55.0	19	6	AX339205
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33	11	55.0	20	6	AR160506
34	11	55.0	20	6	I38898
35	11	55.0	20	6	I87929
36	11	55.0	22	6	AR017782
37	11	55.0	22	6	AR017783
38	11	55.0	22	6	AR017784
39	11	55.0	22	6	AR017785
40	11	55.0	22	6	AR017786
41	11	55.0	22	6	AR017787
42	11	55.0	22	6	AR077185
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44	11	55.0	22	6	AR077187
45	11	55.0	22	6	AR077188

## ALIGNMENTS

RESULT 1

A84604

LOCUS

DEFINITION Sequence 14 from Patent WO9845450.

ACCESSION A84604

VERSION A84604.1 GI:6733517

KEYWORDS

ORGANISM

REFERENCE 1 (bases 1 to 20)

AUTHORS Atkinson,E.M. and Kealey,J.T.

TITLE PURIFIED TELOMERASE

JOURNAL Patent: WO 9845450-A 14 15-OCT-1998;

GERON CORP (US)

20 bp

DNA

linear

PAT 21-JAN-2000

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
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Db
1 CGTTCCTCTTCTGCGGCGCT 20

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LOCUS      AR063827
DEFINITION Sequence 3 from patent US 5846723.
ACCESSION  AR063827
VERSION     AR063827.1 GI:5993135
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Kim N.Woo., Wu P., Kealey, J.T., Pruzan, R. and Weinrich, S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 3 08-DEC-1998;
FEATURES    Location/Qualifiers
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RESULT 3
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ACCESSION  AR079894
VERSION     AR079894.1 GI:10006647
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Weinrich, S.L., Atkinson, E.M. III, Lichtsteiner, S.P., Vassero, A.P.,
          Pruzan, R.A. and Kealey, J.T.
TITLE      Purified telomerase
JOURNAL    Patent: US 5968506-A 7 19-OCT-1999;
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QY
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Db
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ACCESSION  AR063826
VERSION     AR063826.1 GI:5993134
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Kim, N.Woo., Wu, P., Kealey, J.T., Pruzan, R. and Weinrich, S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 2 08-DEC-1998;
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DEFINITION Sequence 7 from Patent WO9845450.
ACCESSION  AB4597
VERSION     AB4597.1 GI:6733513
KEYWORDS
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Atkinson, E.M. and Kealey, J.T.
TITLE      PURIFIED TELOMERASE
JOURNAL    Patent: WO 9845450-A 7 15-OCT-1998;
          GERON CORP (US)
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db
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LOCUS      AR079898
DEFINITION Sequence 14 from patent US 5968506.
ACCESSION  AR079898
VERSION     AR079898.1 GI:10006651
KEYWORDS
SOURCE      Unknown.
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ORGANISM Unknown.  
 REFERENCE Unclassified.  
 AUTHORS 1 (bases 1 to 20)  
 TITLE Weintrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vassero,A.P.,  
 JOURNAL Pruzan,R.A. and Kealey,J.T.  
 FEATURES Purified telomerase  
 Patent: US 5968506-A 14 19-OCT-1999;  
 Location/Qualifiers  
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BASE COUNT 0 a 8 c 4 g 7 t 1 others

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QY 2 GTTCTCTCTCGCGGCT 20  
 Db 2 GTTCTCTCTCGCGGCT 20

RESULT 7  
 ARI46661/c  
 LOCUS ARI46661 29 bp DNA linear PAT 08-AUG-2001  
 DEFINITION Sequence 14 from patent US 6218522.  
 ACCESSION ARI46661  
 VERSION ARI46661.1 GI:15109850  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 29)  
 AUTHORS Saiga,A., Orita,S., Igarashi,H., Okumura,K. and Sakaguchi,G.  
 TITLE DNA molecule relating to suppression of gene expression and novel  
 protein  
 JOURNAL Patent: US 6218522-A 14 17-APR-2001;  
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QY 6 CTCTCTCTCGCGCC 19  
 Db 19 CTCTCTCTCGCGCC 6

RESULT 8  
 AR067594  
 LOCUS AR067594 20 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 1 from patent US 5851769.  
 ACCESSION AR067594  
 VERSION AR067594.1 GI:5998816  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Gray,J.W. and Weier,H.-U.G.  
 TITLE Quantitative DNA fiber mapping  
 JOURNAL Patent: US 5851769-A 1 22-DEC-1998;  
 FEATURES Location/Qualifiers  
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BASE COUNT 2 a 8 c 2 g 8 t

Query Match 65.0%; Score 13; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCCTCTCGCGC 15  
 Db 1 TTCCCTCTCGCGC 13

RESULT 9  
 AR092735/c  
 LOCUS AR092735 31 bp DNA linear PAT 08-SEP-2000  
 DEFINITION Sequence 15 from patent US 5998194.  
 ACCESSION AR092735  
 VERSION AR092735.1 GI:10019487  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 31)  
 AUTHORS Summers,R.G. Jr., Katz,L., Donadio,S. and Staver,M.J.  
 TITLE Polyketide-associated sugar biosynthesis genes  
 JOURNAL Patent: US 5998194-A 15 07-DEC-1999;  
 FEATURES Location/Qualifiers  
 source 1..31  
 /organism="unknown"

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTTCCTGCGGCT 20  
 Db 19 CTTCCTGCGGCT 7

RESULT 10  
 AR024197/c  
 LOCUS AR024197 42 bp DNA linear PAT 05-DEC-1998  
 DEFINITION Sequence 8 from patent US 5795863.  
 ACCESSION AR024197  
 VERSION AR024197.1 GI:3977491  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Wolf,D.  
 TITLE Recombinant agents affecting thrombosis  
 JOURNAL Patent: US 5795863-A 8 18-AUG-1998;  
 FEATURES Location/Qualifiers  
 source 1..42  
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BASE COUNT 12 a 9 c 17 g 4 t

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QY 4 TCCTCTCTCGCG 16  
 Db 22 TCCTCTCTCGCG 10

RESULT 11  
 AR024198/c  
 LOCUS AR024198 45 bp DNA linear PAT 05-DEC-1998  
 DEFINITION Sequence 9 from patent US 5795863.  
 ACCESSION AR024198  
 VERSION AR024198.1 GI:3977492  
 KEYWORDS



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 286.661 Seconds  
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292.710 Million cell updates/sec

Title: US-08-770-564a-4

Perfect score: 12 CGTTCCTCTCC 12

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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 3	12	100.0	25	12	US-10-355-577-396546
C 4	11	91.7	17	9	US-60-427-836-683575
C 5	11	91.7	18	9	US-10-303-778-7608
C 6	11	91.7	18	9	US-10-303-778-7627
C 7	11	91.7	18	9	US-10-310-188-65996
C 8	11	91.7	20	9	US-10-315-474-66
C 9	11	91.7	25	6	US-09-660-222-124398
C 10	11	91.7	25	6	US-09-660-222-124402
C 11	11	91.7	25	6	US-09-660-222-124403
C 12	11	91.7	25	6	US-09-660-222-124417
C 13	11	91.7	25	6	US-09-660-222-124417
C 14	11	91.7	25	7	US-09-953-570-22842
C 15	11	91.7	25	7	US-09-953-570-22842
C 16	11	91.7	25	7	US-09-954-445A-7403
C 17	11	91.7	25	7	US-09-954-445A-21805
C 18	11	91.7	25	7	US-09-954-445A-31524
C 19	11	91.7	25	7	US-09-954-445A-79209
C 20	11	91.7	25	9	US-10-098-263B-24096

21	11	91.7	25	9	US-10-098-263B-81647	Sequence 81647, A
22	11	91.7	25	9	US-10-098-263B-81648	Sequence 81648, A
23	11	91.7	25	9	US-10-098-263B-96226	Sequence 96226, A
24	11	91.7	25	9	US-10-098-263B-114611	Sequence 114611, A
25	11	91.7	25	9	US-10-355-577-96775	Sequence 96775, A
26	11	91.7	25	9	US-10-355-577-101273	Sequence 101273, A
27	11	91.7	25	9	US-10-355-577-101274	Sequence 101274, A
28	11	91.7	25	9	US-10-355-577-164671	Sequence 164671, A
29	11	91.7	25	9	US-10-355-577-178073	Sequence 178073, A
30	11	91.7	25	9	US-10-355-577-198249	Sequence 198249, A
31	11	91.7	25	9	US-10-355-577-318084	Sequence 318084, A
32	11	91.7	25	9	US-10-355-577-394493	Sequence 394493, A
33	11	91.7	25	9	US-10-355-577-394494	Sequence 394494, A
34	11	91.7	25	9	US-10-355-577-396545	Sequence 396545, A
35	11	91.7	25	9	US-10-355-577-498091	Sequence 498091, A
36	11	91.7	25	9	US-10-355-577-581372	Sequence 581372, A
37	11	91.7	25	9	US-10-355-577-587426	Sequence 587426, A
38	11	91.7	25	9	US-10-355-577-650483	Sequence 650483, A
39	11	91.7	25	9	US-10-355-577-650484	Sequence 650484, A
40	11	91.7	25	9	US-10-355-577-653296	Sequence 653296, A
41	11	91.7	25	9	US-10-355-577-658872	Sequence 658872, A
42	11	91.7	25	9	US-10-355-577-667847	Sequence 667847, A
43	11	91.7	25	9	US-10-355-577-667848	Sequence 667848, A
44	11	91.7	25	9	US-10-355-577-730882	Sequence 730882, A
45	11	91.7	25	9	US-10-355-577-734855	Sequence 734855, A

#### ALIGNMENTS

```

RESULT 1
US-09-954-445A-45573/c
; Sequence 45573, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Method of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 45573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-45573

Query Match          100.0%; Score 12; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTCCTCTCC 12
Db      15 CGTTCCTCTCC 4

RESULT 2
US-10-355-577-396546/c
; Sequence 396546, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Method of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 396546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

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US-10-355-577-396546

Query Match 100.0%; Score 12; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCC 12  
DB 24 CGTTCCTCTCC 13

RESULT 3

US-60-427-836-683575  
Sequence 683575, Application US/60427836  
GENERAL INFORMATION:  
APPLICANT: Xue Wei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Rat.  
FILE REFERENCE: 3527  
CURRENT APPLICATION NUMBER: US/60/427,836  
NUMBER OF SEQ ID NOS: 2002-11-20  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 683575  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-60-427-836-683575

Query Match 100.0%; Score 12; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCC 12  
DB 12 CGTTCCTCTCC 23

RESULT 4

US-10-303-778-7608  
Sequence 7608, Application US/10303778  
GENERAL INFORMATION:  
APPLICANT: RosettaGenomics  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL  
FILE REFERENCE: 47416  
CURRENT APPLICATION NUMBER: US/10/303,778  
NUMBER OF SEQ ID NOS: 2002-11-26  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7608  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Avian infectious bronchitis virus  
US-10-303-778-7608

Query Match 91.7%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.1e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTCC 12  
DB 7 GTTCCTCTCC 17

RESULT 5

US-10-303-778-7627  
Sequence 7627, Application US/10303778  
GENERAL INFORMATION:  
APPLICANT: RosettaGenomics  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL  
FILE REFERENCE: 47416  
CURRENT APPLICATION NUMBER: US/10/303,778

CURRENT FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 17608  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7627  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-303-778-7627

Query Match 91.7%; Score 11; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.1e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTCC 12  
DB 7 GTTCCTCTCC 17

RESULT 6

US-10-310-188-65996/c  
Sequence 65996, Application US/10310188  
GENERAL INFORMATION:  
APPLICANT: RosettaGenomics  
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN-  
FILE REFERENCE: 47487  
CURRENT APPLICATION NUMBER: US/10/310,188  
NUMBER OF SEQ ID NOS: 2002-12-19  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 65996  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-310-188-65996

Query Match 91.7%; Score 11; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.1e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTCC 12  
DB 12 GTTCCTCTCC 2

RESULT 7

US-10-315-474-66/c  
Sequence 66, Application US/10315474  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION  
FILE REFERENCE: RTS-0318  
CURRENT APPLICATION NUMBER: US/10/315,474  
NUMBER OF SEQ ID NOS: 2002-12-10  
SEQ ID NO 66  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-315-474-66

Query Match 91.7%; Score 11; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTCC 12  
DB 12 GTTCCTCTCC 2

```
RESULT 8
US-10-315-474-137
; Sequence 137, Application US/10315474
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
; FILE REFERENCE: RTS-0338
; CURRENT APPLICATION NUMBER: US/10/315,474
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 137
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-315-474-137

Query Match          91.7%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCC 12
DB 9 GTTCCTCTTCC 19

RESULT 9
US-09-660-222-124398
; Sequence 124398, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; PRIOR FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124398

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTC 11
DB 12 CGTTCCTCTTC 22

RESULT 10
US-09-660-222-124402
; Sequence 124402, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; PRIOR FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124402
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124402

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTC 11
DB 6 CGTTCCTCTTC 16

RESULT 11
US-09-660-222-124403
; Sequence 124403, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; PRIOR FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124403

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTC 11
DB 4 CGTTCCTCTTC 14

RESULT 12
US-09-660-222-124417
; Sequence 124417, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; PRIOR FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124417
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124417

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGTCTCTCTTC 11  
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 Db 3 GGTCTCTCTTC 13

RESULT 13  
 US-09-953-570-22842/c  
 ; Sequence 22842, Application US/09953570  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast  
 ; FILE REFERENCE: 3110.1  
 ; CURRENT APPLICATION NUMBER: US/09/953,570  
 ; CURRENT FILING DATE: 2001-09-13  
 ; PRIOR APPLICATION NUMBER: 60/232,638  
 ; PRIOR FILING DATE: 2000-09-14  
 ; NUMBER OF SEQ ID NOS: 138410  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 22842  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces Cerevisiae  
 US-09-953-570-22842

Query Match 91.7%; Score 11; DB 7; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTCTTC 12  
 |||||  
 Db 19 GTTCTCTCTTC 9

RESULT 14  
 US-09-953-570-131778/c  
 ; Sequence 131778, Application US/09953570  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast  
 ; FILE REFERENCE: 3110.1  
 ; CURRENT APPLICATION NUMBER: US/09/953,570  
 ; CURRENT FILING DATE: 2001-09-13  
 ; PRIOR APPLICATION NUMBER: 60/232,638  
 ; PRIOR FILING DATE: 2000-09-14  
 ; NUMBER OF SEQ ID NOS: 138410  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 131778  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces Cerevisiae  
 US-09-953-570-131778

Query Match 91.7%; Score 11; DB 7; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTCTTC 12  
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 Db 17 GTTCTCTCTTC 7

RESULT 15  
 US-09-954-445A-7403/c  
 ; Sequence 7403, Application US/09954445A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana  
 ; FILE REFERENCE: 3116.1  
 ; CURRENT APPLICATION NUMBER: US/09/954,445A  
 ; CURRENT FILING DATE: 2000-09-17  
 ; PRIOR APPLICATION NUMBER: 60/233,620  
 ; PRIOR FILING DATE: 2000-09-18  
 ; NUMBER OF SEQ ID NOS: 131820

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 7403  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-09-954-445A-7403

Query Match 91.7%; Score 11; DB 7; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTCTTC 12  
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 Db 12 GTTCTCTCTTC 2

Search completed: June 26, 2003, 04:15:11  
 Job time : 289.969 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 46.9721 Seconds  
(without alignments)  
195.867 Million cell updates/sec

Title: US-08-770-564A-2

Perfect score: 30  
Sequence: 1 CGTTCCTCTCTCGCGCGCTGAACGCTGA 30

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents, NA:\*

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2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	2	US-08-770-565-2
2	20	66.7	20	2	US-08-770-565-3
3	20	66.7	20	2	US-08-770-565-12
4	20	66.7	20	2	US-08-833-377-7
5	19	63.3	20	2	US-08-833-377-14
6	14	46.7	29	3	US-09-121-321-14
7	14	46.7	29	4	US-08-933-803A-14
8	13	43.3	20	2	US-08-534-479-1
9	13	43.3	32	1	US-08-576-626A-15
10	13	43.3	41	2	US-08-487-037-8
11	13	43.3	45	1	US-08-487-037-9
12	12	40.0	12	2	US-08-770-565-4
13	12	40.0	20	1	US-08-031-143B-6
14	12	40.0	20	1	US-08-031-143B-33
15	12	40.0	20	4	US-09-851-896-86
16	12	40.0	20	5	PCT-US94-02891-6
17	12	40.0	20	5	PCT-US94-02891-33
18	12	40.0	33	4	US-08-090-369-15
19	12	40.0	33	4	US-09-482-971-15
20	12	40.0	36	1	US-09-384-327-15
21	12	40.0	36	2	US-08-458-372-15
22	12	40.0	36	2	US-08-956-047-19
23	12	40.0	36	6	5506118-6
24	12	40.0	38	4	US-09-638-202A-18
25	12	40.0	43	1	US-08-456-566-1
26	12	40.0	43	1	US-09-009-044-1
27	12	40.0	49	2	US-08-956-047-10

c 28	11	36.7	11	1	US-08-126-594-5	Sequence 5, Appl
c 29	11	36.7	11	1	US-08-465-811A-5	Sequence 5, Appl
c 30	11	36.7	11	2	US-08-619-542B-5	Sequence 5, Appl
c 31	11	36.7	11	2	US-08-619-542B-48	Sequence 48, Appl
c 32	11	36.7	12	1	US-08-126-594-6	Sequence 6, Appl
c 33	11	36.7	12	1	US-08-465-811A-6	Sequence 6, Appl
c 34	11	36.7	12	2	US-08-619-542B-6	Sequence 6, Appl
c 35	11	36.7	14	1	US-08-294-424-33	Sequence 33, Appl
c 36	11	36.7	17	4	US-09-277-457-28	Sequence 28, Appl
c 37	11	36.7	18	4	US-09-251-645-21	Sequence 21, Appl
c 38	11	36.7	19	4	US-09-442-143A-38	Sequence 38, Appl
c 39	11	36.7	19	4	US-09-442-143A-41	Sequence 41, Appl
c 40	11	36.7	20	1	US-08-068-945A-8	Sequence 8, Appl
c 41	11	36.7	20	1	US-08-442-806-8	Sequence 8, Appl
c 42	11	36.7	20	2	US-08-206-790A-18	Sequence 18, Appl
c 43	11	36.7	20	3	US-08-589-939-40	Sequence 40, Appl
c 44	11	36.7	20	4	US-09-258-377-30	Sequence 30, Appl
c 45	11	36.7	20	5	PCT-US95-02943-18	Sequence 18, Appl

#### ALIGNMENTS

RESULT 1  
US-08-770-565-2  
; Sequence 2, Application US/08770565  
; Patent No. 5846723  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Puzean, Ronald  
; APPLICANT: Weinlich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002300US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-565-2

Query Match 100.0%; Score 30; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGCGCGCTGAACGCTGA 30

Db 1 CGTTCCTCTTCTGCGGCGCTGAACGGTGA 30

## RESULT 2

US-08-770-565-3

Sequence 3, Application US/08770565  
Patent No. 5846723

## GENERAL INFORMATION:

APPLICANT: Klm, Nam Woo

APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Methods for Detecting the RNA Component of

TITLE OF INVENTION: Telomerase

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

CLASSIFICATION: 435

FILING DATE: 20-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002300US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-565-3

Query Match 66.7%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTTCTGCGGCGCT 20  
Db 1 CGTTCCTCTTCTGCGGCGCT 20

## RESULT 3

US-08-770-565-12

Sequence 12, Application US/08770565  
Patent No. 5846723

## GENERAL INFORMATION:

APPLICANT: Klm, Nam Woo

APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Methods for Detecting the RNA Component of

TITLE OF INVENTION: Telomerase

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

CLASSIFICATION: 435

FILING DATE: 20-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002300US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-565-12

Query Match 66.7%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 CCGGGCGGCGCTGAACGGTGA 30  
Db 1 CCGGGCGGCGCTGAACGGTGA 20

## RESULT 4

US-08-833-377-7

Sequence 7, Application US/08833377

Patent No. 5968506

## GENERAL INFORMATION:

APPLICANT: Weinrich, Scott L.

APPLICANT: Atkinson III, Edward M.

APPLICANT: Lichtsteiner, Serge P.

APPLICANT: Vassero, Alain P.

APPLICANT: Pruzan, Ronald A.

APPLICANT: Kealey, James T.

TITLE OF INVENTION: Purified Telomerase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,377

FILING DATE: 04-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/510,736

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.



REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-00110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note="Oligo 14ab"  
US-08-833-377-7

Query Match 66.7%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCGCGCCT 20  
DB 1 CGTCTCTTCTCGCGCCT 20

RESULT 5  
US-08-833-377-14  
Sequence 14, Application US/08833377  
Patent No. 5968506  
GENERAL INFORMATION:  
APPLICANT: Weinrich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichtsteiner, Serge P.  
APPLICANT: Vaaserot, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,377  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Scorello, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-00110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA

FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note="N = 5' biotinylated cytidine"  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note="biotinylated Oligo 14ab"  
US-08-833-377-14

Query Match 63.3%; Score 19; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.096;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCGCGCCT 20  
DB 2 GTTCTCTTCTCGCGCCT 20

RESULT 6  
US-09-121-321-14/C  
Sequence 14, Application US/09121321  
Patent No. 6090783  
GENERAL INFORMATION:  
APPLICANT: Saiga, Akihiko  
APPLICANT: Orita, Satoshi  
APPLICANT: Igarashi, Hisanaga  
APPLICANT: Okumura, Kouichi  
APPLICANT: Sakaguchi, Gaku  
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/121,321  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/933,803  
FILING DATE: 19-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-12CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-09-121-321-14

Query Match 46.7%; Score 14; DB 3; Length 29;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CTCCTCTCGGCGC 19  
DB 19 CTCCTCTCGGCGC 6

## RESULT 7

US-08-933-803A-14/C

Sequence 14, Application US/08933803A

Patent No. 6218522

GENERAL INFORMATION:

APPLICANT: Saiga, Akihiko

APPLICANT: Orita, Satoshi

APPLICANT: Igatahshi, Hisanaga

APPLICANT: Okumura, Kouichi

APPLICANT: Sakaguchi, Gaku

TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSER: FISH &amp; NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933, 803A

FILING DATE: 19-SEP-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Haley, James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-12CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9090

TELEFAX: 212-596-9090

INFORMATION FOR SEQ. ID NO. 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

US-08-933-803A-14

Query Match 46.7%; Score 14; DB 4; Length 29;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CTCCTCTCGGCGC 19  
DB 19 CTCCTCTCGGCGC 6

## RESULT 8

US-08-534-479-1

Sequence 1, Application US/08534479

Patent No. 5851769

GENERAL INFORMATION:

APPLICANT: GRAY, JOE M.

APPLICANT: MEIER, HEINZ-URICH G.

TITLE OF INVENTION: QUANTITATIVE FIBER MAPPING

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN &amp; CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/534,479

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MACKNIGHT, KAMRIN T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: LBL-01754

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-534-479-1

Query Match 43.3%; Score 13; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCCTCTCTCTGC 15  
DB 1 TTCCTCTCTCTGC 13

## RESULT 9

US-08-576-626A-15/C

Sequence 15, Application US/08576626A

Patent No. 5998194

GENERAL INFORMATION:

APPLICANT: Summers, R.C.

APPLICANT: Katz, L.

APPLICANT: Staver, M.J.

TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: Illinois

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/576,626A

FILING DATE: 21-DEC-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Dianne Casulo

REGISTRATION NUMBER: P-40,943

REFERENCE/DOCKET NUMBER: 5857, US. 01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (847) 938-3137  
TELEFAX: (847) 938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-576-626A-15

Query Match 43.3%; Score 13; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTCTCTGCGCGCT 20  
DB 19 TTCTCTGCGCGCT 7

RESULT 10

US-08-487-037-8/c  
Sequence 8, Application US/08487037  
Patent No. 5795863  
GENERAL INFORMATION:  
APPLICANT: Wolf, David L.  
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSES: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,037  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0002.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-037-8

Query Match 43.3%; Score 13; DB 1; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTCTTCTCTGCG 16  
DB 22 TTCTCTTCTCTGCG 10

RESULT 11  
US-08-487-037-9/c  
Sequence 9, Application US/08487037  
Patent No. 5795863

GENERAL INFORMATION:  
APPLICANT: Wolf, David L.  
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSES: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,037  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0002.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-037-9

Query Match 43.3%; Score 13; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTTCTCTGCG 16  
DB 22 TTCTTTTCTCTGCG 10

RESULT 12  
US-08-770-565-4  
Sequence 4, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinlich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSES: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-4

Query Match 40.0%; Score 12; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCCTCTTCC 12  
DB 1 GGTTCCTCTTCC 12

RESULT 13  
US-08-031-143B-6/c  
Sequence 6, Application US/08031143B  
Patent No. 5518880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
APPLICANT: MCBRIDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,143B  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: OLIGONUCLEOTIDE  
DESCRIPTION: NO  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R

US-08-031-143B-6  
Query Match 40.0%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCT 13  
DB 18 GTTCCTCTTCT 7

RESULT 14  
US-08-031-143B-33  
Sequence 33, Application US/08031143B  
Patent No. 5518880  
GENERAL INFORMATION:  
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;  
APPLICANT: MCBRIDE, O. WESLEY  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND  
TREATMENT OF XSCID  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVE.  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT # 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,143B  
FILING DATE: 12-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: OLIGONUCLEOTIDE  
DESCRIPTION: NO  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
INDIVIDUAL ISOLATE: IL-2R  
US-08-031-143B-33  
Query Match 40.0%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCT 13  
DB 3 GTTCCTCTTCT 14

RESULT 15  
US-08-851-896-86  
Sequence 86, Application US/09851896  
Patent No. 6410325

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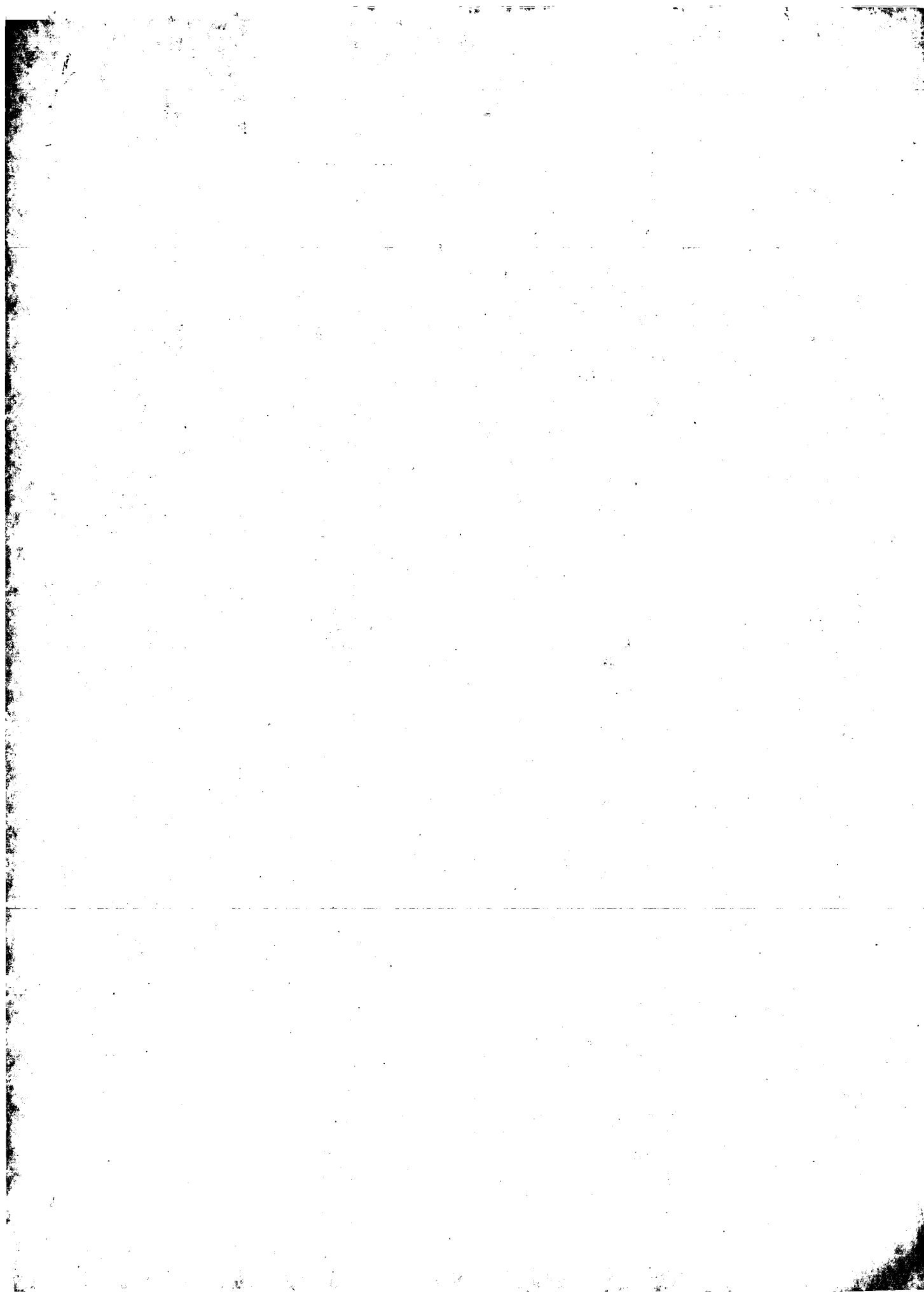
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-896-86

Query Match      40.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. Se+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 TCCTGGGCGCTG 21
        |||||
Db       8 TCCTGGGCGCTG 19

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Search completed: June 23, 2003, 10:17:02  
 Job time : 50.9721 secs



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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 199.363 Seconds  
(without alignments)  
338.880 Million cell updates/sec

Title: US-08-770-564A-2

Perfect score: 30  
Sequence: 1 CGTTCCTCTCTCGCGCGCTGAACGCTGA 30

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N Geneseq\_101002.\*

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	30	100.0	30 19 AAV41169	RNA component of h
2	20	66.7	20 19 AAV71226	Antisense oligonuc
3	20	66.7	20 19 AAV41170	RNA component of h
4	20	66.7	20 20 AA223632	Human clone 28-1 t
5	20	66.7	20 20 AA223636	Human clone 28-1 t
6	20	66.7	20 22 AAS09477	Antisense oligonuc
7	20	66.7	20 22 AAS09480	Antisense oligonuc
8	14	46.7	29 17 AAT42916	Primer 8201RN, amp
9	13	43.3	21 17 AAT36484	Upstream PCR prime

10	13	43.3	21 21 AAA72585	Upstream PCR prime
11	13	43.3	21 22 AAA47842	Human p53 PCR prim
12	13	43.3	31 18 AAT72696	Sugar biosynthesis
13	13	43.3	50 22 AAL28060	Human SNP oligonuc
14	13	43.3	50 22 AAL34593	Human SNP oligonuc
15	12	40.0	12 19 AAV41171	RNA component of h
16	12	40.0	20 15 AAQ71941	Human IL-2R gamma
17	12	40.0	20 15 AAQ71914	Human IL-2R gamma
18	12	40.0	20 19 AAV45148	Homo sapiens P-TEN
19	12	40.0	20 20 AAX94325	PCR primer used to
20	12	40.0	21 22 AAH63356	RBSP2 polymorphism
21	12	40.0	24 15 AAQ57316	Enzymatic RNA mole
22	12	40.0	24 24 ABQ01901	Oligonucleotide ad
23	12	40.0	24 24 ABQ07713	Oligonucleotide ad
24	12	40.0	24 24 ABQ07754	Oligonucleotide ad
25	12	40.0	25 22 AAL62055	Soybean 318013 reg
26	12	40.0	27 22 AAF87709	Human glutathione
27	12	40.0	30 22 AAH19632	Human t-PA primer
28	12	40.0	31 21 AAA79024	Human genomic DNA
29	12	40.0	33 14 AAQ49474	Modified tissue pl
30	12	40.0	36 16 AAQ80463	Primer (PhoAUP2) c
31	12	40.0	36 16 AAQ80463	Oligodeoxyribonuc
32	12	40.0	36 20 AAX03944	Tissue plasminogen
33	12	40.0	36 21 AAA39099	Human tissue plas
34	12	40.0	36 22 AAH45119	ERYCIII PCR primer
35	12	40.0	37 18 AAT95360	Mouse anti-Ptha MA
36	12	40.0	38 18 AAT95360	Synthetic Fn3 gene
37	12	40.0	38 24 ABL94482	Ribonectin 3 codi
38	12	40.0	40 17 AAT70784	Stenotic carotid a
39	12	40.0	40 17 AAT70788	Stenotic carotid a
40	12	40.0	40 17 AAT70789	Human tetrapeptide
41	12	40.0	41 24 ABA04330	Human tetrapeptide
42	12	40.0	41 24 ABA04330	Human tetrapeptide
43	12	40.0	43 17 AAT35002	Mutagenic oligonuc
44	12	40.0	43 17 AAT35002	Primer (VILIO) for
45	12	40.0	49 16 AAQ80460	

## ALIGNMENTS

```
RESULT 1
ID AAV41169 strand; DNA; 30 BP.
AC AAV41169;
DT 08-OCT-1998 (first entry)
DE RNA component of human telomerase (htr) antisense oligo 14.
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraseption; sterilisation; immunosuppression; therapeutic; htr;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
XX
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI, 1998-377670/32.
DR
```

```
XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Claim 11; Page 65; 80pp; English.
XX
CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridize to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridize to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilization, for
CC immunosuppression, and for selectively down-regulation, for
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 30 BP; 4 A; 10 C; 8 G; 8 T; 0 other;
Query Match 100.0%; Score 30; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTTCTCGGCGCTGAAACGGTGA 30
Db 1 CGTTCCTCTTCTCGGCGCTGAAACGGTGA 30
RESULT 2
AAV71226
ID AAV71226 standard; DNA; 20 BP.
XX
AC AAV71226;
XX
DT 15-FEB-1999 (first entry)
XX
DE Antisense oligonucleotide 14ab for human telomerase RNA component.
XX
KW Human; telomerase RNA component; anticancer therapy; purification;
KW assay; vaccine; cancer; antisense oligonucleotide; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "bioclinylated"
XX
XX WO9845450-A1.
XX
XX 15-OCT-1998.
XX
XX 04-APR-1997; 97WO-US06012.
XX
XX 04-APR-1997; 97WO-US06012.
XX
XX (GERO-) GERON CORP.
XX
PI Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA,
PI Vassero AP, Weinrich SL;
```

```
XX
DR WPI; 1998-594485/50.
XX
XX Purification of telomerase on affinity material - useful for, e.g.
PT diagnosis and treatment of cancer
XX
PS Claim 6; Page 61; 76pp; English.
XX
CC The present sequence represents an antisense oligonucleotide
CC directed against the human telomerase RNA component gene sequences.
CC The oligonucleotide can be used as an affinity agent in the methods of
CC the invention, which are used to purify human telomerase. The methods
CC involve the use of several sequential steps, including the use of two
CC matrices that bind molecules bearing negative charges, a matrix that
CC binds molecules bearing positive charges, an affinity purification step
CC and a size separation. Telomerase is a particular target of anticancer
CC therapies, and is useful in assays for characterizing (pre)cancerous
CC cells. Telomerase can also be used to screen for specific modulators,
CC for biochemical analysis of its activity, and in preparation of
CC antibodies. Fragments of telomerase, or nucleic acid encoding them,
CC are used in vaccines, and for treating over expression of telomerase,
CC particularly in cancer.
XX
SQ Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;
Query Match 66.7%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTTCTCGGCGCT 20
Db 1 CGTTCCTCTTCTCGGCGCT 20
RESULT 3
AAV41170
ID AAV41170 standard; DNA; 20 BP.
XX
XX AAV41170;
XX
DT 08-OCT-1998 (first entry)
XX
XX RNA component of human telomerase (hTR) antisense oligo 14ab.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilization; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9828442-A1.
XX
XX 02-JUL-1998.
XX
XX 19-DEC-1997; 97WO-US23619.
XX
XX 20-DEC-1996; 96US-0770565.
XX
XX 20-DEC-1996; 96US-0770564.
XX
XX (GERO-) GERON CORP.
XX
XX Kealey JT, Kim NM, Pruzan R, Weinrich SL, Wu F,
XX WPI; 1998-37670/32.
XX
XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Claim 11; Page 65; 80pp; English.
```



CC Sequences shown in AA41169 to AA41181 represent antisense  
CC oligonucleotides to the RNA component of human telomerase (htr). These  
CC antisense oligonucleotides specifically hybridize to a nucleotide  
CC sequence within an accessible region of the htr, but that does not  
CC hybridize to a sequence within the template region of htr. These  
CC oligonucleotides may specifically be used for detection of an RNA  
CC component of human telomerase in a sample. This is useful for diagnosing  
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),  
CC and providing prognosis for a cancer patient. The inhibitory  
CC oligonucleotides can inhibit the telomerase activity level in a cell by  
CC interfering with transcription of the RNA component, decreasing the  
CC half-life of the telomerase RNA component transcript, inhibiting assembly  
CC of the RNA component into the telomerase holoenzyme, or inhibiting the  
CC polymerase activity of telomerase. These antisense oligonucleotides can  
CC be used for inhibiting telomerase activity in both cultured cells and in  
CC cells in vivo. They can be used in therapeutics for treating or  
CC preventing cancer, for contraception or sterilization, for  
CC immunosuppression, and for selectively down-regulating specific branches  
CC of the immune system, e.g. a specific subset of T-cells, in  
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,  
CC parasites or fungi.

SO Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 19; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.49;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCCTGCGGCT 20  
DB 1 CGTTCCTCTTCCTGCGGCT 20

RESULT 4

ID AA223632 standard; DNA; 20 BP.

AA223632;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide 14ab.

KW Telomerase; human; immune response; cancer; vaccine; treatment;  
KW disease; primer; ss.

OS Synthetic.

OS Homo sapiens.

PN US968506-A.

PD 19-OCT-1999.

PF 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;  
PI Vassero AP;

DR MPI; 1999-590379/50.

PT Compositions comprising human telomerase, useful for treating diseases  
PT associated with overexpression of telomerase e.g. cancer -

PS Disclosure; Column 45-46; 34pp; English.

CC This invention describes a novel composition comprising human telomerase  
CC having at least 2000-fold (preferably at least 6000-fold) increased  
CC relative purity compared with crude extract of cells from  
CC adenovirus-transformed kidney cell line. The composition is useful for

CC eliciting an immune response in animals and may therefore be used as a  
CC vaccine for treating diseases associated with the overexpression of  
CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used  
CC in the isolation of human clone 28-1 which contains a fragment of the  
CC human telomerase described in the method of the invention.

SO Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 20; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.49;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCCTGCGGCT 20  
DB 1 CGTTCCTCTTCCTGCGGCT 20

RESULT 5

ID AA223636 standard; DNA; 20 BP.

AA223636;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide oligo 14ab.

KW Telomerase; human; immune response; cancer; vaccine; treatment;  
KW disease; primer; ss.

OS Synthetic.

OS Homo sapiens.

PN US968506-A.

PD 19-OCT-1999.

PF 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;  
PI Vassero AP;

DR MPI; 1999-590379/50.

PT Compositions comprising human telomerase, useful for treating diseases  
PT associated with overexpression of telomerase e.g. cancer -

PS Disclosure; Column 49-50; 34pp; English.

CC This invention describes a novel composition comprising human telomerase  
CC having at least 2000-fold (preferably at least 6000-fold) increased  
CC relative purity compared with crude extract of cells from  
CC adenovirus-transformed kidney cell line. The composition is useful for  
CC eliciting an immune response in animals and may therefore be used as a  
CC vaccine for treating diseases associated with the overexpression of  
CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used  
CC in the isolation of human clone 28-1 which contains a fragment of the  
CC human telomerase described in the method of the invention.

SO Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 20; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.49;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGGGCT 20  
 DB 1 CGTTCCTCTCTCGGGGCT 20

## RESULT 6

AAS09477  
 ID AAS09477 standard; DNA; 20 BP.

AC AAS09477;  
 DT 24-OCT-2001 (first entry)

DE Antisense oligonucleotide for human telomerase, Oligo 14ab #1.

KM Human; Telomerase; vaccine; antibody; cancer; EP2H;  
 KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

OS Homo sapiens.

FN US6261556-B1.

PD 17-JUL-2001.

PF 18-OCT-1999; 99US-0420056.

PR 04-APR-1997; 97US-0833377.  
 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Weinlich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA;  
 PI Kealey JT;

DR WPI; 2001-450477/48.

PT Purified human telomerase, useful for inducing immune response in  
 PT animals, comprises several thousand folds increased purity compared  
 PT with cytoplasmic crude cell preparations

PS Disclosure; Column 2; 29pp; English.

XX The sequence represents an antisense oligonucleotide used in  
 CC the purification of human telomerase. The invention relates  
 CC to a purified human telomerase core enzyme protein comprising  
 CC 2000-fold increased purity compared with a crude extract of cells from  
 CC adenovirus-transformed kidney cell line (293 cells) and when associated  
 CC with telomerase RNA component has DNA polymerase activity and a molecular  
 CC weight of 200-2000 kDa. The purified telomerase is useful  
 CC for inducing a humoral or cell-mediated immune response in an animal.  
 CC Purified telomerase or immunogenic fragments are useful as vaccines for  
 CC treating diseases associated with over-expression of telomerase, such as  
 CC cancer and for producing antibodies that recognize telomerase, which are  
 CC useful as affinity agents in isolating the proteins and for detecting the  
 CC presence of proteins in a sample, such as cell or tissue. Identification  
 CC of telomerase aids in diagnosis of cancer or pre-cancerous states.  
 CC Telomerase and/or telomerase associated proteins are also useful for  
 CC screening compounds to identify agents that alter the association of  
 CC telomerase-associated proteins, such as nucleolin or EP2H with  
 CC telomerase.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 22; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.49;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGGGCT 20  
 DB 1 CGTTCCTCTCTCGGGGCT 20

RESULT 7  
 AAS09480  
 ID AAS09480 standard; DNA; 20 BP.

AC AAS09480;

DT 24-OCT-2001 (first entry)

DE Antisense oligonucleotide for human telomerase, Oligo 14ab #2.

KM Human; Telomerase; vaccine; antibody; cancer; EP2H;  
 KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

OS Homo sapiens.

FN US6261556-B1.

PD 17-JUL-2001.

PF 18-OCT-1999; 99US-0420056.

PR 04-APR-1997; 97US-0833377.  
 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Weinlich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA;  
 PI Kealey JT;

DR WPI; 2001-450477/48.

PT Purified human telomerase, useful for inducing immune response in  
 PT animals, comprises several thousand folds increased purity compared  
 PT with cytoplasmic crude cell preparations

PS Disclosure; Column 16; 29pp; English.

XX The sequence represents a biotinylated antisense oligonucleotide  
 CC used in the purification of human telomerase. The invention  
 CC relates to a purified human telomerase core enzyme protein comprising  
 CC 2000-fold increased purity compared with a crude extract of cells from  
 CC adenovirus-transformed kidney cell line (293 cells) and when associated  
 CC with telomerase RNA component has DNA polymerase activity and a molecular  
 CC weight of 200-2000 kDa. The purified telomerase is useful  
 CC for inducing a humoral or cell-mediated immune response in an animal.  
 CC Purified telomerase or immunogenic fragments are useful as vaccines for  
 CC treating diseases associated with over-expression of telomerase, such as  
 CC cancer and for producing antibodies that recognize telomerase, which are  
 CC useful as affinity agents in isolating the proteins and for detecting the  
 CC presence of proteins in a sample, such as cell or tissue. Identification  
 CC of telomerase aids in diagnosis of cancer or pre-cancerous states.  
 CC Telomerase and/or telomerase associated proteins are also useful for  
 CC screening compounds to identify agents that alter the association of  
 CC telomerase-associated proteins, such as nucleolin or EP2H with  
 CC telomerase.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 22; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.49;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGGGCT 20  
 DB 1 CGTTCCTCTCTCGGGGCT 20

```

RESULT 8
AAAT42916/c
ID   AAT42916 standard; DNA; 29 BP.
XX
XX
AC   AAT42916;
XX
XX
DT   16-JUN-1997 (first entry)
XX
XX
DE   Primer 8201RN, amplifies TSP-1 and gene regulation sequences.
XX
XX
KW   gene expression; regulation; plasmid; viral infection;
KW   human T-cell leukaemia; HIV; antiviral agent; detection; cancer;
KW   gene therapy; TSP; ss.
XX
XX
OS   Synthetic.
XX
XX
PN   WO960522-A1.
XX
XX
PD   03-OCT-1996.
XX
XX
PF   19-MAR-1996; 96WO-JP00719.
XX
XX
PR   27-APR-1995; 95JP-0104299.
PR   24-MAR-1995; 95JP-0065559.
XX
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
XX
PI   Igarashi H, Okumura K, Orita S, Saiga A, Sakaguchi G;
XX
XX
DR   WPI; 1996-455367/45.
XX
XX
PT   DNA molecule with gene expression regulation activity - for use in
XX
XX
PT   e.g. treatment of human T-cell leukaemia and HIV, as antiviral agent
XX
XX
PT   and for detecting cancer
XX
XX
PS   Example 1; Page 48; 77pp; Japanese.
XX
XX
SQ   The sequences given in AAT42904-16 are primers which were used in the
CC   construction of the plasmid of the invention. The plasmid contains a
CC   DNA sequence encoding the protein TSP-1 in conjunction with a DNA
CC   molecule with gene expression regulation activity. The plasmid is
CC   used for regulation of gene expression, and treatment of viral
CC   infection pref. human T-cell leukaemia and HIV. The plasmid also encodes
CC   a protein which is used as an antiviral agent, and also in a method for
CC   detecting cancer. The DNA molecule and protein have potential uses in
CC   gene therapy, and the plasmid may also have potential use in the
CC   treatment of TSP.
XX
XX
SQ   Sequence 29 BP; 8 A; 5 C; 10 G; 6 T; 0 other;
XX
XX
Query Match      46.7%; Score 14; DB 17; Length 29;
Best Local Similarity 100.0%; Pred.No.5.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 CTCCTTCCTGCGCC 19
      19 CTCCTTCCTGCGCC 6
DB

```

```

XX
XX
OS   Synthetic.
XX
XX
PN   US552676-A.
XX
XX
PD   18-JUN-1996.
XX
XX
PF   29-MAR-1989; 89US-0330566.
XX
XX
PR   06-DEC-1989; 89US-0446584.
PR   29-MAR-1989; 89US-0330566.
PR   17-AUG-1992; 92US-0928661.
PR   22-MAR-1993; 93US-0047041.
XX
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
XX
PI   Baker SJ, Fearon ER, Nigro JM, Vogelstein B;
XX
XX
DR   WPI; 1996-299851/30.
XX
XX
PT   Nucleic acid assay for cancer detection - based on comparing
XX
XX
PT   neoplastic p53 gene with wild-type p53 gene
XX
XX
PS   Example 4; Column 10; 38pp; English.
XX
XX
SQ   The primer pair AAT36484/85 was used for the PCR amplification of a
CC   111 bp fragment of the human p53 gene, which may contain the tumour
CC   nude mouse xenograft (Cx3) mutation, Val 143 Ala, where the wild
CC   type codon 143 GTG is substd. with GCG. This mutation also
CC   introduces a new HhaI site (GGCC at nucleotides 427-430), so that
CC   HhaI cleavage of a PCR prod. amplified from a mutant template
CC   produces 68 and 43 nucleotide subfragments, which can be detected
CC   by gel electrophoresis separation, followed by radioactive probe
CC   hybridisation. This assay can be used to diagnose the presence of
CC   the Val 143 Ala mutation, and therefore the Cx3 tumour.
XX
XX
SQ   Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;
XX
XX
Query Match      43.3%; Score 13; DB 17; Length 21;
Best Local Similarity 100.0%; Pred.No.1.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 TTCCTTCCTTCGC 15
      1 TTCCTTCCTTCGC 13
DB

```

```

RESULT 9
AAT36484
ID   AAT36484 standard; DNA; 21 BP.
XX
XX
AC   AAT36484;
XX
XX
DT   09-OCT-1996 (first entry)
XX
XX
DE   Upstream PCR primer for p53 gene region contg. Val 143 Ala mutation.
XX
XX
KW   Primer; PCR; polymerase chain reaction; amplification; human;
KW   p53 gene; tumour; cancer; Cx3; mutation; Val 143 Ala; assay;
KW   HhaI cleavage site; detection; gel electrophoresis; diagnosis;
KW   radioactive probe hybridisation; nude mouse xenograft; ss.
XX
XX

```

```

RESULT 10
AAA72585
ID   AAA72585 standard; DNA; 21 BP.
XX
XX
AC   AAA72585;
XX
XX
DT   27-NOV-2000 (first entry)
XX
XX
DE   Upstream PCR primer for mutant p53 gene fragment amplification.
XX
XX
KW   Human; p53; chromosome 17p; neoplastic tissue detection; lung; breast;
KW   brain; colorectal; bladder; mesenchyme; prostate; stomach; cancer;
KW   tumour; leukaemia; osteosarcoma; PCR primer; ss.
XX
XX
OS   Homo sapiens.
XX
XX
PN   US6090566-A.
XX
XX
PD   18-JUL-2000.
XX
XX
PF   02-JUN-1995; 95US-0459676.
XX
XX
PR   22-MAR-1993; 93US-0047041.
PR   06-DEC-1989; 89US-0446584.
PR   17-AUG-1992; 92US-0928661.
PR   29-MAR-1989; 89US-0330566.
XX
XX

```

XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA Nigro JM, Fearon ER, Baker SJ, Vogelstein B;  
 PI WPI; 2000-531419/48.  
 XX  
 XX Determining neoplastic tissue by detecting alteration in sequence of  
 PT neoplastic p53 proteins and wild type p53, comparing antibody binding  
 PT to p53 proteins or testing antigen complexing ability of p53 proteins  
 PT  
 XX  
 PS Example 4; Column 10; 19pp; English.  
 CC A method for determining whether a human tissue is neoplastic comprises  
 CC detecting an alteration in the amino acid sequence of the p53 proteins in  
 CC a neoplastic tissue and wild type tissue by comparing binding of a  
 CC monoclonal antibody to the two p53 proteins and detecting loss of binding  
 CC in the mutant compared to the wild type protein. Alternatively a mutation  
 CC may be detected by testing the ability of the p53 proteins to bind an  
 CC antigen. Several genetic alterations occur during colorectal tumour  
 CC formation, the most common of which are deletions of the short arm of  
 CC chromosome 17. Allelic deletions of chromosome 17p particularly in the  
 CC p53 gene occur in a wide variety of cancers. The method of the invention  
 CC is useful for the diagnosis of neoplastic tissues such as lung, breast,  
 CC brain, colorectal, bladder, mesenchyme, prostate or stomach tumours and  
 CC also in the diagnosis of leukaemia and osteosarcoma.  
 CC The present sequence represents a PCR primer used to amplify a fragment  
 CC of the human p53 gene from a tumour which has an allelic deletion of  
 CC chromosome 17p, yet still expresses p53. The primer is used to determine  
 CC that the tumour carries a point mutation at codon 143 of the p53 gene.  
 CC  
 SQ Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;  
 Query Match 43.3%; Score 13; DB 21; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TTCCCTTCTCTGC 15  
 DB 1 TTCCCTTCTCTGC 13  
 RESULT 11  
 ID AAH47842 standard; DNA; 21 BP.  
 AC AAH47842;  
 XX  
 XX 21-SEP-2001 (first entry)  
 DT  
 XX Human p53 PCR primer 1.  
 DE Human; p53; PCR primer; immunological detection; ss.  
 KW Homo sapiens.  
 OS  
 XX JP2001128685-A.  
 PN  
 XX 15-MAY-2001.  
 PD  
 XX 05-NOV-1999; 99JP-0315678.  
 PF  
 XX 05-NOV-1999; 99JP-0315678.  
 PR  
 XX (IATR ) IATRON LAB INC.  
 PA  
 XX WPI; 2001-373029/39.  
 DR  
 XX A method for detection of variation of human p53 gene.  
 PT  
 XX Claim 2; Page 10; 12pp; Japanese.  
 PS  
 XX

CC The present sequence is that of a PCR primer for detection of variation  
 CC in the human p53 gene useful to the invention. The invention relates to  
 CC detection of variation in the human p53 gene with an antibody which  
 CC specifically react with human p53 protein by steps of: immunological  
 CC detection of a sample with immunological staining; separation of stained  
 CC and un-stained cells; extraction of genome DNA from stained cells;  
 CC PCR amplification of a p53 DNA fragment which may contain an area of  
 CC variation of human p53 gene from the genome DNA obtained in the  
 CC preceding extraction step; and analysis of the reaction product.  
 CC  
 SQ Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;  
 Query Match 43.3%; Score 13; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TTCCCTTCTCTGC 15  
 DB 1 TTCCCTTCTCTGC 13

RESULT 12  
 ID AAT72696 standard; DNA; 31 BP.  
 AC AAT72696;  
 XX  
 XX 18-SEP-1997 (first entry)  
 DT  
 XX Sugar biosynthesis gene eryBII PCR primer.  
 DE  
 XX  
 XX Polyketide; glycosylation; eryBII; L-mycarose; antimicrobial;  
 KW antibiotic; antifungal; fungicide; anticancer; cytostatic;  
 KW anthelmintic; Saccharopolyspora erythraea; primer; PCR;  
 KW polymerase chain reaction; px86; oleandomycin; ss.  
 OS Synthetic.  
 XX  
 XX MO9723630-A2.  
 PN  
 XX 03-JUL-1997.  
 PD  
 XX 23-DEC-1996; 96WO-US20238.  
 PF  
 XX 21-DEC-1995; 95US-0576626.  
 PR  
 XX (ABBO ) ABBOTT LAB.  
 PA  
 XX Donadio S, Katz L, Staver MJ, Summers RG;  
 PI WPI; 1997-351066/32.  
 DR  
 XX New genes involved in sugar biosynthesis and attachment - used to  
 PT generate polyketide antimicrobials etc. with altered pattern of  
 PT glycosylation  
 PT  
 XX  
 PS Example 3; Page 25; 85pp; English.  
 CC 2 PCR primers (AAT72696-97) were used to amplify a 1.0 kb DNA  
 CC segment comprising nucleotides 2385-3410 of a Saccharopolyspora  
 CC erythraea gene segment (AAT72684), covering the eryBII gene that  
 CC encodes an enzyme (AAM19736) involved in L-mycarose biosynthesis.  
 CC The amplified DNA was utilised in the construction of plasmid pXB4  
 CC and hence of plasmid pXB6, which was used to transform Streptomyces  
 CC antibioticus ATCC 11891, resulting in prodn. of the novel  
 CC polyketide 3-des-oleandomycin-3-mycarosyl oleandomycin.  
 CC  
 SQ Sequence 31 BP; 10 A; 8 C; 11 G; 2 T; 0 other;  
 Query Match 43.3%; Score 13; DB 18; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	8	CTTCCTGCGGCT	20
Db	19	CTTCCTGCGGCT	7

## RESULT 13

ID AAL28060 standard; DNA; 50 BP.

AC AAL28060;  
...

DT 24-JAN-2002 (first entry)

Human SNP oligonucleotide #1268

KW immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001

28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 1743; 4143pp; English

CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogene,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesin, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.

50 BP; 11 A; 14 C; 8 G; 17 T; 0 other;

Query Match	43.3%	Score 13:	DB 22:	Length 50:
Best Local Similarity	100.0%	Pred. NO.	1.7e+03:	
Matches 13;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	16	GGCCTGAACGGT	28
Db	21	GGCCTGAACGGT	9

RESULT 14  
AAL34593/c  
ID AAL34593 standard; DNA; 50 BP.

AC AAL34593 ;

DT 24-JAN-2002 (first entry)

Human SNP oligonucleotide #7801.

immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
 amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 complement related protein; cyclochrome; kinesin; cytokine; interferon;  
 interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 multifactorial disease; autoimmune disease; infection;  
 nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001

PF 28-DEC-2000; 2000WO-US35498

PR 28-DEC-1999; 99US-0173419

PR 27-DEC-2000; 2000US-0173419

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 3646; 4143pp; English

CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesin, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.

**SQ** Sequence 50 BP; 17 A; 12 C; 15 G; 6 T; 0 other;

Query Match	43.3%	Score 13	DB 22	length 50
Best Local Similarity	100.0%	Pred. No.	1.7e+03	
Matches 13	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	7	TCTTCCTGGGCC	1
Db	21	TCTTCCTGGGCC	9

## RESULT 15

```

AAV41171
ID AAV41171 standard; DNA; 12 BP.
XX
AC AAV41171:
XX
DN 08-OCT-1998 (first entry)
XX
DE RNA component of human telomerase (hTR) antisense oligo 14d.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN MO9828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97MO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
XX
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX
DR WPI; 1998-37670/32.
XX
PT New polynucleotide(s) antisense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Claim 11; Page 65; 80pp; English.
XX
CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 12 BP; 0 A; 6 C; 1 G; 5 T; 0 other;

```

Query Match 40.0%; Score 12; DB 19; Length 12;  
 Best Local Similarity 100.0%; Freq. No. 5; 7e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 CGTCTCTTCC 12
   |||||
DB 1 CGTCTCTTCC 12

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 348.884 Seconds

(without alignments)  
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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

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Minimum DB seq length: 0

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Post-Processing: listing first 45 summaries

Database :

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8: gb\_pl:\*

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13: gb\_un:\*

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29: em\_vl:\*

30: em\_hcg\_hum:\*

31: em\_hcg\_inv:\*

32: em\_hcg\_other:\*

33: em\_hcg\_mus:\*

34: em\_hcg\_pin:\*

35: em\_hcg\_rod:\*

36: em\_hcg\_mam:\*

37: em\_hcg\_vrt:\*

38: em\_sy:\*

39: em\_hcgo\_hum:\*

40: em\_hcgo\_mus:\*

41: em\_hcgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	6	AR063826
2	20	66.7	20	6	AR4604
3	20	66.7	20	6	AR063827
4	20	66.7	20	6	AR063836
5	20	66.7	20	6	AR079894
6	19	63.3	20	6	AR4597
7	19	63.3	20	6	AR079898
8	14	46.7	29	6	AR146661
9	13	43.3	20	6	AR067594
10	13	43.3	31	6	AR092735
11	13	43.3	42	6	AR024197
12	13	43.3	45	6	AR024198
13	12	40.0	12	6	AR063828
14	12	40.0	19	6	A35686
15	12	40.0	20	6	I21035
16	12	40.0	20	6	I21062
17	12	40.0	24	6	AX445453
18	12	40.0	25	6	AX196979
19	12	40.0	31	6	BD002728
20	12	40.0	33	6	AR162875
21	12	40.0	33	6	AR194025
22	12	40.0	36	6	A41698
23	12	40.0	36	6	E59618
24	12	40.0	36	6	I05106
25	12	40.0	36	6	I07406
26	12	40.0	36	6	I07637
27	12	40.0	36	6	I71445
28	12	40.0	37	6	AX283664
29	12	40.0	38	6	AX375329
30	12	40.0	42	6	BD006272
31	12	40.0	42	6	AX166899
32	12	40.0	43	6	A51765
33	12	40.0	43	6	AR070601
34	12	40.0	43	6	I89763
35	12	40.0	49	6	A41685
36	11	36.7	11	6	AR051288
37	11	36.7	11	6	AR051324
38	11	36.7	11	6	I16936
39	11	36.7	11	6	I45730
40	11	36.7	12	6	AR051289
41	11	36.7	12	6	I16937
42	11	36.7	12	6	I45731
43	11	36.7	14	6	AR036791
44	11	36.7	17	6	AR199264
45	11	36.7	18	6	AR166765

#### ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	FEATURES
1	AR063826	Sequence 2 from patent US 5846723.	30 bp	DNA	linear	PAT 29-SEP-1999	Unknown.	Kim,N.Moo., Wu,P., Kealey,J.T., Pruzan,R. and Weinrich,S.L.	Methods for detecting the RNA component of telomerase	Patent: US 5846723-A 2 08-DEC-1998;	Location/Qualifiers
2	AR063826	Sequence 2 from patent US 5846723.	30 bp	DNA	linear	PAT 29-SEP-1999	Unknown.	Kim,N.Moo., Wu,P., Kealey,J.T., Pruzan,R. and Weinrich,S.L.	Methods for detecting the RNA component of telomerase	Patent: US 5846723-A 2 08-DEC-1998;	Location/Qualifiers

Source 1.30  
/organism="unknown"

BASE COUNT 4 a 10 c 8 g 8 t  
ORIGIN

Query Match 100.0%; Score 30; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 8.9e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTGCGGCTGAACGGTGA 30  
Db 1 CGTTCCTCTTCTGCGGCTGAACGGTGA 30

## RESULT 2

LOCUS A84604 Sequence 14 from Patent WO9845450. 20 bp DNA linear PAT 21-JAN-2000  
DEFINITION A84604.1 GI:6733517  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Atkinson,E.M. and Kealey,J.T.  
TITLE PURIFIED TELOMERASE  
JOURNAL Patent: WO 9845450-A 14 15-OCT-1998;  
GERON CORP (US)  
FEATURES  
Source 1.20  
Location/Qualifiers  
/organism="unknown"  
/db\_xref="taxon:32644"

BASE COUNT 0 a 9 c 4 g 7 t  
ORIGIN

Query Match 66.7%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTGCGGCT 20  
Db 1 CGTTCCTCTTCTGCGGCT 20

## RESULT 3

LOCUS AR063827 Sequence 3 from patent US 5846723. 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION AR063827  
ACCESSION AR063827.1 GI:5993135  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.  
TITLE Methods for detecting the RNA component of telomerase  
JOURNAL Patent: US 5846723-A 3 08-DEC-1998;  
FEATURES  
Source 1.20  
Location/Qualifiers  
/organism="unknown"

BASE COUNT 0 a 9 c 4 g 7 t  
ORIGIN

Query Match 66.7%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTGCGGCT 20  
Db 1 CGTTCCTCTTCTGCGGCT 20

## RESULT 4

LOCUS AR063836 Sequence 12 from patent US 5846723. 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION AR063836  
ACCESSION AR063836.1 GI:5993144  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.  
TITLE Methods for detecting the RNA component of telomerase  
JOURNAL Patent: US 5846723-A 12 08-DEC-1998;  
FEATURES  
Source 1.20  
Location/Qualifiers  
/organism="unknown"

BASE COUNT 0 a 9 c 4 g 7 t  
ORIGIN

Query Match 66.7%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTGCGGCT 20  
Db 1 CGTTCCTCTTCTGCGGCT 20

RESULT 4  
LOCUS AR063836 Sequence 12 from patent US 5846723. 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION AR063836  
ACCESSION AR063836.1 GI:5993144  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.  
TITLE Methods for detecting the RNA component of telomerase  
JOURNAL Patent: US 5846723-A 12 08-DEC-1998;  
FEATURES  
Source 1.20  
Location/Qualifiers  
/organism="unknown"

BASE COUNT 4 a 6 c 7 g 3 t  
ORIGIN

Query Match 66.7%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGTTCCTCTTCTGCGGCTGAACGGTGA 30  
Db 1 CGTTCCTCTTCTGCGGCTGAACGGTGA 20

RESULT 5  
LOCUS AR079894 Sequence 7 from patent US 5968506. 20 bp DNA linear PAT 31-AUG-2000  
DEFINITION AR079894  
ACCESSION AR079894.1 GI:10006647  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vaessero,A.P., Pruzan,R.A. and Kealey,J.T.  
TITLE Purified telomerase  
JOURNAL Patent: US 5968506-A 7 19-OCT-1999;  
FEATURES  
Source 1.20  
Location/Qualifiers  
/organism="unknown"

BASE COUNT 0 a 9 c 4 g 7 t  
ORIGIN

Query Match 66.7%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTGCGGCT 20  
Db 1 CGTTCCTCTTCTGCGGCT 20

## RESULT 6

LOCUS A84597 Sequence 7 from Patent WO9845450. 20 bp DNA linear PAT 21-JAN-2000  
DEFINITION A84597  
ACCESSION A84597.1 GI:6733513  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Atkinson,E.M. and Kealey,J.T.  
TITLE PURIFIED TELOMERASE

BASE COUNT 0 a 9 c 4 g 7 t  
ORIGIN

Query Match 66.7%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTGCGGCT 20  
Db 1 CGTTCCTCTTCTGCGGCT 20

## RESULT 6

LOCUS A84597 Sequence 7 from Patent WO9845450. 20 bp DNA linear PAT 21-JAN-2000  
DEFINITION A84597  
ACCESSION A84597.1 GI:6733513  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Atkinson,E.M. and Kealey,J.T.  
TITLE PURIFIED TELOMERASE

BASE COUNT 0 a 9 c 4 g 7 t  
ORIGIN

Query Match 66.7%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTGCGGCT 20  
Db 1 CGTTCCTCTTCTGCGGCT 20



JOURNAL Patent: WO 9845450-A 7 15-OCT-1998;  
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 Location/Qualifiers  
 source 1..20  
 /organism="unidentified"  
 /db\_xref="taxon:32644"  
 modified\_base 1  
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 /mod\_base=OTHER

BASE COUNT 0 a 8 c 4 g 7 t 1 others  
 ORIGIN

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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCCTTCTCGCGGCT 20  
 DB 2 GTTCCCTTCTCGCGGCT 20

RESULT 7  
 LOCUS AR079898 20 bp DNA linear PAT 31-AUG-2000  
 DEFINITION Sequence 14 from patent US 5968506.  
 ACCESSION AR079898  
 VERSION AR079898.1 GI:10006651  
 KEYWORDS

SOURCE Unknown.  
 ORGANISM Unidentified.  
 1 (bases 1 to 20)  
 REFERENCES Weirich,S.L., Atkinson,E.M. II, Lichtsteiner,S.P., Vassero,A.P.,  
 Pruzan,R.A. and Kealey,J.T.  
 TITLE Purified telomerase  
 JOURNAL Patent: US 5968506-A 14 19-OCT-1999;  
 FEATURES Location/Qualifiers  
 source 1..20  
 /organism="unknown"

BASE COUNT 0 a 8 c 4 g 7 t 1 others  
 ORIGIN

Query Match 63.3%; Score 19; DB 6; Length 20;  
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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCCTTCTCGCGGCT 20  
 DB 2 GTTCCCTTCTCGCGGCT 20

RESULT 8  
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 DEFINITION Sequence 14 from patent US 6218522.  
 ACCESSION ARI46661  
 VERSION ARI46661.1 GI:15109850  
 KEYWORDS

SOURCE Unknown.  
 ORGANISM Unidentified.  
 1 (bases 1 to 29)  
 REFERENCES Saiga,A., Orita,S., Igarashi,H., Okumura,K. and Sakaguchi,G.  
 TITLE DNA molecule relating to suppression of gene expression and novel  
 JOURNAL Protein Patent: US 6218522-A 14 17-APR-2001;  
 FEATURES Location/Qualifiers  
 source 1..29  
 /organism="unknown"

BASE COUNT 8 a 5 c 10 g 6 t  
 ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCTCCCGCGGCC 19  
 DB 19 CTCTCCCGCGGCC 6

RESULT 9  
 LOCUS AR067594 20 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 1 from patent US 5851769.  
 ACCESSION AR067594  
 VERSION AR067594.1 GI:5998816  
 KEYWORDS

SOURCE Unknown.  
 ORGANISM Unidentified.  
 1 (bases 1 to 20)  
 REFERENCES Gray,J.W. and Weller,H.-U.G.  
 TITLE Quantitative DNA fiber mapping  
 JOURNAL Patent: US 5851769-A 1 22-DEC-1998;  
 FEATURES Location/Qualifiers  
 source 1..20  
 /organism="unknown"

BASE COUNT 2 a 8 c 2 g 8 t  
 ORIGIN

Query Match 43.3%; Score 13; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCCTTCTCGC 15  
 DB 1 TTCCCTTCTCGC 13

RESULT 10  
 LOCUS AR092735/c 31 bp DNA linear PAT 08-SEP-2000  
 DEFINITION Sequence 15 from patent US 5998194.  
 ACCESSION AR092735  
 VERSION AR092735.1 GI:10019487  
 KEYWORDS

SOURCE Unknown.  
 ORGANISM Unidentified.  
 1 (bases 1 to 31)  
 REFERENCES Summers,R.G. Jr., Katz,L., Donadio,S. and Staver,M.J.  
 TITLE Polyketide-associated sugar biosynthesis genes  
 JOURNAL Patent: US 5998194-A 15 07-DEC-1999;  
 FEATURES Location/Qualifiers  
 source 1..31  
 /organism="unknown"

BASE COUNT 10 a 8 c 11 g 2 t  
 ORIGIN

Query Match 43.3%; Score 13; DB 6; Length 31;  
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QY 8 CTTCCTGCGGCT 20  
 DB 19 CTTCCTGCGGCT 7

RESULT 11  
 LOCUS AR024197/c 42 bp DNA linear PAT 05-DEC-1998  
 DEFINITION Sequence 8 from patent US 5795863.  
 ACCESSION AR024197  
 VERSION AR024197.1 GI:3977491  
 KEYWORDS

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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 42)
AUTHORS     Wolf, D.
TITLE       Recombinant agents affecting thrombosis
JOURNAL     Patent: US 5795863-A 8 18-AUG-1998;
FEATURES    Location/Qualifiers
            source
              1..42
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BASE COUNT  12 a 12 g 17 g 4 t
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 TCCTCTCTCTGCG 16
Db          22 TCCTCTCTCTGCG 10

RESULT 12
LOCUS      AR024198 45 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 9 from patent US 5795863.
ACCESSION  AR024198
VERSION     AR024198.1 GI:3977492
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 45)
AUTHORS     Wolf, D.
TITLE       Recombinant agents affecting thrombosis
JOURNAL     Patent: US 5795863-A 9 18-AUG-1998;
FEATURES    Location/Qualifiers
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BASE COUNT  14 a 14 g 18 g 4 t
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QY          4 TCCTCTCTCTGCG 16
Db          22 TCCTCTCTCTGCG 10

RESULT 13
LOCUS      AR063828 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5846723.
ACCESSION  AR063828
VERSION     AR063828.1 GI:5993136
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim, N. W., Wu, F., Keasley, J. T., Pruzan, R., and Weintrich, S. L.
TITLE       Methods for detecting the RNA component of telomerase
JOURNAL     Patent: US 5846723-A 4 08-DEC-1998;
FEATURES    Location/Qualifiers
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BASE COUNT  0 a 6 c 1 g 5 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.2e+04;

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 CGTCTCTCTTCC 12
Db          1 CGTCTCTCTTCC 12

RESULT 14
LOCUS      A35686/c 19 bp DNA linear PAT 02-DEC-1996
DEFINITION Synthetic human IFN-alpha 2 gene oligo.
ACCESSION  A35686
VERSION     A35686.1 GI:1927068
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Camde, R. and Edge, M. D.
TITLE       Analogous interferon polypeptides, process for their preparation
JOURNAL     Patent: EP 0194006-A 131 10-SEP-1986;
FEATURES    Imperial Chemical Industries PLC
            Location/Qualifiers
            source
              1..19
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              /db_xref="taxon:32630"
BASE COUNT  4 a 5 c 6 g 4 t
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 CTCTCTCTGCGG 17
Db          15 CTCTCTCTGCGG 4

RESULT 15
LOCUS      I21035/c 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 6 from patent US 5518880.
ACCESSION  I21035
VERSION     I21035.1 GI:1601389
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Leonard, W. J., Noguchi, M., and McBride, O. Wesley.
TITLE       Methods for diagnosis of XSCID and kits thereof
JOURNAL     Patent: US 5518880-A 6 21-MAY-1996;
FEATURES    Location/Qualifiers
            source
              1..20
              /organism="unknown"
BASE COUNT  8 a 1 c 9 g 2 t
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 GTTCTCTCTTCT 13
Db          18 GTTCTCTTCTCT 7

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Job time : 356.346 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 477.769 Seconds  
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Title: US-08-770-564a-3

Perfect score: 1 CGTTCCTCTCTGCGGCT 20

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Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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12: /cgn2\_6/prodata/1/pna/US60\_NEW\_COMB.seq2:\*  
13: /cgn2\_6/prodata/1/pna/US60\_NEW\_COMB.seq3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.4	72.0	25	12	US-60-427-808-363970, Sequence 363970,
2	14.4	72.0	25	12	US-60-427-808-469548, Sequence 469548,
3	14.2	71.0	22	9	US-10-310-188-18988, A Sequence 18988, A
4	14.2	71.0	25	9	US-10-098-2638-114611, Sequence 114611,
5	14.2	71.0	25	9	US-10-355-577-421837, Sequence 421837,
6	14.2	71.0	25	12	US-60-427-808-324892, Sequence 324892,
7	14.2	71.0	25	12	US-60-427-808-504791, Sequence 504791,
8	14.2	71.0	25	12	US-60-427-836-347776, Sequence 347776,
9	14.2	71.0	50	5	US-09-749-2808-7801, Sequence 7801, Ap
10	14	70.0	19	1	PCT-US03-04088-26, Sequence 26, Appl
11	14	70.0	18	9	PCT-US03-04088-290, Sequence 290, Appl
12	13.8	69.0	23	10	US-10-310-188-1208, Sequence 1208, Ap
13	13.8	69.0	23	10	US-10-287-787-17323, Sequence 17323, A
14	13.8	69.0	24	10	US-10-287-787-17324, Sequence 17324, A
15	13.8	69.0	25	6	US-09-660-222-118104, Sequence 118104,
16	13.8	69.0	25	9	US-10-098-2638-23782, Sequence 23782, A
17	13.8	69.0	25	9	US-10-355-577-593121, Sequence 593121,
18	13.8	69.0	25	9	US-10-355-577-646261, Sequence 646261,
19	13.8	69.0	25	9	US-10-355-577-749521, Sequence 749521,
20	13.8	69.0	25	12	US-60-427-808-614542, Sequence 614542,

21	13.8	69.0	25	12	US-60-427-808-829890, Sequence 829890,
22	13.8	69.0	25	12	US-60-427-836-165430, Sequence 165430,
23	13.8	69.0	33	9	US-10-341-967-6, Sequence 6, Appl1
24	13.8	69.0	39	8	US-10-447-242-23365, Sequence 23365, A
25	13.8	69.0	47	9	US-10-349-143-3619, Sequence 3619, Ap
26	13.6	68.0	24	9	US-10-310-188-76318, Sequence 76318, A
27	13.6	68.0	25	7	US-09-953-570-107932, Sequence 107932,
28	13.6	68.0	25	7	US-09-954-4454-5462, Sequence 5462, Ap
29	13.6	68.0	25	9	US-10-098-2638-69585, Sequence 69585, A
30	13.6	68.0	25	12	US-60-427-808-194584, Sequence 194584,
31	13.6	68.0	25	12	US-60-427-808-636422, Sequence 636422,
32	13.6	68.0	25	12	US-60-427-808-636423, Sequence 636423,
33	13.6	68.0	25	12	US-60-427-808-636425, Sequence 636425,
34	13.6	68.0	50	9	US-10-325-899-38659, Sequence 3869, Ap
35	13.4	67.0	20	6	US-09-905-688-11, Sequence 11, Appl
36	13.4	67.0	21	4	US-08-825-746-11, Sequence 11, Appl
37	13.4	67.0	25	7	US-09-953-570-16633, Sequence 16633, A
38	13.4	67.0	25	7	US-09-953-570-16639, Sequence 16639, A
39	13.4	67.0	25	7	US-09-953-570-16672, Sequence 16672, A
40	13.4	67.0	25	7	US-09-953-570-16673, Sequence 16673, A
41	13.4	67.0	25	9	US-10-355-577-397620, Sequence 397620,
42	13.4	67.0	25	9	US-10-355-577-766703, Sequence 766703,
43	13.4	67.0	25	12	US-60-427-836-194000, Sequence 194000,
44	13.4	67.0	25	12	US-60-427-836-352087, Sequence 352087,
45	13.4	67.0	25	12	US-60-427-836-384194, Sequence 384194,

## ALIGNMENTS

RESULT 1  
US-60-427-808-363970  
; Sequence 363970, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 363970  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-363970

Query Match 72.0%; Score 14.4; DB 12; Length 25;  
Best Local Similarity 93.8%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTCCTCTCTCTGCGGC 18  
DB 5 TTCCTCTCTCTGCGGC 20

RESULT 2  
US-60-427-808-469548  
; Sequence 469548, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 469548  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-469548

Query Match 72.0%; Score 14.4; DB 12; Length 25;  
Best Local Similarity 93.8%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTCCTCTCTCGG 17  
DB 9 GTTCCTCTCTGTGG 24

RESULT 3  
US-10-310-188-18988  
; Sequence 18988, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES  
; FILE REFERENCE: 47487  
; CURRENT APPLICATION NUMBER: US/10/310,188  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18988  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-18988

Query Match 71.0%; Score 14.2; DB 9; Length 22;  
Best Local Similarity 84.2%; Pred. No. 1.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGC 19  
DB 4 CTTCTCTCTCTCGGCGC 22

RESULT 4  
US-10-098-263B-114611  
; Sequence 114611, Application US/10098263B  
; GENERAL INFORMATION:  
; APPLICANT: Mitterman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 114611  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-114611

Query Match 71.0%; Score 14.2; DB 9; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCCTCTCTCGGCGC 20  
DB 6 GTTCCTCTCTCGACCT 24

RESULT 5  
US-10-355-577-421837/c  
; Sequence 421837, Application US/10355577  
; GENERAL INFORMATION:  
; APPLICANT: Mitterman, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
; FILE REFERENCE: 3121  
; CURRENT APPLICATION NUMBER: US/10/355,577  
; CURRENT FILING DATE: 2003-01-31

; NUMBER OF SEQ ID NOS: 997516  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 421837  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-355-577-421837

Query Match 71.0%; Score 14.2; DB 9; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGC 19  
DB 20 GTTACCTCTCTCGGCGC 2

RESULT 6  
US-60-427-808-324892  
; Sequence 324892, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 324892  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-324892

Query Match 71.0%; Score 14.2; DB 12; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCCTCTCTCGGCGC 20  
DB 3 GTTACCTCTCTCGACCT 21

RESULT 7  
US-60-427-808-504791  
; Sequence 504791, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 504791  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-504791

Query Match 71.0%; Score 14.2; DB 12; Length 25;  
Best Local Similarity 84.2%; Pred. No. 1.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCCTCTCTCGGCGC 20  
DB 6 GTTACCTCTCTCGACCT 24

RESULT 8  
US-60-427-836-347776/c  
; Sequence 347776, Application US/60427836  
; GENERAL INFORMATION:

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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 347776
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-60-427-836-347776

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Query Match          71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      2 GTTCTCTTCTGCGGCT 20
DB      20 GGTCTTCTGCTGCGGCT 2

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RESULT 9
US-09-749-2808-7801/c
; Sequence 7801, Application US/097492808
; GENERAL INFORMATION:
; APPLICANT: Shimketers, Richard A.
; APPLICANT: Leach, Martin
; TITLE OF INVENTION: Nucleic Acids Containing Single
; FILE REFERENCE: 15966-610
; CURRENT APPLICATION NUMBER: US/09/749,2808
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/173,419
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 10038
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 7801
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (25)...(26)
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43294227
; US-09-749-2808-7801

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Query Match          71.0%; Score 14.2; DB 5; Length 50;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      1 CGTTCTCTTCTGCGGCT 19
DB      27 CATGCGCTTCTGCGGCT 9

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RESULT 10
PCT-US03-04088-26/c
; Sequence 26, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
; Expression Using Short Interfering RNA (siRNA)

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```

; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; PCT-US03-04088-26

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Query Match          70.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      7 TCTTCTGCGGCT 20
DB      19 TCTTCTGCGGCT 6

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RESULT 11
PCT-US03-04088-290
; Sequence 290, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
; Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial

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Fri Jun 27 07:42:29 2003

us-08-770-564a-3.inpn

Page 4

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense  
OTHER INFORMATION: region  
PCT-US03-04088-290

Query Match 70.0%; Score 14; DB 1; Length 19;  
Best Local Similarity 64.3%; Pred. No. 1.6e+04;  
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCTGCGGCT 20  
DB 1 UCUUCGCGGCTU.14

RESULT 12  
US-10-310-188-1208/c  
Sequence 1208, Application US/10310188  
GENERAL INFORMATION:  
APPLICANT: Rosecrans  
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES  
FILE REFERENCE: 47487  
CURRENT APPLICATION NUMBER: US/10/310,188  
CURRENT FILING DATE: 2002-12-19  
NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: Patent version 3.1  
SEQ ID NO 1208  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-310-188-1208

Query Match 69.0%; Score 13.8; DB 9; Length 18;  
Best Local Similarity 88.2%; Pred. No. 1.9e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCCTCTGCGGCT 20  
DB 18 TCCTCTGCGGCT 2

RESULT 13  
US-10-287-787-17323  
Sequence 17323, Application US/10287787  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Caulobacter crescentus complete genome.  
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/287,787  
CURRENT FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 27958  
SOFTWARE: Proprietary  
SEQ ID NO 17323  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Caulobacter crescentus complete genome.  
FEATURE:  
LOCATION: (2648691)...(2648713)  
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 19213  
US-10-287-787-17323

Query Match 69.0%; Score 13.8; DB 10; Length 23;  
Best Local Similarity 88.2%; Pred. No. 1.9e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTTCTCTGCGGCT 18  
DB 1 GTTCTCTGCGGCT 17

RESULT 14  
US-10-287-787-17324/c  
Sequence 17324, Application US/10287787

GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Caulobacter crescentus complete genome.  
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/287,787  
CURRENT FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 27958  
SOFTWARE: Proprietary  
SEQ ID NO 17324  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Caulobacter crescentus complete genome.  
FEATURE:  
LOCATION: (2648691)...(2648713)  
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1921  
US-10-287-787-17324

Query Match 69.0%; Score 13.8; DB 10; Length 24;  
Best Local Similarity 88.2%; Pred. No. 1.9e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTTCTCTGCGGCT 18  
DB 24 GTTCTCTGCGGCT 8

RESULT 15  
US-09-660-222-118104  
Sequence 118104, Application US/09660222  
GENERAL INFORMATION:  
APPLICANT: Miltmann et al.  
TITLE OF INVENTION: Methods of Genetic Analysis of Human  
FILE REFERENCE: 3102.1  
CURRENT APPLICATION NUMBER: US/09/660,222  
CURRENT FILING DATE: 2000-09-12  
PRIOR FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 140981  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 118104  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: Genbank X56654  
US-09-660-222-118104

Query Match 69.0%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.9e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTCTCTGCGGCT 17  
DB 2 CGTCTCTGCGGCT 18

Search completed: June 26, 2003, 04:15:08  
Job time : 487.077 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 2545.58 Seconds  
(without alignments)  
296.308 Million cell updates/sec

Title: US-08-770-564A-2  
Perfect score: 30  
Sequence: 1 CGTTCCTTCTTCGCGCGCTGAAACGTGA 30

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues  
Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_MA Main:\*

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2: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq:\*  
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6: /cgn2\_6/ptodata/2/pna/US082\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US083\_COMB.seq:\*  
8: /cgn2\_6/ptodata/2/pna/US084\_COMB.seq:\*  
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20: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq:\*  
21: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq:\*  
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23: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq:\*  
24: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq:\*  
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1	30	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appl1
2	30	100.0	30	11 US-08-770-564A-2	Sequence 2, Appl1
3	30	100.0	31	9 US-08-521-634-17	Sequence 17, Appl1
4	20	66.7	20	1 PCT-US97-23619-3	Sequence 3, Appl1
5	20	66.7	20	1 PCT-US97-23619-27	Sequence 27, Appl1
6	20	66.7	20	11 US-08-770-564A-3	Sequence 3, Appl1
7	20	66.7	20	11 US-08-770-564A-15	Sequence 15, Appl1
8	16.6	55.3	50	1 PCT-US01-47856-304	Sequence 304, App
9	16.6	55.3	40	40 US-10-131-827-304	Sequence 304, App
10	16.6	55.3	50	40 US-10-131-831-304	Sequence 304, App
11	16	53.3	25	36 US-09-956-604-116016	Sequence 116016, App
12	16	53.3	25	36 US-09-956-604-116016	Sequence 116016, App
13	16	53.3	25	36 US-09-956-604-116016	Sequence 116016, App
14	16	53.3	25	36 US-09-956-604-116016	Sequence 116016, App
15	15.8	52.7	20	41 US-10-174-020-71	Sequence 71, Appl1
16	15.8	52.7	20	41 US-10-174-020-138	Sequence 138, App
17	15.8	52.7	40	1 PCT-US99-11295-97	Sequence 97, Appl1
18	15.8	52.7	40	28 US-09-701-626A-97	Sequence 97, Appl1
19	15.6	52.0	44	1 PCT-US02-16223-24	Sequence 24, Appl1
20	15.6	52.0	44	37 US-09-992-430B-55	Sequence 55, Appl1
21	15.6	52.0	44	41 US-10-154-460-24	Sequence 24, Appl1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

22 15.6 52.0 47 3 US-07-972-453-38 Sequence 38, Appl  
 23 15.6 52.0 49 3 US-07-972-453-40 Sequence 40, Appl  
 24 15.4 51.3 25 17 US-09-396-196F-14541 Sequence 14541, A  
 25 15.4 51.3 25 17 US-09-396-196F-71995 Sequence 71995, A  
 26 15.4 51.3 25 17 US-09-396-196G-14541 Sequence 14541, A  
 27 15.4 51.3 25 17 US-09-396-196G-71995 Sequence 71995, A  
 28 15.4 51.3 39 29 US-09-724-750-23365 Sequence 23365, A  
 29 15.4 51.3 39 29 US-09-724-750-23365 Sequence 23365, A  
 30 15.2 50.7 24 1 PCT-US01-30828-5 Sequence 18, Appl  
 31 15.2 50.7 24 1 PCT-US01-42432-18 Sequence 413, App  
 32 15.2 50.7 32 16 US-09-225-201B-413 Sequence 413, App  
 33 15.2 50.7 50 1 PCT-US01-47856-4600 Sequence 4600, App  
 34 15.2 50.7 50 40 US-10-131-827-4600 Sequence 4600, App  
 35 15.2 50.7 50 40 US-10-131-831-4600 Sequence 4600, App  
 36 15 50.0 25 17 US-09-396-196F-18575 Sequence 18575, A  
 37 15 50.0 25 17 US-09-396-196F-18575 Sequence 18575, A  
 38 15 50.0 25 79 US-60-353-987-348389 Sequence 348389, A  
 39 15 50.0 25 79 US-60-353-987-435780 Sequence 435780, A  
 40 15 50.0 25 79 US-60-353-987-546037 Sequence 546037, A  
 41 15 50.0 25 79 US-60-353-987-546261 Sequence 546261, A  
 42 15 50.0 25 79 US-60-353-987-902019 Sequence 902019, A  
 43 15 50.0 25 79 US-60-353-987-902020 Sequence 902020, A  
 44 15 50.0 50 30 US-09-783-606-496 Sequence 496, App  
 45 15 50.0 50 30 US-09-796-460-496 Sequence 496, App

## ALIGNMENTS

## RESULT 1

PCT-US97-23619-2  
 Sequence 2, Application PC/TUS9723619

GENERAL INFORMATION:  
 APPLICANT:  
 APPLICANT:  
 APPLICANT:  
 APPLICANT:  
 TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
 TITLE OF INVENTION: RNA Component of Telomerase  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSES: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US97/23619  
 FILING DATE: Not yet assigned  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/770,564  
 FILING DATE: 20-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/770,565  
 FILING DATE: 20-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Storella, John R.  
 REGISTRATION NUMBER: 32,944  
 REFERENCE/DOCKET NUMBER: 15389-27PC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 FEATURE:  
 NAME/KEY: 1..30  
 LOCATION: 1..30  
 OTHER INFORMATION: /note="oligo 14"  
 PCT-US97-23619-2

Query Match 100.0%; Score 30; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.017;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTGCGGCGCTGAAACGGTGA 30  
 DB 1 CGTTCCTCTCTGCGGCGCTGAAACGGTGA 30

## RESULT 2

US-08-770-564A-2  
 Sequence 2, Application US/08770564A

GENERAL INFORMATION:

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ron

TITLE OF INVENTION: Inhibitory Polynucleotides Directed

TITLE OF INVENTION: Against the RNA Component of Telomerase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESSES:

ADDRESSES: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,564A

FILING DATE: 20-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002200US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-564A-2

Query Match 100.0%; Score 30; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.017;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 3

US-08-521-634-17/c



Sequence 17, Application US/08521634  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/521,634  
FILING DATE: 31-AUG-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,115  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 7-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy J.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 15389-000850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-521-634-17

Query Match 100.0%; Score 30; DB 9; Length 31;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCGCGGCTGAACGGTGA 30  
DB 31 CGTTCCTCTTCGCGGCTGAACGGTGA 2

RESULT 4  
PCT-US97-23619-3  
Sequence 3, Application PC/TUS9723619  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note="oligo 14a"  
PCT-US97-23619-3

Query Match 66.7%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCGCGGCT 20  
DB 1 CGTTCCTCTTCGCGGCT 20

RESULT 5  
PCT-US97-23619-27  
Sequence 27, Application PC/TUS9723619  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note="oligo 14bc"  
PCT-US97-23619-27

Query Match  
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCTGGCGCCTGAACGGTGA 30  
DB 1 CCTGGCGCCTGAACGGTGA 20

RESULT 6  
US-08-770-564A-3  
Sequence 3, Application US/0870564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ron  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-770-564A-3

Query Match  
Best Local Similarity 100.0%; Score 20; DB 11; Length 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCTGGGCGCT 20  
DB 1 CGTTCCTCTCTCTGGGCGCT 20

RESULT 7  
US-08-770-564A-15  
Sequence 15, Application US/0870564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ron  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564A-15

Query Match  
Best Local Similarity 100.0%; Score 20; DB 11; Length 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCTGGCGCCTGAACGGTGA 30  
DB 1 CCTGGCGCCTGAACGGTGA 20

RESULT 8

PCT-US01-47856-304/C  
; Sequence 304, Application PC/TUS0147856  
; GENERAL INFORMATION:  
; APPLICANT: BIOCARDIA, INC.  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Queternous, Thomas  
; APPLICANT: Johnson, Frances  
; APPLICANT: Fry, Kirk  
; APPLICANT: Matcuk, George  
; APPLICANT: Prentice, James  
; APPLICANT: Phillips, Julie  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Altman, Peter  
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING  
; FILE REFERENCE: 506612000140  
; CURRENT APPLICATION NUMBER: PCT/US01/47856  
; CURRENT FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/241,994  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 8832  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 304  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US01-47856-304

Query Match 55.3%; Score 16.6; DB 1; Length 50;  
Best Local Similarity 82.6%; Pred. No. 1.1e+04;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 7 TCTTCCTGGCGCTGAACGGTG 29  
Db 46 TCTTTTGTGGCTGAACGATG 24

RESULT 9  
US-10-131-827-304/C  
; Sequence 304, Application US/10131827  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 304  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-304

Query Match 55.3%; Score 16.6; DB 40; Length 50;  
Best Local Similarity 82.6%; Pred. No. 1.1e+04;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 7 TCTTCCTGGCGCTGAACGGTG 29  
Db 46 TCTTTTGTGGCTGAACGATG 24

RESULT 10  
US-10-131-831-304/C  
; Sequence 304, Application US/10131831  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING  
; TITLE OF INVENTION: TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000121  
; CURRENT APPLICATION NUMBER: US/10/131,831  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9190  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 304  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-831-304

Query Match 55.3%; Score 16.6; DB 40; Length 50;  
Best Local Similarity 82.6%; Pred. No. 1.1e+04;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 7 TCTTCCTGGCGCTGAACGGTG 29  
Db 46 TCTTTTGTGGCTGAACGATG 24

RESULT 11  
US-09-956-604-116016/C  
; Sequence 116016, Application US/09956604  
; GENERAL INFORMATION:  
; APPLICANT: Mittermann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli  
; FILE REFERENCE: 3117.1  
; CURRENT APPLICATION NUMBER: US/09/956,604  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/234,049  
; PRIOR FILING DATE: 2000-09-19  
; NUMBER OF SEQ ID NOS: 141629  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 116016  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
US-09-956-604-116016

Query Match 53.3%; Score 16; DB 36; Length 25;  
Best Local Similarity 79.2%; Pred. No. 1.7e+04;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5 CCTTTCCTGGCGCTGAACGGT 28  
Db 24 CCTATTCAGCGCGCTGAATGTT 1

RESULT 12  
US-09-956-604A-116016/C  
; Sequence 116016, Application US/09956604A  
; GENERAL INFORMATION:  
; APPLICANT: Mittermann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli  
; FILE REFERENCE: 3117.1  
; CURRENT APPLICATION NUMBER: US/09/956,604A  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/234,049  
; PRIOR FILING DATE: 2000-09-19

Fri Jun 27 07:42:19 2003

us-08-770-564a-2.rnmp

Page 6

NUMBER OF SEQ ID NOS: 141629  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 116016  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-09-956-604A-116016

Query Match 53.3%; Score 16; DB 36; Length 25;  
Best Local Similarity 79.2%; Pred. No. 1.7e+04;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CCTCTTCTGCGGCGCTGAACGGT 28  
DB 24 CCTATTCACGCGCGCGTAAATGGT 1

RESULT 13  
US-09-956-604B-116016/c  
Sequence 116016, Application US/09956604B  
GENERAL INFORMATION:  
APPLICANT: Miltmann, Michael  
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli  
FILE REFERENCE: 3117.1  
CURRENT APPLICATION NUMBER: US/09/956,604B  
CURRENT FILING DATE: 2001-09-19  
PRIOR APPLICATION NUMBER: 60/234,049  
PRIOR FILING DATE: 2000-09-19  
NUMBER OF SEQ ID NOS: 141629  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 116016  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-09-956-604B-116016

Query Match 53.3%; Score 16; DB 36; Length 25;  
Best Local Similarity 79.2%; Pred. No. 1.7e+04;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CCTCTTCTGCGGCGCTGAACGGT 28  
DB 24 CCTATTCACGCGCGCGTAAATGGT 1

RESULT 14  
US-60-234-049-104243/c  
Sequence 104243, Application US/60234049  
GENERAL INFORMATION:  
APPLICANT: Miltmann, Michael  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis of  
FILE REFERENCE: 3117  
CURRENT APPLICATION NUMBER: US/60/234,049  
CURRENT FILING DATE: 2000-09-19  
NUMBER OF SEQ ID NOS: 141629  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 104243  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Escherichia coli  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: GenBank U00096  
US-60-234-049-104243

Query Match 53.3%; Score 16; DB 67; Length 25;  
Best Local Similarity 79.2%; Pred. No. 1.7e+04;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CCTCTTCTGCGGCGCTGAACGGT 28  
DB 24 CCTATTCACGCGCGCGTAAATGGT 1

RESULT 15  
US-10-174-020-71  
Sequence 71, Application US/10174020  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monla  
TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EX  
FILE REFERENCE: RTS-0369  
CURRENT APPLICATION NUMBER: US/10/174,020  
CURRENT FILING DATE: 2002-06-17  
NUMBER OF SEQ ID NOS: 149  
SEQ ID NO 71  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-174-020-71

Query Match 52.7%; Score 15.8; DB 41; Length 20;  
Best Local Similarity 89.5%; Pred. No. 2e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTGCGGCGC 19  
DB 2 CGTTCCTTCTGCGGCGC 20

Search completed: June 25, 2003, 06:20:20  
Job time : 2551.19 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 91.1952 Seconds

(without alignments)  
482.732 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30  
Sequence: 1 CGTTCCTCTCTGCGGCGTGAACGGTGA 30

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCR\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCITUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15	50.0	25 9	US-10-098-263B-89577
2	15	50.0	25 9	US-10-098-263B-89578
3	14.6	48.7	39 9	US-09-832-355A-71
4	14.4	48.0	30 9	US-10-251-385-115
5	14.2	47.3	25 9	US-10-098-263B-114611
6	14	46.7	35 9	US-09-978-600-120
7	14	46.7	40 9	US-09-918-696-13
8	13.8	46.0	25 9	US-10-215-112-5699
9	13.8	46.0	25 9	US-10-098-263B-23782
10	13.8	46.0	25 9	US-10-098-263B-127465
11	13.8	46.0	25 9	US-10-098-263B-127466
12	13.8	46.0	25 9	US-10-023-096-3
13	13.6	45.3	25 9	US-10-098-263B-48187
14	13.6	45.3	25 9	US-10-098-263B-69585
15	13.6	45.3	25 9	US-10-098-263B-115381
16	13.6	45.3	25 9	US-10-098-263B-115382
17	13.6	45.3	25 9	US-10-098-263B-115382
18	13.6	45.3	28 10	US-09-225-201-40
19	13.6	45.3	45 9	US-09-995-847-26

20	13.6	45.3	46 9	US-09-995-847-25	Sequence 25, Appl
21	13.4	44.7	24 9	US-09-754-853A-683	Sequence 683, Appl
22	13.4	44.7	25 9	US-10-098-263B-61269	Sequence 61269, A
23	13.4	44.7	25 9	US-10-098-263B-62932	Sequence 62932, A
24	13.4	44.7	25 9	US-10-098-263B-96093	Sequence 96093, A
25	13.4	44.7	25 9	US-10-098-263B-96094	Sequence 96094, A
26	13.4	44.7	25 9	US-10-098-263B-106347	Sequence 106347, A
27	13.4	44.7	31 9	US-09-912-263-428	Sequence 428, Appl
28	13.2	44.0	23 9	US-09-439-429-17	Sequence 17, Appl
29	13.2	44.0	25 9	US-10-215-112-8421	Sequence 8421, Appl
30	13.2	44.0	25 9	US-10-098-263B-24011	Sequence 24011, A
31	13.2	44.0	25 9	US-10-098-263B-48100	Sequence 48100, A
32	13.2	44.0	25 10	US-09-866-108-5278	Sequence 5278, Appl
33	13.2	44.0	25 10	US-09-866-108-5279	Sequence 5279, Appl
34	13.2	44.0	25 10	US-09-866-108-5280	Sequence 5280, Appl
35	13.2	44.0	25 10	US-09-866-108-5281	Sequence 5281, Appl
36	13.2	44.0	25 10	US-09-866-108-5282	Sequence 5282, Appl
37	13.2	44.0	25 10	US-09-866-108-5283	Sequence 5283, Appl
38	13.2	44.0	25 10	US-09-866-108-5284	Sequence 5284, Appl
39	13.2	44.0	25 10	US-09-866-108-5285	Sequence 5285, Appl
40	13.2	44.0	31 9	US-09-836-705-39	Sequence 39, Appl
41	13.2	44.0	38 9	US-09-903-412-18	Sequence 18, Appl
42	13.2	44.0	38 9	US-09-780-533A-3230	Sequence 3230, Appl
43	13.2	44.0	38 9	US-09-930-423-1849	Sequence 1849, Appl
44	13.2	44.0	38 9	US-10-174-717A-18	Sequence 18, Appl
45	13.2	44.0	38 9	US-10-174-717A-18	Sequence 18, Appl

#### ALIGNMENTS

RESULT 1  
US-10-098-263B-89577  
Sequence 89577, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098, 263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 89577  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-89577

Query Match 50.0%; Score 15; DB 9; Length 25;  
Best Local Similarity 78.3%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 7 TCTTCCTGCGGCGCTGAACGGTG 29  
Db 3 TCTTCCTGCGGCGCTGAACGGTTG 25

RESULT 2  
US-10-098-263B-89578  
Sequence 89578, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098, 263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 89578  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-89578

Query Match 50.0%; Score 15; DB 9; Length 25;  
Best Local Similarity 78.3%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 7 TCTCTCGCGCGCTGAAACGGTG 29  
Db 3 TCTCTCGCGCGCTGAAACGGTG 25

RESULT 3  
US-09-832-355A-71/c  
Sequence 71, Application US/09832355A  
Publication No. US20030027751A1  
GENERAL INFORMATION:  
APPLICANT: Kovesdi, Imre  
APPLICANT: Kovesdi, Paul  
TITLE OF INVENTION: VEGF FUSION PROTEINS  
FILE REFERENCE: 205654  
CURRENT APPLICATION NUMBER: US/09/832,355A  
CURRENT FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 126  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 71  
LENGTH: 39  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1..71)  
OTHER INFORMATION: Synthetic  
US-09-832-355A-71

Query Match 48.7%; Score 14.6; DB 9; Length 39;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCTCTTCTCTGCGGCTGA 22  
Db 32 GTTCTCTTCTCTGCGGCTGA 12

RESULT 4  
US-10-251-385-115/c  
Sequence 115, Application US/10251385  
Publication No. US20030105292A1  
GENERAL INFORMATION:  
APPLICANT: Behar, Dominic P.  
APPLICANT: Chalamera, Derek T.  
APPLICANT: Liaw, Chen W.  
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G  
TITLE OF INVENTION: Receptor  
FILE REFERENCE: AREN-0040  
CURRENT APPLICATION NUMBER: US/10/251,385  
CURRENT FILING DATE: 2002-09-20  
PRIOR APPLICATION NUMBER: US/09/170,496  
PRIOR FILING DATE: 1998-10-13  
NUMBER OF SEQ ID NOS: 294  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 115  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: No. US20030105292A1e1 Sequence  
US-10-251-385-115

Query Match 48.0%; Score 14.4; DB 9; Length 30;  
Best Local Similarity 75.0%; Pred. No. 2.8e+03;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTTCTCTTCTCTGCGGCTGAAC 25  
Db 28 GTTCCCATCTTTGGGCTGAAGC 5

RESULT 5  
US-10-098-263B-114611  
Sequence 114611, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Mittman, Michael  
APPLICANT: Mittman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 114611  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-114611

Query Match 47.3%; Score 14.2; DB 9; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GTTCTCTTCTCTGCGGCT 20  
Db 6 GTTCTCTTCTCTGAGCT 24

RESULT 6  
US-09-978-600-120/c  
Sequence 120, Application US/09978600  
Publication No. US20030087858A1  
GENERAL INFORMATION:  
APPLICANT: HERRNSTADT, CORINNA  
APPLICANT: PARKER, WILLIAM D.  
APPLICANT: DAVIS, ROBERT  
APPLICANT: MILLER, SCOTT W.  
TITLE OF INVENTION: Diagnosis, therapy and cellular and animal models for diseases associated with Mitochondrial Defects  
NUMBER OF SEQUENCES: 206  
CORRESPONDENCE ADDRESS:  
ADDRESS: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/978,600  
FILING DATE: 15-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/413,740  
FILING DATE: 30-MAR-1995  
APPLICATION NUMBER: PCT/US95/04063  
FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Bonham, David B.  
REGISTRATION NUMBER: 34297  
REFERENCE/DOCKET NUMBER: 2105/7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 429-1776  
TELEFAX: (202) 429-0796  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 120:  
US-09-978-600-120

Query Match 46.7%; Score 14; DB 9; Length 35;  
Best Local Similarity 77.3%; Pred. No. 4.2e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TTCTCTTCTCGCGGCTGAAC 25  
DB 29 TCCTCTTCATCGGACGACAC 8

RESULT 7  
US-09-918-696-13  
Sequence 13, Application US/09918696  
Publication No. US20030003076A1  
GENERAL INFORMATION:  
APPLICANT: Shen, Yuchiao  
APPLICANT: Nye, Julie  
APPLICANT: Hermonston, Terry  
TITLE OF INVENTION: ADENOVIRUS E1B-55K SINGLE AMINO ACID MUTANT AND METHODS OF USE  
FILE REFERENCE: ONYX1047-US  
CURRENT APPLICATION NUMBER: US/09/918,696  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: US 60/222,887  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 13  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: ONYX-058  
US-09-918-696-13

Query Match 46.7%; Score 14; DB 9; Length 40;  
Best Local Similarity 77.3%; Pred. No. 4.2e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCGCGGCTGAAC 23  
DB 17 GTTCTTTTACTGCTGTGAAC 38

RESULT 8  
US-09-918-696-14/c  
Sequence 14, Application US/09918696  
Publication No. US20030003076A1  
GENERAL INFORMATION:  
APPLICANT: Shen, Yuchiao  
APPLICANT: Nye, Julie  
APPLICANT: Hermonston, Terry  
TITLE OF INVENTION: ADENOVIRUS E1B-55K SINGLE AMINO ACID MUTANT AND METHODS OF USE  
FILE REFERENCE: ONYX1047-US  
CURRENT APPLICATION NUMBER: US/09/918,696  
CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US 60/222,887  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: ONYX-058; A284A MUTATION  
US-09-918-696-14

Query Match 46.7%; Score 14; DB 9; Length 40;  
Best Local Similarity 77.3%; Pred. No. 4.2e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCGCGGCTGAAC 23  
DB 24 GTTCTTTTACTGCTGTGAAC 3

RESULT 9  
US-10-215-112-5699/c  
Sequence 5699, Application US/10215112  
Publication No. US20030082596A1  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
TITLE OF INVENTION: Method of Genetic Analysis of Probes:  
FILE REFERENCE: 3119  
CURRENT APPLICATION NUMBER: US/10/215,112  
CURRENT FILING DATE: 2002-08-08  
NUMBER OF SEQ ID NOS: 14936  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5699  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-215-112-5699

Query Match 46.0%; Score 13.8; DB 9; Length 25;  
Best Local Similarity 88.2%; Pred. No. 5.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TTCTGCGGCGCTGAAC 25  
DB 24 TCCTGCGGCGCTGTAC 8

RESULT 10  
US-10-098-263B-23782/c  
Sequence 23782, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 23782  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-23782

Query Match 46.0%; Score 13.8; DB 9; Length 25;  
Best Local Similarity 88.2%; Pred. No. 5.2e+03;

Fri Jun 27 07:42:18 2003

US-08-770-564a-2.rnpb

Page 4

	Matches	15;	Conservative	0;	Mismatches	2;	Indels	0;	Caps	0;
OY		1	CGTTCCTTCCCTGCGS	17						
					*	4				
Db		20	CGTCCCTTCTCTGGGG	4						

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RESULT 11
US-10-098-263B-127465/c
Sequence 127465: Application US/10098263B
Publication NO: US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman; Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 127465
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-127465

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US-10-098-66322-1	Score	DB	Length	Gaps
Query Match	46.0%	13.8;	29;	0;
Best Local Similarity	42.0%	Pred.No.2e+03;	Indels	0;
Best Local	0;	Mismatches		
Matches	18;	Conservative		
QY	6	CTCTTCCTGCGCGCTGAAACGTGA	30	
Db	25	CTCTTGCTGCGGACGAAGACTGTGA	1	

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RESULT 12
US-10-098-263B-127466/c Application US//10098263B
; Sequence 127466, US20030104410x1
; Publication 127466
; Applicant Information: Michael
APPLICANT: Miltman, Human Microarray
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT FILING DATE: 2003-01-08
PRIORITY FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131086
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 127466
SEQUENCE: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-127466

Query Match          46.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 72.0%; Pred.No.5.2e+03; Indels 0; Gaps 0;
Matches 18; Conservative

        6 CTCTTCTGCGGCCTGAACGGGCA 30
      ||| ||||| ||||| ||||| |||||
QY      25 CTCTTGCTGGGCTCGAGACTGTGCA 1

RESULT 13
US-10-023-096-3/c Application US//10023096
; Sequence 3, AP020160941A1
; Patent No. US20020160941A1
; Applicant Information: Marian L.
APPLICANT: Kruszel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D

```

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APPLICANT: Doyle, Darrell J. Expression, and Uses of Human
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
CLASSIFICATION:
Prior Application Number: US/08/724,586
APPLICATION DATE: 30-SEPT-1996
FILING DATE: 05-MAY-1994
APPLICATION NUMBER: US 08/338,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 31,10505/P58185C
TELEPHONE: (202) 393,5350
TELEFAX: (202) 393,5350
INFORMATION FOR SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 Nucleic acid
TYPE: nucleic acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHESIS: NO
ANTI-SENSE: NO
US-10-023-096-3
Query Match 46.0%; Score 13.8; DB 9; Length 36;
Best Local Similarity 72.0%; Pred. No. 5.2e+03; Indels 0; Gaps 0
Matches 18; Conservative
4 TCCCTCTTCTGGCGGCTGAACGCT 28
25 TCCCTCTCTACGCCGCGATCCGCT 1
RESULT 14
US-10-098-263B-48187
Sequence 48187 Application US/10098263B
Publication Information:
GENERAL INVENTOR: Maltman, Michael
APPLICANT OF INVENTION: Human Microarray
TITLE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
Prior Filing DATE: 2003-06-27, 6/27, 759
Prior Filing DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 11066
SOFTWARE: Microarray probe Sequence Listing Generator V 1.1
SEQ ID NO 48187
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-48187
Query Match 45.3%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.4e+03;

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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

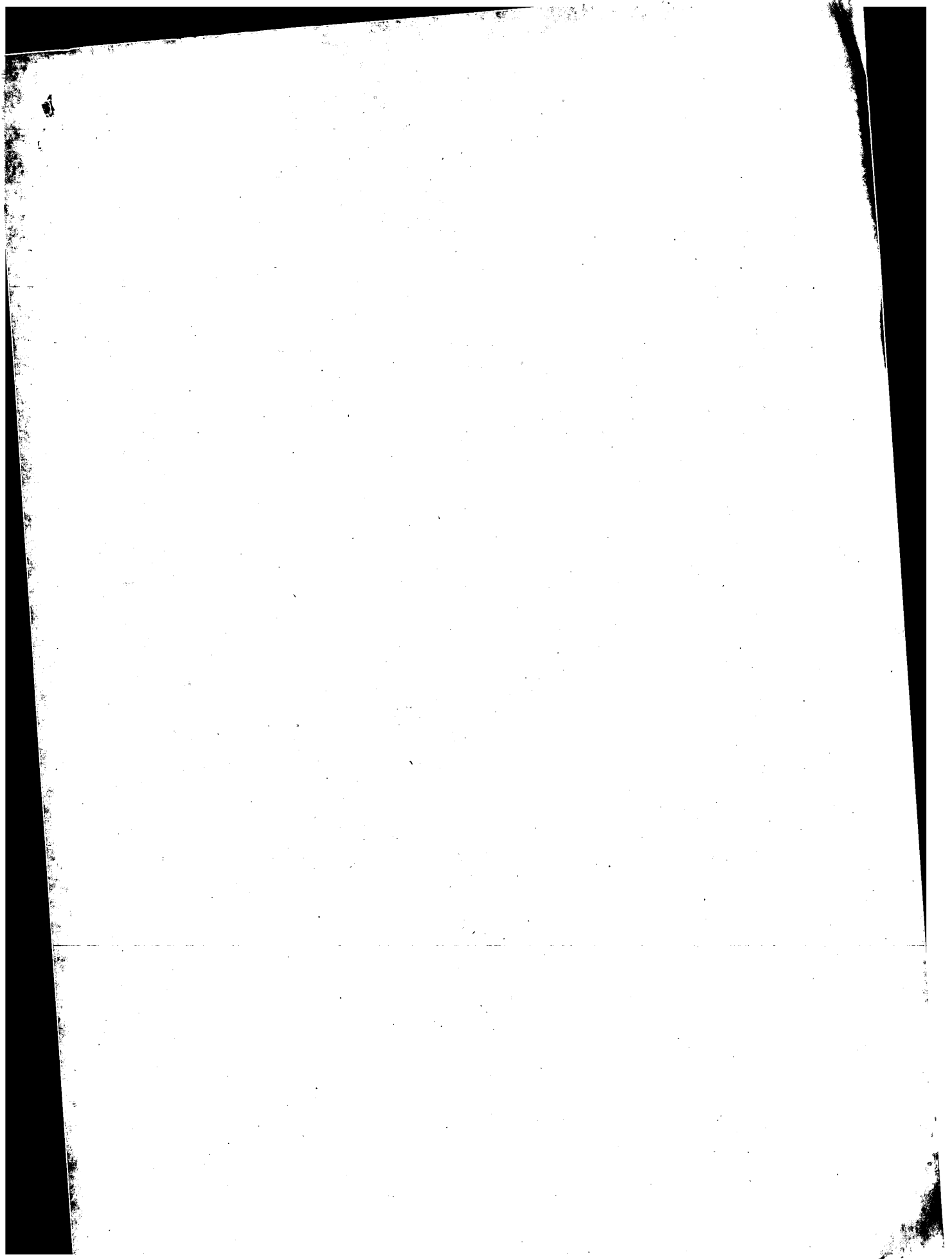
Qy 10 TCCTCGGCTGAAACGGTG 29  
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 Db 1 TCCTCGGCTGAAACGGTTG 20

RESULT 15  
 US-10-098-263B-69585/c  
 ; Sequence 69585, Application US/10098263B  
 ; Publication No. US20030104410A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; PRIOR FILING DATE: 2003-01-08  
 ; PRIOR APPLICATION NUMBER: 60/276,759  
 ; NUMBER OF SEQ ID NOS: 131066  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 69585  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-69585

Query Match 45.3%; Score 13.6; DB 9; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 6.4e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGTCTCTCTCTCGGCGCT 20  
 |||||  
 Db 21 CGTCTCTCTCTCGGCGACT 2

Search completed: June 25, 2003, 22:25:00  
 Job time : 95.1952 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 45.5378 Seconds  
(without alignments)  
202.036 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30  
Sequence: 1 CGTTCCTCTCTCTCGCGCGCTGAACGCTGA 30

Scoring table: IDENTITY NUC  
Gapex 10.0, Gapext 1.0

Searched: 443362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents NA:\*

1: /cgn2\_6/prodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/prodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/5A.COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/5B.COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/5A.COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/5B.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	US-08-770-565-2	Sequence 2, Appl
2	20	66.7	20	US-08-770-565-3	Sequence 3, Appl
3	20	66.7	20	US-08-770-565-12	Sequence 12, Appl
4	20	66.7	20	US-08-833-377-7	Sequence 14, Appl
5	19	63.3	20	US-08-833-377-14	Sequence 14, Appl
6	15.2	50.7	32	US-08-859-998-413	Sequence 413, App
7	15.2	50.7	32	US-09-225-928-413	Sequence 413, App
8	14.6	48.7	29	US-09-121-321-14	Sequence 14, Appl
9	14.6	48.7	29	US-08-933-803A-14	Sequence 14, Appl
10	14.6	48.7	43	US-08-456-566-1	Sequence 1, Appl
11	14.6	48.7	43	US-09-009-044-1	Sequence 1, Appl
12	14.4	48.0	38	US-08-463-115-85	Sequence 85, Appl
13	14.4	48.0	38	US-08-465-388-85	Sequence 85, Appl
14	14.4	48.0	42	US-08-487-037-8	Sequence 8, Appl
15	14.2	47.3	47	US-09-641-638-840	Sequence 840, App
16	14.2	47.3	35	US-08-413-740A-120	Sequence 120, App
17	14.2	46.7	35	PCT-US95-04063-120	Sequence 120, App
18	13.8	46.0	20	US-09-418-641-38	Sequence 38, Appl
19	13.8	46.0	20	US-09-418-641-39	Sequence 39, Appl
20	13.8	46.0	31	US-08-576-626A-15	Sequence 15, Appl
21	13.8	46.0	33	US-08-672-213-8	Sequence 8, Appl
22	13.8	46.0	33	US-08-672-213-49	Sequence 49, Appl
23	13.8	46.0	33	US-08-973-131-38	Sequence 38, Appl
24	13.8	46.0	36	US-08-724-586-3	Sequence 3, Appl
25	13.8	46.0	36	US-09-421-632-3	Sequence 3, Appl
26	13.8	46.0	36	US-09-932-190-3	Sequence 3, Appl
27	13.8	46.0	38	US-08-435-350-102	Sequence 102, App

28	13.8	46.0	41	US-08-656-716-51	Sequence 51, Appl
29	13.8	46.0	41	US-08-835-728D-211	Sequence 211, App
30	13.8	46.0	41	US-09-123-951-51	Sequence 51, Appl
31	13.8	46.0	41	US-09-490-558-211	Sequence 211, App
32	13.6	45.3	28	US-08-859-998-40	Sequence 40, Appl
33	13.6	45.3	28	US-09-225-928-40	Sequence 40, Appl
34	13.4	44.7	20	US-08-534-479-1	Sequence 1, Appl
35	13.4	44.7	31	US-08-039-137-22	Sequence 22, Appl
36	13.4	44.7	32	US-09-233-478-13	Sequence 13, Appl
37	13.2	44.0	20	US-09-009-913-173	Sequence 173, App
38	13.2	44.0	20	US-09-851-886-86	Sequence 86, Appl
39	13.2	44.0	22	US-08-538-875-55	Sequence 55, Appl
40	13.2	44.0	22	US-08-538-875-55	Sequence 55, Appl
41	13.2	44.0	23	US-09-176-862-17	Sequence 17, Appl
42	13.2	44.0	36	US-09-384-327-15	Sequence 15, Appl
43	13.2	44.0	36	US-08-427-097-6	Sequence 6, Appl
44	13.2	44.0	36	US-08-458-372-15	Sequence 15, Appl
45	13.2	44.0	36	US-08-878-957-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-08-770-565-2  
; Sequence 2, Application US/08770565  
; Patent No. 5846723  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Puzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002300US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-770-565-2  
Query Match 100.0%; Score 30; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTCCTCTCTCTCGCGCGCTGAACGCTGA 30

Db 1 CGTCTCTTCTGCGGCTGAAACGGTGA 30

RESULT 2  
US-08-770-565-3  
Sequence 3, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-3  
Query Match 66.7%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CGTCTCTTCTGCGGCT 20  
Db 1 CGTCTCTTCTGCGGCT 20  
RESULT 3  
US-08-770-565-12  
Sequence 12, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-12  
Query Match 66.7%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 11 CTTGGCGGCTGAAACGGTGA 30  
Db 1 CTTGGCGGCTGAAACGGTGA 20  
RESULT 4  
US-08-833-377-7  
Sequence 7, Application US/08833377  
Patent No. 5968506  
GENERAL INFORMATION:  
APPLICANT: Weinrich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichtsteiner, Serge P.  
APPLICANT: Vassero, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,377  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.

REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note= "Oligo 14ab"  
US-08-833-377-7

Query Match 66.7%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCGCGCCT 20  
DB 1 CGTCTCTTCTCGCGCCT 20

RESULT 5  
US-08-833-377-14  
Sequence 14, Application US/08833377  
Patent No. 5968506  
GENERAL INFORMATION:  
APPLICANT: Weinrich, Scott L.  
APPLICANT: Atkinson III, Edward M.  
APPLICANT: Lichtesteiner, Serge P.  
APPLICANT: Vassero, Alain P.  
APPLICANT: Pruzan, Ronald A.  
APPLICANT: Kealey, James T.  
TITLE OF INVENTION: Purified Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,377  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/510,736  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA

FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "N = 5' diocinylated cytidine"  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..20  
OTHER INFORMATION: /note= "diocinylated Oligo 14ab"  
US-08-833-377-14

Query Match 63.3%; Score 19; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCGCGCCT 20  
DB 2 GTTCTCTTCTCGCGCCT 20

RESULT 6  
US-08-859-998-413  
Sequence 413, Application US/0885998  
Patent No. 5994076  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
APPLICANT: Jokhadze, George  
APPLICANT: Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Fieh & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 413:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-08-859-998-413

Query Match 50.7%; Score 15.2; DB 2; Length 32;  
Best Local Similarity 71.4%; Pred. No. 4.4e+02;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCTGCGCGCTGAACGCTGA 30

Db 1 TTCTGTTACTGAGAACTCAAGGGTTA 28

RESULT 7  
US-09-225-928-413  
Sequence 413, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
Jokhadze, George  
Biblashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
EXPRESSION  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,928  
FILING DATE: 05-Jan-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859,998  
FILING DATE: 21-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
TELEPHONE/DOCKET NUMBER: 09096/002001  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 413:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
SEQUENCE DESCRIPTION: SEQ ID NO: 413:  
US-09-225-928-413

Query Match 50.7%; Score 15.2; DB 4; Length 32;  
Best Local Similarity 71.4%; Pred. No. 4.4e+02;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 TTCTCTCTCTGCGCGCTGAAGGCTGA 30  
Db 1 TTCTGTTACTGAGAACTCAAGGGTTA 28

RESULT 8  
US-09-121-321-14/c  
Sequence 14, Application US/09121321  
Patent No. 6090783  
GENERAL INFORMATION:  
APPLICANT: Saiga, Akihiko  
Orita, Satoshi  
Igataashi, Hisanaga  
APPLICANT: Okumura, Kouichi  
Sakaguchi, Gaku  
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF

TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/121,321  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/933,803  
FILING DATE: 19-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-12CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-09-121-321-14

Query Match 48.7%; Score 14.6; DB 3; Length 29;  
Best Local Similarity 81.0%; Pred. No. 7.8e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTGCGCGCTGAAGGCTGA 24  
Db 21 TACTCTCTCTGCGCGCGCATTA 1

RESULT 9  
US-08-933-803A-14/c  
Sequence 14, Application US/08933803A  
Patent No. 6218522  
GENERAL INFORMATION:  
APPLICANT: Saiga, Akihiko  
Orita, Satoshi  
Igataashi, Hisanaga  
APPLICANT: Okumura, Kouichi  
Sakaguchi, Gaku  
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
EXPRESSION AND NOVEL PROTEIN  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,803A  
FILING DATE: 19-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-12CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-08-933-803A-14

Query Match 48.7%; Score 14.6; DB 4; Length 29;  
Best Local Similarity 81.0%; Pred. No. 7.8e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 TCCTCTCTCTCGCGCCTGAAA 24  
DB 21 TACTCTCTCTCGCGCCGCGCAT 1

RESULT 10  
US-08-456-566-1  
Sequence 1, Application US/08456566  
Patent No. 5723122  
GENERAL INFORMATION:  
APPLICANT: Kohnert, Ulrich; Stern, Anne; Martin, Ulrich;  
APPLICANT: Fischer, Stephan  
TITLE OF INVENTION: Use Of The Protease Domain Of Human  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,566  
FILING DATE: 1-JUNE-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5723122man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: BOER 1049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-456-566-1

Query Match 48.7%; Score 14.6; DB 1; Length 43;  
Best Local Similarity 81.0%; Pred. No. 8.3e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 TCCTCTCTCTCGCGCCTGAAACG 27  
DB 23 TCACCTCTCTCGCGCCTGAGACAG 43

RESULT 11  
US-09-009-044-1  
Sequence 1, Application US/0909044  
Patent No. 5908625  
GENERAL INFORMATION:  
APPLICANT: Kohnert, Ulrich; Stern, Anne; Martin, Ulrich;  
APPLICANT: Fischer, Stephan  
TITLE OF INVENTION: Use Of The Protease Domain Of Human  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,044  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,566  
FILING DATE: 1-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5908625man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: BOER 1049  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-009-044-1

Query Match 48.7%; Score 14.6; DB 2; Length 43;  
Best Local Similarity 81.0%; Pred. No. 8.3e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 TCCTCTCTCTCGCGCCTGAAACG 27  
DB 23 TCACCTCTCTCGCGCCTGAGACAG 43

RESULT 12  
US-08-463-115-85  
Sequence 85, Application US/08463115  
Patent No. 5703221  
GENERAL INFORMATION:  
APPLICANT: WILLIAM JOHN MARTIN  
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles

```
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,115
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/887,502
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/704,814
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/301
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-115-85

Query Match 48.0%; Score 14.4; DB 1; Length 38;
Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CTCTTCTGCGCCCTGAACGGTG 29
DB 11 CTCTTCTTGAGCAGCATACGGTG 34

RESULT 13
US-08-465-388-85
Sequence 85, Application US/08465388
Patent No. 5753488
GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/465,388
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/887,502
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/704,814
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-388-85

Query Match 48.0%; Score 14.4; DB 1; Length 38;
Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CTCTTCTGCGCCCTGAACGGTG 29
DB 11 CTCTTCTTGAGCAGCATACGGTG 34

RESULT 14
US-08-487-037-8/c
Sequence 8, Application US/08487037
Patent No. 5795863
GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,037
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-037-8

Query Match 48.0%; Score 14.4; DB 1; Length 42;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCTGCG 16  
Db 25 CGATCCTCTCTGCG 10

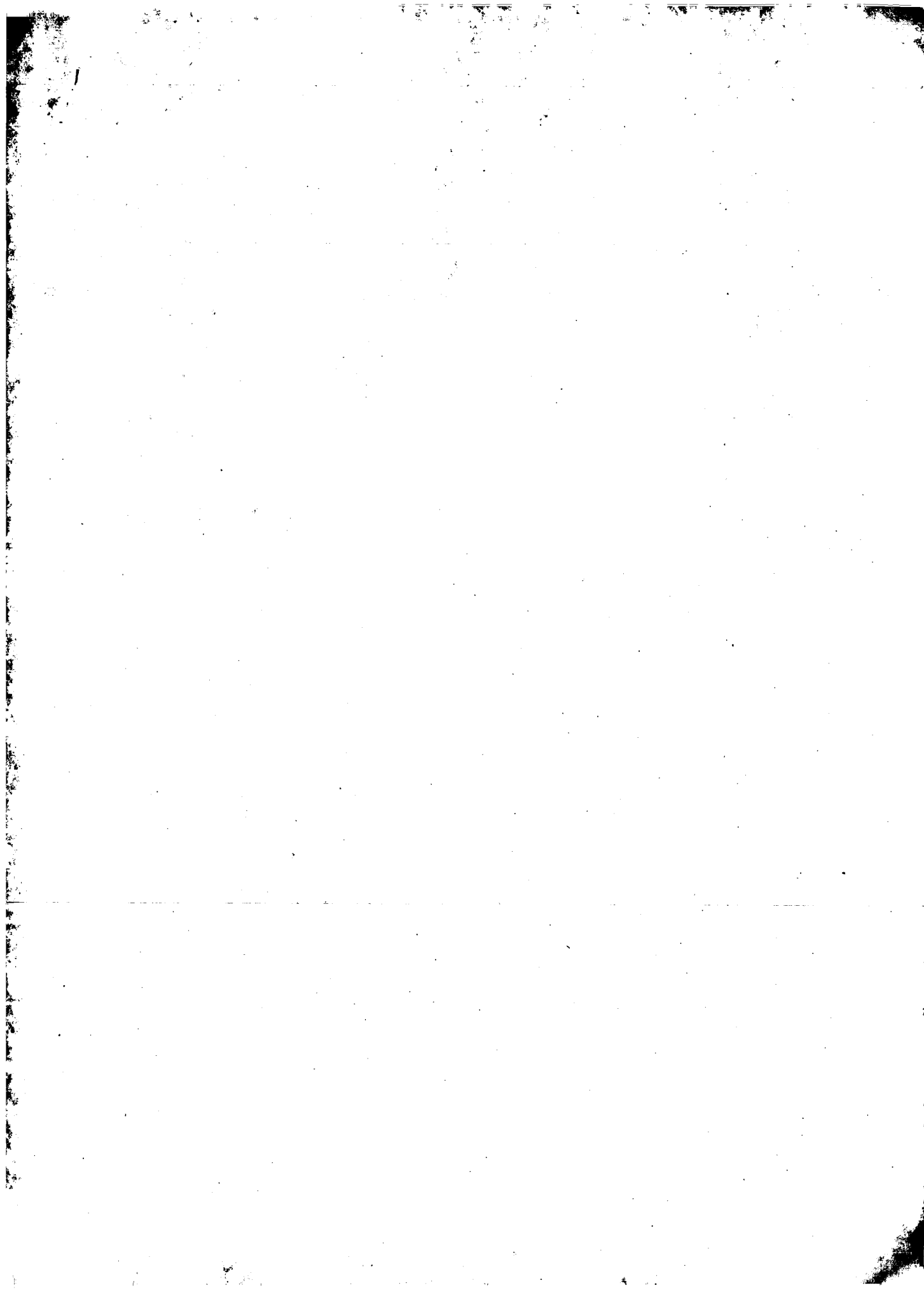
RESULT 15

US-09-641-638-840/C  
Sequence 840, Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bouguetelret, Lydie  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
FILE REFERENCE: GENSET.051CP1  
CURRENT APPLICATION NUMBER: US/09/641,638  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 840  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 10-375-136 : polymorphic base C or T  
US-09-641-638-840

Query Match 47.3%; Score 14.2; DB 4; Length 47;  
Best Local Similarity 76.2%; Pred. No. 1.2e+03;  
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCTTCTCGGCGCTGAACGG 27  
Db 38 TGTTCGCGCGCCCTRAAAGG 18

Search completed: June 25, 2003, 00:24:34  
Job time : 46.5378 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1546.73 Seconds  
(without alignments)  
314.123 Million cell updates/sec

Title: US-08-770-564A-2

Perfect score: 30  
Sequence: 1 CATTCTCTCTCTGCGCGCTGAACGCTGA 30

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
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7: em\_estro:\*  
8: em\_hc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
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16: em\_estom:\*  
17: gb\_ges:\*  
18: em\_ges\_hum:\*  
19: em\_ges\_inv:\*  
20: em\_ges\_pln:\*  
21: em\_ges\_vrt:\*  
22: em\_ges\_fun:\*  
23: em\_ges\_mam:\*  
24: em\_ges\_mus:\*  
25: em\_ges\_ohar:\*  
26: em\_ges\_pro:\*  
27: em\_ges\_rtd:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	ID	Description
C 1	12	40.0	38 17	AZ974736 2M0249A03
C 2	12	40.0	43 17	AZ830358 2M0109M04
C 3	12	40.0	46 17	AL767395 Arabidops
C 4	11	36.7	26 17	AZ942099 2M0202C09
C 5	11	36.7	33 17	BH850686 SALK 0716
C 6	11	36.7	37 17	AZ392980 1M0155P13

Result No.	Score	Query Match length	ID	Description
C 7	11	36.7	40 17	AZ627381 1M0469H09
C 8	11	36.7	43 17	AZ419099 1M0195N23
C 9	11	36.7	45 17	AZ423992 1M0203A16
C 10	11	36.7	46 17	BT488502 603021011
C 11	11	36.7	50 9	AT102629
C 12	11	36.7	50 13	BT685073
C 13	10	33.3	21 17	AZ474246
C 14	10	33.3	27 17	AZ630179
C 15	10	33.3	28 14	N92455
C 16	10	33.3	29 17	AZ794049
C 17	10	33.3	31 14	T96040
C 18	10	33.3	32 17	AZ587757
C 19	10	33.3	32 17	AZ792853
C 20	10	33.3	32 17	BH847691
C 21	10	33.3	35 17	AZ391153
C 22	10	33.3	35 17	AZ581591
C 23	10	33.3	37 17	AZ625706
C 24	10	33.3	37 17	AZ761912
C 25	10	33.3	41 17	AZ608460
C 26	10	33.3	41 17	BH625029
C 27	10	33.3	42 17	BH640418
C 28	10	33.3	43 14	H41505
C 29	10	33.3	43 14	T77849
C 30	10	33.3	44 17	AZ761199
C 31	10	33.3	45 17	AZ657409
C 32	10	33.3	45 17	AZ843544
C 33	10	33.3	45 17	AL754108
C 34	10	33.3	46 9	AA052407
C 35	10	33.3	46 9	AT003193
C 36	10	33.3	46 14	R87862
C 37	10	33.3	47 14	H80650
C 38	10	33.3	47 17	AZ784478
C 39	10	33.3	47 17	AZ845343
C 40	10	33.3	48 17	AZ443723
C 41	10	33.3	48 17	BH840628
C 42	10	33.3	49 9	AA902962
C 43	10	33.3	50 9	AI252059
C 44	10	33.3	50 9	AU102657
C 45	10	33.3	50 9	AU102702

## ALIGNMENTS

RESULT 1  
LOCUS AZ974736 38 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0249A03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0249A03 R, DNA sequence.  
ACCESSION AZ974736  
VERSION AZ974736.1 GI:13845963  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 38)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00



## COMMENT

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence is recovered from the left border of the T-DNA. It  
indicates an insertion within the locus defined by clone fsk1. The  
sequences are generated at the MPI for Plant Breeding Research in  
the context of the GABI-Kat project. GABI-Kat is part of the German  
Plant Genomics program designated 'GABI'. Information on line  
availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

## FEATURES

## source

1..46

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone\_1lb="GK-219A03-014202"

/clone\_1lb="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector pM161. The lines contain one or more T-DNA

insertions. The DNA fragment(s) resulting from the PCR

were directly sequenced to determine the genomic sequence

flanking the insertion. Sequences displaying significant

similarity to the A. thaliana nuclear genome sequence were

processed for submission. T-DNA derived sequences were

removed"

## BASE COUNT

7 a 19 c 2 g 18 t

## ORIGIN

Query Match 40.0%; Score 12; DB 17; Length 46;  
Best Local Similarity 100.0%; Pred.No. 1.2e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy

2 GTTCTCTTCTCT 13

## Db

29 GTTCTCTTCTCT 40

## RESULT 4

## LOCUS

AZ942099 26 bp DNA linear GSS 26-APR-2001

## DEFINITION

2M0202C09F Mouse 10kb plasmid UUGCM library Mus musculus genomic

## ACCESSION

AZ942099

## VERSION

AZ942099.1 GI:13805115

## KEYWORDS

GSS.

## SOURCE

house mouse.

## ORGANISM

Mus musculus.

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## TITLE

1 (bases 1 to 26)

## JOURNAL

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,

## COMMENT

Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly,

## JOURNAL

M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.

## COMMENT

and Wright, D., Weiss, R.,

## JOURNAL

Mouse whole genome scaffolding with paired end reads from 10kb

## COMMENT

Plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

University of Utah Genome Center

## JOURNAL

Contact: Robert B. Weiss

## COMMENT

University of Utah

## JOURNAL

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

## COMMENT

84112, USA

## JOURNAL

Tel: 801 585 5606

## COMMENT

Fax: 801 585 7177

## JOURNAL

Email: ddunne@genetics.utah.edu

## COMMENT

Insert Length: 10000 Std Error: 0.00

## JOURNAL

Plate: 0202 row: C column: 09

## COMMENT

Seq primer: CGTTGTAAACGACGCCAGT

## JOURNAL

Class: plasmid ends

## COMMENT

High quality sequence stop: 26.

/db\_xref="taxon:10090"

/clone="UUGC2M0202C09"

/clone\_1lb="Mouse 10kb plasmid UUGC2M library"

/sex="Female"

/lab\_host="B. coli strain X10-Gold, T1-resistant, F-"

/note="Vector: pMD29v, Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g14732114|g14732114|AF19072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent B. coli X10-Gold (Stratagene) cells

and selected for ampicillin resistance."

## BASE COUNT

10 a 0 c 16 g 0 t

## ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 26;  
Best Local Similarity 100.0%; Pred.No. 3.6e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy

3 TTCTCTTCTCT 13

## Db

12 TTCTCTTCTCT 2

## RESULT 5

## LOCUS

BH850686 33 bp DNA linear GSS 13-JUN-2002

## DEFINITION

SALK\_071692.32.90.x Arabidopsis thaliana TDNA insertion lines

## ACCESSION

BH850686

## VERSION

BH850686

## KEYWORDS

GSS.

## SOURCE

thale cress.

## ORGANISM

Arabidopsis thaliana

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

## TITLE

Rosidae; euroside II; Brassicales; Brassicaceae; Arabidopsis.

## JOURNAL

1 (bases 1 to 33)

## COMMENT

A Sequence-Indexed Library of Insertion Mutations in the

## JOURNAL

Arabidopsis Genome

## COMMENT

Unpublished (2001)

## JOURNAL

Contact: Joseph R. Ecker

## COMMENT

Salk Institute Genomic Analysis Laboratory (SIGAL)

## JOURNAL

The Salk Institute for Biological Studies

## COMMENT

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

## JOURNAL

Tel: 858 453 4100 x1752

## COMMENT

Fax: 858 558 6379

## JOURNAL

Email: ecker@salk.edu

## COMMENT

This is single pass sequence recovered from the left border of

## JOURNAL

TDNA.

## JOURNAL

Class: TDNA tagged.

## COMMENT

Location/Qualifiers

## JOURNAL

1..33

## COMMENT

/organism="Arabidopsis thaliana"

## JOURNAL

/strain="Columbia 0"

## COMMENT

/db\_xref="taxon:3702"

## JOURNAL

/clone="SALK\_071692.32.90.x"

/clone.lib="Arabidopsis thaliana TDM insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDM insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

BASE COUNT 5 a 16 c 1 g 11 t

ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 33;  
Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCT 13  
|||||  
19 TTCTCTTCTCT 29

RESULT 6  
AZ392980 37 bp DNA linear GSS 03-OCT-2000  
LOCUS AZ392980.1  
DEFINITION clone UUGC1M0155P13 R, DNA sequence.

ACCESSION AZ392980  
VERSION AZ392980.1 GI:10508052  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [duun@genetics.utah.edu](mailto:duun@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0155 row: F column: 13  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 37.  
Location/Qualifiers

#### FEATURES

1..37  
source  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0155P13"  
/clone.lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="B. Coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 15 a 0 c 22 g 0 t

ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 37;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCT 13  
|||||  
16 TTCTCTTCTCT 6

RESULT 7  
AZ627381 40 bp DNA linear GSS 13-DEC-2000  
LOCUS AZ627381  
DEFINITION clone UUGC1M0469H09 F, DNA sequence.

ACCESSION AZ627381  
VERSION AZ627381.1 GI:11749571  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [duun@genetics.utah.edu](mailto:duun@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0469 row: H column: 09  
Seq primer: CGTTTAAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 40.  
Location/Qualifiers

#### FEATURES

1..40  
source  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0469H09"  
/clone.lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="B. Coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 16 c 3 g 13 t

ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 40;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCCTCTCTCG 14  
|||||  
9 TCCTCTCTCG 19

RESULT 8  
AZ419099/c 43 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0195N23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
DEFINITION Clone UUGCIM0195N23 F, DNA sequence.  
ACCESSION AZ419099  
VERSION AZ419099.1 GI:10543112  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0195 row: N column: 23  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 43.

FEATURES  
source Location/Qualifiers  
1..43  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0195N23"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 21 a 0 c 22 g 0 t

ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 43;  
Best Local Similarity 100.0%; Pred. No. 4.1e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCCTCTTCT 13  
|||||  
33 TTCCTCTTCT 23

RESULT 9  
AZ423992 45 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0203A16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
DEFINITION Clone UUGCIM0203A16 F, DNA sequence.  
ACCESSION AZ423992  
VERSION AZ423992.1 GI:10548005  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 45)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0203 row: A column: 16  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 45.

FEATURES  
source Location/Qualifiers  
1..45  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0203A16"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD2 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 11 c 6 g 20 t  
 Query Match 36.7%; Score 11; DB 17; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
 BI48502/c 46 bp mRNA linear EST 28-AUG-2001  
 LOCUS 603021011p1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5191659 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI48502  
 VERSION BI48502.1 GI:15327720  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE NIH-MGC http://mgc.nci.nih.gov/ (bases 1 to 46)  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rcmail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM11479 row: e column: 04  
 High quality sequence stop: 46.  
 Location/Qualifiers

FEATURES  
 source 1..46  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="5191659"  
 /clone\_id="NIH\_MGC\_114"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMV-Sport6; Site 1: NciI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb. Insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Incytegen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

BASE COUNT 9 a 8 c 25 g 4 t

Query Match 36.7%; Score 11; DB 13; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTTCTCC 12  
 DB 12 GTTCTTCTCC 2

RESULT 11  
 AU102629/c 50 bp mRNA linear EST 30-AUG-2001  
 LOCUS AU102629 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 DEFINITION CA504232, mRNA sequence.  
 ACCESSION AU102629  
 VERSION AU102629.1 GI:13552150  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sase, J., Hata  
 H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
 Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)  
 21270072  
 CONTACT: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
 S. Construction and characterization of a full length-enriched and  
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
 Location/Qualifiers

FEATURES  
 source 1..50  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="CA504232"  
 /clone\_id="Sugano Homo sapiens cDNA library"  
 /note="Differential display comparison of untreated and  
 dimethylformate treated U937 cells"

BASE COUNT 13 a 10 c 18 g 9 t

Query Match 36.7%; Score 11; DB 9; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTCG 14  
 DB 19 TCCTCTTCTCG 9

RESULT 12  
 BI685073 50 bp mRNA linear EST 18-SEP-2001  
 LOCUS 603310058F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5345990 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI685073  
 VERSION BI685073.1 GI:15647701  
 KEYWORDS EST.

SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/ (bases 1 to 50)  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rcmail.nih.gov  
 Tissue Procurement: Jeffrey Green M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:



http://image.llnl.gov  
Plate: LLAM1879 row: c column: 15  
High quality sequence stop: 50.  
Location/Qualifiers

## FEATURES

source

1.50  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:534590"  
/clone\_1ib="NCI CGAP Mam6"  
/sex="Female, virgin"  
/tissue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Jeffrey Green, W.D., NIH"

## BASE COUNT

3 a 20 c 17 g 10 t

## ORIGIN

Query Match 36.7%; Score 11; DB 13; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TCCTGCGGCT 20  
|||||  
Db 6 TCCTGCGGCT 16

## RESULT 13

A2474246

LOCUS

21 bp DNA linear GSS 04-OCT-2000  
1M0290L08 Mouse 10kb plasmid UNGCM library Mus musculus genomic

DEFINITION

clone UNGCM0290L08 R, DNA sequence.

ACCESSION

A2474246

VERSION

A2474246.1 GI:10632371

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

## REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weis,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0290 row: L column: 08

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1.21

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UNGCM0290L08"

/clone\_1ib="Mouse 10kb plasmid UNGCM library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

## FEATURES

source

1.21

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UNGCM0290L08"

/clone\_1ib="Mouse 10kb plasmid UNGCM library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

## BASE COUNT

9 a 5 c 4 g 3 t

## ORIGIN

Query Match 33.3%; Score 10; DB 17; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GGCTGAAC 25  
|||||  
Db 4 GGCTGAAC 13

## RESULT 14

A2630179

LOCUS

27 bp DNA linear GSS 13-DEC-2000  
1M0483B10R Mouse 10kb plasmid UNGCM library Mus musculus genomic

DEFINITION

clone UNGCM0483B10 R, DNA sequence.

ACCESSION

A2630179

VERSION

A2630179.1 GI:11752369

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

## REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weis,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0483 row: B column: 10

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 27.

Location/Qualifiers

1.27

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UNGCM0483B10"

/clone\_1ib="Mouse 10kb plasmid UNGCM library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

## FEATURES

source

1.27

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UNGCM0483B10"

/clone\_1ib="Mouse 10kb plasmid UNGCM library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/nbases/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (914732114[SP|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 9 t

ORIGIN

Query Match 33.3%; Score 10; DB 17; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 TTCTCTTCC 12  
|||||  
4 TTCTCTTCC 13

Db

RESULT 15  
N92455  
LOCUS  
DEFINITION  
N92455 28 bp mRNA linear EST 20-AUG-1996  
IMAGE:308305.3, similar to SB:X06323 cdel MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);, mRNA sequence.  
N92455  
N92455.1 GI:1264764  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 28)  
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,B., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Scheilenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,B., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Warrar,M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
97044478  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert Length: 866 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 1.  
Location/Qualifiers  
1  
28  
/organism="Homo sapiens"  
/db\_xref="GDB:1251718"  
/db\_xref="taxon:9606"  
/clone="IMAGE:308305"  
/clone\_lib="Soares\_fetal\_lung\_NBHL19W"  
/dev\_stage="19 weeks"

FEATURES  
source

/lab host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAGTGGAGCGCCGCAATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Patricia Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."

BASE COUNT 7 a 9 c 4 g 8 t

ORIGIN

Query Match 33.3%; Score 10; DB 14; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 GTTCTCTTC 11  
|||||  
3 GTTCTCTTC 12

Db

Search completed: June 23, 2003, 10:10:14  
Job time: 1554.89 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 / Search time 1316.89 Seconds  
(without alignments)  
158.668 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30  
Sequence: 1 CATTCTCTTCTCGCGCTGAACGTGA 30

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
10: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
11: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*  
12: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*  
13: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	60.0	19	1	PCT-US03-04088-26
2	18	60.0	19	1	PCT-US03-04088-290
3	13	43.3	20	6	US-09-905-688-11
4	13	43.3	20	6	US-10-310-788-34029
5	13	43.3	21	4	US-08-825-746-11
6	13	43.3	25	7	US-09-954-445A-45573
7	13	43.3	25	9	US-10-355-577-198249
8	13	43.3	25	9	US-10-355-577-198680
9	13	43.3	25	9	US-10-355-577-223567
10	13	43.3	25	9	US-10-355-577-364423
11	13	43.3	25	9	US-10-355-577-422449
12	13	43.3	25	9	US-10-355-577-498091
13	13	43.3	25	12	US-60-417-190-13946
14	13	43.3	25	12	US-60-417-190-13947
15	13	43.3	25	12	US-60-417-190-48932
16	13	43.3	25	12	US-60-417-190-48933
17	13	43.3	25	12	US-60-417-190-48939
18	13	43.3	25	12	US-60-417-190-48940
19	13	43.3	25	12	US-60-427-808-112999
20	13	43.3	25	12	US-60-427-808-218754

21	13	43.3	25	12	US-60-427-808-275929	Sequence 275929,
22	13	43.3	25	12	US-60-427-808-469548	Sequence 469548,
23	13	43.3	25	12	US-60-427-808-564830	Sequence 564830,
24	13	43.3	25	12	US-60-427-836-440978	Sequence 440978,
25	13	43.3	25	12	US-60-427-836-455883	Sequence 455883,
26	13	43.3	25	12	US-60-427-836-549003	Sequence 549003,
27	13	43.3	25	12	US-60-427-836-599225	Sequence 599225,
28	13	43.3	25	12	US-60-427-836-683575	Sequence 683575,
29	13	43.3	25	13	US-60-470-475-51737	Sequence 51737, A
30	13	43.3	25	13	US-60-470-475-51738	Sequence 51738, A
31	13	43.3	25	13	US-60-470-475-55703	Sequence 55703, A
32	13	43.3	25	13	US-60-470-475-57853	Sequence 57853, A
33	13	43.3	25	13	US-60-470-475-61267	Sequence 61267, A
34	13	43.3	25	13	US-60-470-475-61272	Sequence 61272, A
35	13	43.3	25	13	US-60-470-475-73706	Sequence 73706, A
36	13	43.3	25	13	US-60-470-475-89881	Sequence 98881, A
37	13	43.3	29	9	US-10-294-719-499	Sequence 499, App
38	13	43.3	50	5	US-09-749-280B-1268	Sequence 1268, Ap
39	13	43.3	50	5	US-09-749-280B-7801	Sequence 7801, Ap
40	13	43.3	50	9	US-10-325-899-3869	Sequence 3869, Ap
41	12	40.0	15	10	US-10-367-892-6314	Sequence 6314, Ap
42	12	40.0	15	10	US-10-367-892-19280	Sequence 19280, A
43	12	40.0	19	9	US-10-293-338-4597	Sequence 4597, Ap
44	12	40.0	20	1	PCT-US02-24310-154	Sequence 154, App
45	12	40.0	20	9	US-10-303-778-15311	Sequence 15311, A

#### ALIGNMENTS

RESULT 1  
PCT-US03-04088-26/c  
Sequence 26, Application PC/TUS0304088  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Beigelman, James  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
FILE OF INVENTION: Expression Using Short Interfering RNA (siRNA)  
FILE REFERENCE: 02-708-A (400/080)  
CURRENT APPLICATION NUMBER: PCT/US03/04088  
PRIOR FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: US 60/396,600  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 26  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
PCT-US03-04088-26

Query Match 60.0%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 TCTTCTGGCGGCTGAAA 24  
Db 19 TCTTCTGGCGGCTGAAA 2

RESULT 2  
PCT-US03-04088-290  
; Sequence 290, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: McSwigen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT FILING DATE: 2003-04-28  
; PCT-US03/04088  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 290  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense  
PCT-US03-04088-290

Query Match 60.0%; Score 18; DB 1; Length 19;  
Best Local Similarity 72.2%; Pred. No. 8.7;  
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 7 TCTTCTGGCGGCTGAAA 24  
Db 1 UCUCUCUGCGGCTGAAA 18

RESULT 3  
US-09-905-688-11  
; Sequence 11, Application US/09905688  
; GENERAL INFORMATION:  
; APPLICANT: CERNIAK, BOGDAN  
; TITLE OF INVENTION: METHODS OF DETECTING AND DIAGNOSING BLADDER CANCER AND  
; IDENTIFYING NEOPLASTIC PROGRESSION  
; FILE REFERENCE: UTSC:663US  
; CURRENT APPLICATION NUMBER: US/09/905,688  
; CURRENT FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-905-688-11

Query Match 43.3%; Score 13; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TTCTCTTCTCTGC 15  
Db 1 TTCTCTTCTCTGC 13

RESULT 4  
US-10-310-188-34029/c  
; Sequence 34029, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE  
; FILE REFERENCE: 47487  
; CURRENT APPLICATION NUMBER: US/10/310,188  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 34029  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-34029

Query Match 43.3%; Score 13; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TTCTCTTCTCTGC 15  
Db 19 TTCTCTTCTCTGC 7

RESULT 5  
US-08-825-746-11  
; Sequence 11, Application US/08825746  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Baker, Suzanne  
; APPLICANT: Pearson, Eric  
; APPLICANT: Nigro, Janice M.  
; TITLE OF INVENTION: Methods for Restoring Wild-Type p53 Gene Function  
; FILE REFERENCE: 001107.05877  
; CURRENT APPLICATION NUMBER: US/08/825,746  
; CURRENT FILING DATE: 1997-04-03  
; PRIOR APPLICATION NUMBER: 08/035,366  
; PRIOR FILING DATE: 1993-03-22  
; PRIOR APPLICATION NUMBER: 07/860,758  
; PRIOR FILING DATE: 1992-03-21  
; PRIOR APPLICATION NUMBER: 07/715,182  
; PRIOR FILING DATE: 1991-06-14  
; PRIOR APPLICATION NUMBER: 07/928,661  
; PRIOR FILING DATE: 1992-08-17  
; PRIOR APPLICATION NUMBER: 07/446,584  
; PRIOR FILING DATE: 1989-12-06  
; PRIOR APPLICATION NUMBER: 07/330,566  
; PRIOR FILING DATE: 1989-03-29  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PasteSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-08-825-746-11

Query Match 43.3%; Score 13; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCTTCTCTGC 15  
 |||||  
 Db 1 TTCCTTCTCTGC 13

RESULT 6  
 US-09-954-445A-45573/c  
 ; Sequence 45573, Application US/0995445A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana  
 ; FILE REFERENCE: 3116.1  
 ; CURRENT APPLICATION NUMBER: US/09/954,445A  
 ; CURRENT FILING DATE: 2000-09-17  
 ; PRIOR APPLICATION NUMBER: 60/233,620  
 ; PRIOR FILING DATE: 2000-09-18  
 ; NUMBER OF SEQ ID NOS: 131820  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO: 45573  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-09-954-445A-45573

Query Match 43.3%; Score 13; DB 7; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCT 13  
 |||||  
 Db 15 CGTCTCTCTCT 3

RESULT 7  
 US-10-355-577-198249  
 ; Sequence 198249, Application US/10355577  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
 ; FILE REFERENCE: 3121  
 ; CURRENT APPLICATION NUMBER: US/10/355,577  
 ; CURRENT FILING DATE: 2003-01-31  
 ; NUMBER OF SEQ ID NOS: 997516  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO: 198249  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; US-10-355-577-198249

Query Match 43.3%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTCTCTG 14  
 |||||  
 Db 9 GTTCTCTCTCTG 21

RESULT 8  
 US-10-355-577-198680  
 ; Sequence 198680, Application US/10355577  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
 ; FILE REFERENCE: 3121  
 ; CURRENT APPLICATION NUMBER: US/10/355,577  
 ; CURRENT FILING DATE: 2003-01-31  
 ; NUMBER OF SEQ ID NOS: 997516  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO: 198680  
 ; LENGTH: 25  
 ; TYPE: DNA

; ORGANISM: Homo sapien  
 ; US-10-355-577-198680

Query Match 43.3%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCGGCGCTGAACG 26  
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 Db 13 GCGGCGCTGAACG 25

RESULT 9  
 US-10-355-577-223567/c  
 ; Sequence 223567, Application US/10355577  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
 ; FILE REFERENCE: 3121  
 ; CURRENT APPLICATION NUMBER: US/10/355,577  
 ; CURRENT FILING DATE: 2003-01-31  
 ; NUMBER OF SEQ ID NOS: 997516  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO: 223567  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; US-10-355-577-223567

Query Match 43.3%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTCTGCG 17  
 |||||  
 Db 25 CCTCTTCTCTGCG 13

RESULT 10  
 US-10-355-577-364423  
 ; Sequence 364423, Application US/10355577  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
 ; FILE REFERENCE: 3121  
 ; CURRENT APPLICATION NUMBER: US/10/355,577  
 ; CURRENT FILING DATE: 2003-01-31  
 ; NUMBER OF SEQ ID NOS: 997516  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO: 364423  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; US-10-355-577-364423

Query Match 43.3%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GCGTGAACGGTG 29  
 |||||  
 Db 7 GCGTGAACGGTG 19

RESULT 11  
 US-10-355-577-422449  
 ; Sequence 422449, Application US/10355577  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
 ; FILE REFERENCE: 3121  
 ; CURRENT APPLICATION NUMBER: US/10/355,577  
 ; CURRENT FILING DATE: 2003-01-31

```

; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 422449
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-422449

```

```

Query Match          43.3%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      14 GCGGCTGAAACG 26
         |||||
DB      3 GCGGCTGAAACG 15

```

```

RESULT 12
US-10-355-577-498091
; Sequence 498091, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Micmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 498091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-498091

```

```

Query Match          43.3%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 GTTCCTCTCCTG 14
         |||||
DB      3 GTTCCTCTCCTG 15

```

```

RESULT 13
US-60-417-190-13946
; Sequence 13946, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13946
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-13946

```

```

Query Match          43.3%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 TCCTCTTCTGCG 16
         |||||
DB      2 TCCTCTTCTGCG 14

```

```

RESULT 14
US-60-417-190-13947

```

```

; Sequence 13947, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13947
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-13947

```

```

Query Match          43.3%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 TCCTCTTCTGCG 16
         |||||
DB      1 TCCTCTTCTGCG 13

```

```

RESULT 15
US-60-417-190-48932
; Sequence 48932, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48932
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48932

```

```

Query Match          43.3%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 TTCCTCTTCTGCG 15
         |||||
DB      13 TTCCTCTTCTGCG 25

```

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Search completed: June 23, 2003, 19:12:10
Job time : 1319.89 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 2516.18 Seconds  
(without alignments)  
299.770 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30  
Sequence: 1 CGTTCCTCTTCCCTGCGGCGCTGAACGGTGA 30

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

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1: /cgn2_6/ptodata/2/pna/US0600_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
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10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*
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19: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
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21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
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36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
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40: /cgn2_6/ptodata/2/pna/US101A_COMB.seq:*
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42: /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US102B_COMB.seq:*

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Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appl1
2	30	100.0	30	11 US-08-770-564A-2	Sequence 2, Appl1
3	30	100.0	31	9 US-08-521-634-17	Sequence 17, Appl1
4	20	66.7	20	1 PCT-US97-23619-3	Sequence 3, Appl1
5	20	66.7	20	1 PCT-US97-23619-7	Sequence 27, Appl1
6	20	66.7	20	11 US-08-770-564A-3	Sequence 3, Appl1
7	20	66.7	20	11 US-08-770-564A-15	Sequence 15, Appl1
8	14	46.7	25	17 US-09-396-196F-119937	Sequence 119937, A
9	14	46.7	25	17 US-09-396-196G-119937	Sequence 119937, A
10	14	46.7	25	36 US-09-956-584-18655	Sequence 18655, A
11	14	46.7	25	36 US-09-956-584-237631	Sequence 237631, A
12	14	46.7	25	67 US-60-234-017-52883	Sequence 52883, A
13	14	46.7	25	67 US-60-234-017-208542	Sequence 208542, A
14	14	46.7	29	13 US-08-913-665-14	Sequence 14, Appl1
15	13	43.3	20	1 PCT-US02-18427-11	Sequence 11, Appl1
16	13	43.3	20	41 US-10-167-241-11	Sequence 11, Appl1
17	13	43.3	21	41 US-10-157-058-11	Sequence 11, Appl1
18	13	43.3	25	36 US-09-953-115-27778	Sequence 27778, A
19	13	43.3	25	67 US-60-233-620-45573	Sequence 45573, A
20	13	43.3	25	79 US-60-353-987-198249	Sequence 198249, A
21	13	43.3	25	79 US-60-353-987-198680	Sequence 198680, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

22 13 43.3 25 79 US-60-353-987-223567 Sequence 223567,  
23 13 43.3 25 79 US-60-353-987-364423 Sequence 364423,  
24 13 43.3 25 79 US-60-353-987-422449 Sequence 422449,  
25 13 43.3 25 79 US-60-353-987-498091 Sequence 498091,  
26 13 43.3 31 18 US-09-454-623-15 Sequence 15, Appl  
27 13 43.3 42 26 US-09-671-346-8 Sequence 8, Appl  
28 13 43.3 45 26 US-09-671-346-9 Sequence 9, Appl  
29 13 43.3 50 40 US-10-131-827-3869 Sequence 3869, Ap  
30 13 43.3 50 40 US-10-131-827-3869 Sequence 3869, Ap  
31 13 43.3 50 40 US-10-131-827-3869 Sequence 3869, Ap  
32 12 40.0 12 11 PCT-US97-23619-4 Sequence 4, Appl  
33 12 40.0 12 11 PCT-US97-23619-4 Sequence 4, Appl  
34 12 40.0 15 1 PCT-US01-06051-14 Sequence 14, Appl  
35 12 40.0 15 1 PCT-US02-25940-6314 Sequence 6314, Ap  
36 12 40.0 15 1 PCT-US02-25940-19280 Sequence 19280, A  
37 12 40.0 15 1 PCT-US02-25942-1021 Sequence 1021, Ap  
38 12 40.0 15 1 PCT-US02-25942-1585 Sequence 1585, Ap  
39 12 40.0 15 42 US-10-227-583-6316 Sequence 6316, Ap  
40 12 40.0 15 42 US-10-227-583-6316 Sequence 6316, Ap  
41 12 40.0 15 42 US-10-227-587-1021 Sequence 1021, Ap  
42 12 40.0 15 42 US-10-227-587-1021 Sequence 1021, Ap  
43 12 40.0 20 1 PCT-US02-14110-86 Sequence 86, Appl  
44 12 40.0 20 15 US-09-198-452A-3651 Sequence 3651, Ap  
45 12 40.0 20 17 US-09-366-483B-21 Sequence 21, Appl

## ALIGNMENTS

RESULT 1  
PCT-US97-23619-2  
Sequence 2, Application PC/TUS9723619  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
NUMBER OF SEQUENCES: 29  
TITLE OF INVENTION: RNA Component of Telomerase  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

Query Match 100.0%; Score 30; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
PCT-US97-23619-2 /note="olligo 14"

QY 1 CGTTCCTCTTCCTGCGGCTGAAACGGTGA 30  
DB 1 CGTTCCTCTTCCTGCGGCTGAAACGGTGA 30

RESULT 2  
US-08-770-564A-2  
Sequence 2, Application US/08770564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ron  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSES: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564A-2

Query Match 100.0%; Score 30; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTCCTCTTCCTGCGGCTGAAACGGTGA 30  
DB 1 CGTTCCTCTTCCTGCGGCTGAAACGGTGA 30

RESULT 3  
US-08-521-634-17/c



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/ Sequence 17, Application US/08521634
/ GENERAL INFORMATION:
/ APPLICANT: Villeponteau, Bryant
/ APPLICANT: Peng, Junli
/ APPLICANT: Funk, Walter
/ APPLICANT: Andrews, William
/ TITLE OF INVENTION: Mammalian Telomerase
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Townsend and Townsend and Crew
/ STREET: One Market Plaza, Steuart Tower, Suite 2000
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/521,634
/ FILING DATE: 31-AUG-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/482,115
/ FILING DATE: 7-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/472,802
/ FILING DATE: 7-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/330,123
/ FILING DATE: 27-OCT-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/272,102
/ FILING DATE: 7-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dunn, Tracy J.
/ REGISTRATION NUMBER: 34,587
/ REFERENCE/DOCKET NUMBER: 15389-000850
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-326-2400
/ TELEFAX: 415-326-2422
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 31 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (oligonucleotide)
/ US-08-521-634-17

Query Match      100.0%; Score 30; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCGCGGCGCTGAAGGTGA 30
DB      31 CGTTCCTCTTCGCGGCGCTGAAGGTGA 2

RESULT 4
PCT-US97-23619-3
/ Sequence 3, Application PC/TUS9723619
/ GENERAL INFORMATION:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ TITLE OF INVENTION: Methods for Detecting and Inhibiting the
/ TITLE OF INVENTION: RNA Component of Telomerase
```

```
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US97/23619
/ FILING DATE: Not yet assigned
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/770,564
/ FILING DATE: 20-DEC-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/770,565
/ FILING DATE: 20-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Storella, John R.
/ REGISTRATION NUMBER: 32,944
/ REFERENCE/DOCKET NUMBER: 15389-27PC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..20
/ OTHER INFORMATION: /note="oligo 14ab"
/ PCT-US97-23619-3

Query Match      66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCGCGGCGCT 20
DB      1 CGTTCCTCTTCGCGGCGCT 20

RESULT 5
PCT-US97-23619-27
/ Sequence 27, Application PC/TUS9723619
/ GENERAL INFORMATION:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ TITLE OF INVENTION: Methods for Detecting and Inhibiting the
/ TITLE OF INVENTION: RNA Component of Telomerase
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
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```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="01igo 14bc"
PCT-US97-23619-27

Query Match      66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CCTGCGGCTGAACGGTGA 30
DB      1 CCTGCGGCTGAACGGTGA 20

RESULT 6
US-08-770-564A-3
Sequence 3, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
REFERENCE/DOCKET NUMBER: 015389-002200US
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```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-564A-3

Query Match      66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTCCTCTCTCGGGGCT 20
DB      1 CGTTCCTCTCTCGGGGCT 20

RESULT 7
US-08-770-564A-15
Sequence 15, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-15

Query Match      66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CCTGCGGCTGAACGGTGA 30
DB      1 CCTGCGGCTGAACGGTGA 20

RESULT 8
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US-09-396-196F-119937/c
; Sequence 119937, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; PRIOR FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-119937

Query Match
Best Local Similarity 100.0%; Score 14; DB 17; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCCTCTCTGTC 15
DB 25 GTTCCCTCTCTGTC 12

RESULT 9
US-09-396-196G-119937/c
; Sequence 119937, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-119937

Query Match
Best Local Similarity 100.0%; Score 14; DB 17; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCCTCTCTGTC 15
DB 25 GTTCCCTCTCTGTC 12

RESULT 10
US-09-956-584-18655/c
; Sequence 18655, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18655
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-18655

Query Match
Best Local Similarity 100.0%; Score 14; DB 36; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTG 14
DB 18 CGTTCCTCTCTG 5

RESULT 11
US-09-956-584-237631/c
; Sequence 237631, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 237631
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-237631

Query Match
Best Local Similarity 100.0%; Score 14; DB 36; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GCCTGAACGGTGA 30
DB 24 GCCTGAACGGTGA 11

RESULT 12
US-60-234-017-52883/c
; Sequence 52883, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltman, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U41285
US-60-234-017-52883

Query Match
Best Local Similarity 100.0%; Score 14; DB 67; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTG 14
DB 18 CGTTCCTCTCTG 5
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RESULT 13  
US-60-234-017-208542/c  
; Sequence 208542, Application US/60234017  
; GENERAL INFORMATION:  
; APPLICANT: Miltman, M  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus  
; FILE REFERENCE: 3115  
; CURRENT APPLICATION NUMBER: US/60/234,017  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 605887  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 208542  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Genbank A1465630  
US-60-234-017-208542

Query Match 46.7%; Score 14; DB 67; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 17 GCCTGAACGGTGA 30  
Db 24 GCCTGAACGGTGA 11

RESULT 14  
US-08-913-665-14/c  
; Sequence 14, Application US/08913665  
; GENERAL INFORMATION:  
; APPLICANT: Saiga, Akihiko  
; APPLICANT: Orita, Satoshi  
; APPLICANT: Igarashi, Hisanaga  
; APPLICANT: Okumura, Kouichi  
; APPLICANT: Sakaguchi, Gaku  
; TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
; TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & BEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,665  
; FILING DATE: 19-SEP-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley, James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: SHGN-12  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9090  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"  
US-08-913-665-14

Query Match 46.7%; Score 14; DB 13; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTCCTCCTCGGCGC 19  
Db 19 CTCCTCCTCGGCGC 6

RESULT 15  
PCT-US02-18427-11  
; Sequence 11, Application PC/TUS0218427  
; GENERAL INFORMATION:  
; APPLICANT: CZERNIAK, BOGDAN  
; APPLICANT: JOHNSTON, DENNIS  
; TITLE OF INVENTION: METHODS OF DETECTING, DIAGNOSING AND TREATING CANCER  
; TITLE OF INVENTION: AND IDENTIFYING NEOPLASTIC PROGRESSION  
; FILE REFERENCE: UTFC-712-MO  
; CURRENT APPLICATION NUMBER: PCT/US02/18427  
; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: 60/297,813  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; PCT-US02-18427-11

Query Match 43.3%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCCTCTCTCTC 15  
Db 1 TTCCTCTCTCTC 13

Search completed: June 23, 2003, 16:08:16  
Job time : 2520.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 241.076 Seconds  
(without alignments)  
182.610 Million cell updates/sec

Title: US-08-770-564A-2

Perfect score: 30  
Sequence: 1 CGTTCCTCTCTGCGGCGCTGAACGCTGA 30

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

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Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PTCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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- 6: /cgn2\_6/ptodata/1/pubpna/PTCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	40.0	20	9 US-10-139-496-25	Sequence 25, Appl
C 2	12	40.0	24	9 US-09-940-185-1908	Sequence 1908, Ap
C 3	12	40.0	25	9 US-09-754-853A-686	Sequence 686, App
C 4	12	40.0	25	9 US-10-098-263B-49318	Sequence 49318, A
C 5	12	40.0	25	9 US-10-098-263B-114611	Sequence 114611,
C 6	12	40.0	38	9 US-09-903-412-18	Sequence 18, Appl
C 7	12	40.0	38	9 US-09-930-423-2074	Sequence 2074, Ap
C 8	12	40.0	38	9 US-10-174-717A-18	Sequence 18, Appl
C 9	12	40.0	38	10 US-09-096-749A-18	Sequence 18, Appl
C 10	11	36.7	12	9 US-09-938-744-2	Sequence 2, Appl
C 11	11	36.7	18	10 US-09-969-373-1923	Sequence 1923, Ap
C 12	11	36.7	19	9 US-09-879-389B-4	Sequence 4, Appl
C 13	11	36.7	19	9 US-09-902-563-38	Sequence 38, Appl
C 14	11	36.7	19	9 US-09-902-563-41	Sequence 41, Appl
C 15	11	36.7	19	9 US-10-096-255-38	Sequence 38, Appl
C 16	11	36.7	19	9 US-10-096-255-41	Sequence 41, Appl
C 17	11	36.7	19	10 US-09-947-770-26	Sequence 26, Appl
C 18	11	36.7	20	9 US-09-919-197-23	Sequence 23, Appl
C 19	11	36.7	24	9 US-10-101-487-12	Sequence 12, Appl

20	11	36.7	24	9 US-10-101-487-13	Sequence 13, Appl
21	11	36.7	24	10 US-09-818-954A-4	Sequence 4, Appl
22	11	36.7	25	9 US-09-943-388-16	Sequence 16, Appl
23	11	36.7	25	9 US-09-990-940-48	Sequence 48, Appl
C 24	11	36.7	25	9 US-10-215-112-2042	Sequence 2042, Ap
C 25	11	36.7	25	9 US-10-215-112-5699	Sequence 5699, Ap
C 26	11	36.7	25	9 US-10-215-112-10249	Sequence 10249, A
C 27	11	36.7	25	9 US-10-215-112-10695	Sequence 10695, A
C 28	11	36.7	25	9 US-10-215-112-12736	Sequence 12736, A
C 29	11	36.7	25	9 US-10-098-263B-9249	Sequence 9249, Ap
C 30	11	36.7	25	9 US-10-098-263B-17568	Sequence 17568, A
C 31	11	36.7	25	9 US-10-098-263B-24096	Sequence 24096, A
C 32	11	36.7	25	9 US-10-098-263B-26793	Sequence 26793, A
C 33	11	36.7	25	9 US-10-098-263B-38102	Sequence 38102, A
C 34	11	36.7	25	9 US-10-098-263B-38729	Sequence 38729, A
C 35	11	36.7	25	9 US-10-098-263B-48043	Sequence 48043, A
C 36	11	36.7	25	9 US-10-098-263B-48044	Sequence 48044, A
C 37	11	36.7	25	9 US-10-098-263B-48100	Sequence 48100, A
C 38	11	36.7	25	9 US-10-098-263B-50057	Sequence 50057, A
C 39	11	36.7	25	9 US-10-098-263B-50058	Sequence 50058, A
C 40	11	36.7	25	9 US-10-098-263B-56723	Sequence 56723, A
C 41	11	36.7	25	9 US-10-098-263B-56724	Sequence 56724, A
C 42	11	36.7	25	9 US-10-098-263B-67054	Sequence 67054, A
C 43	11	36.7	25	9 US-10-098-263B-81647	Sequence 81647, A
C 44	11	36.7	25	9 US-10-098-263B-81648	Sequence 81648, A
C 45	11	36.7	25	9 US-10-098-263B-96226	Sequence 96226, A

#### ALIGNMENTS

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RESULT 1
US-10-139-496-25/c
; Sequence 25, Application US/10139496
; Publication No. US20030082646A1
; GENERAL INFORMATION:
; APPLICANT: Carey, Thomas E.
; APPLICANT: Nay, Thanku S.
; APPLICANT: Gray, Jennifer P.
; TITLE OF INVENTION: Antigenic Targets of Autoimmune Sensorineural Hearing Loss (AISNL)
; FILE REFERENCE: Development of Tests for Diagnosis and Management of AISNL
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 09/222,179
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-139-496-25

Query Match          40.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTCCCTCTCTG 14
Db      17 TTCCCTCTCTG 6

RESULT 2
US-09-940-185-1908/c
; Sequence 1908, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides

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/ FILE REFERENCE: A-69605-1
/ CURRENT APPLICATION NUMBER: US/09/940.185
/ CURRENT FILING DATE: 2001-08-27
/ PRIOR APPLICATION NUMBER: US 60/227,948
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: US 60/228,854
/ PRIOR FILING DATE: 2000-08-29
/ NUMBER OF SEQ ID NOS: 4768
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 1908
/ LENGTH: 24
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-1908
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Query Match      40.0%; Score 12; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      17 GCCTGAACCGT 28
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Db       20 GCCTGAACCGT 9
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RESULT 3
US-09-754-853a-686/c
/ Sequence 686, Application US/09754853a
/ Publication No. US20030005491A1
/ GENERAL INFORMATION:
/ APPLICANT: Hauge, Brian M.
/ APPLICANT: Parnell, Laurence D.
/ APPLICANT: Parsons, Jeremy D.
/ APPLICANT: Wang, Ming Li
/ TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
/ TITLE OF INVENTION: Soybean Cyst Nematode Resistance
/ FILE REFERENCE: 38-10(15810)B
/ CURRENT APPLICATION NUMBER: US/09/754.853a
/ CURRENT FILING DATE: 2001-01-05
/ PRIOR APPLICATION NUMBER: US 60/174,880
/ PRIOR FILING DATE: 2000-01-07
/ NUMBER OF SEQ ID NOS: 1119
/ SEQ ID NO 686
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 318013_region_A3_151839_17_Reverse_Primer_Seq
US-09-754-853a-686
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Query Match      40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      3 TTCTCTCTCTG 14
         |||||
Db      12 TTCTCTCTCTG 1
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RESULT 4
US-10-098-263b-49318/c
/ Sequence 49318, Application US/10098263b
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098.263b
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
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/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 49318
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263b-49318
```

```
Query Match      40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      6 CTCTCTCTGCGG 17
         |||||
Db      14 CTCTCTCTGCGG 3
```

```
RESULT 5
US-10-098-263b-114611
/ Sequence 114611, Application US/10098263b
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098.263b
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 114611
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263b-114611
```

```
Query Match      40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      2 GTTCTCTTCTCT 13
         |||||
Db      6 GTTCTCTTCTCT 17
```

```
RESULT 6
US-09-903-412-18/c
/ Sequence 18, Application US/09903412
/ Publication No. US20030027319A1
/ GENERAL INFORMATION:
/ APPLICANT: Koide, Shohel
/ TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
/ FILE REFERENCE: 109.050US1
/ CURRENT APPLICATION NUMBER: US/09/903.412
/ CURRENT FILING DATE: 2001-07-11
/ PRIOR APPLICATION NUMBER: US 60/217,474
/ PRIOR FILING DATE: 2000-07-11
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 38
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide FN3R.
US-09-903-412-18
```

```
Query Match      40.0%; Score 12; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      14 GCGGCTGAAC 25
         |||||
```

Db 28 GCGGCGCTGAAC 17

# RESULT 7

US-09-930-423-2074  
 ; Sequence 2074, Application US/09930423  
 ; Publication No. US20030092003A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwigen, Jim  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
 ; FILE REFERENCE: MBH00,918-A 400/027  
 ; CURRENT APPLICATION NUMBER: US/09/930,423  
 ; CURRENT FILING DATE: 2001-08-15  
 ; NUMBER OF SEQ ID NOS: 4553  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 2074  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (31)..(31)  
 ; OTHER INFORMATION: n stands for inosine  
 US-09-930-423-2074

## Query Match

Best Local Similarity 40.0%; Score 12; DB 9; Length 38;  
 Pred. No. 1.3e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCTGGCGGCTGA 22  
 ||:|||||:  
 Db 1 CCTGGCGGCTGA 12

# RESULT 8

US-10-174-717A-18/c  
 ; Sequence 18, Application US/10174717A  
 ; Publication No. US20030108948A1  
 ; APPLICANT: Koide, Shohel  
 ; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
 ; STREET: 121 South Eighth Street, St. 1600  
 ; CITY: Minneapolis  
 ; STATE: MN  
 ; COUNTRY: USA  
 ; ZIP: 55402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: WINDOWS  
 ; SOFTWARE: FastSeq Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/174,717A  
 ; FILING DATE: 18-Jun-2002  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/096,749  
 ; FILING DATE: June 12, 1998  
 ; APPLICATION NUMBER: 60/049,410  
 ; FILING DATE: June 12, 1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ann S. Vikenins  
 ; REGISTRATION NUMBER: 37,748  
 ; REFERENCE/DOCKET NUMBER: 109.034US4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (612) 373-6900  
 ; TELEFAX: (612) 339-3061  
 ; INFORMATION FOR SEQ ID NO: 18:  
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: Internal  
 ORIGINAL SOURCE:  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
 US-10-174-717A-18

Query Match 40.0%; Score 12; DB 9; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCGGCGCTGAAC 25  
 |||||||||  
 Db 28 GCGGCGCTGAAC 17

# RESULT 9

US-09-096-749A-18/c  
 ; Sequence 18, Application US/09096749A  
 ; Patent No. US20020019517A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koide, Shohel  
 ; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
 ; STREET: 121 South Eighth Street, Ste. 1600  
 ; CITY: Minneapolis  
 ; STATE: MN  
 ; COUNTRY: USA  
 ; ZIP: 55402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/096,749A  
 ; FILING DATE: June 12, 1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ann S. Vikenins  
 ; REGISTRATION NUMBER: 37,748  
 ; REFERENCE/DOCKET NUMBER: 109.034US1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (612) 373-6900  
 ; TELEFAX: (612) 339-3061  
 ; INFORMATION FOR SEQ ID NO: 18:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 38 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE:  
 ; ORIGINAL SOURCE:  
 ; US-09-096-749A-18

Query Match 40.0%; Score 12; DB 10; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCGGCGCTGAAC 25  
 |||||||||

Db 28 GCGGCTGAAAC 17

RESULT 10  
US-09-938-744-2/c  
; Sequence 2, Application US/09938744  
; Patent No. US20020172954A1  
; GENERAL INFORMATION:  
; APPLICANT: Mao, Yumin  
; TITLE OF INVENTION: METHOD FOR LARGE SCALE CDNA CLONING AND  
; FILE REFERENCE: A34606-PCR-USA-A 072975.0111  
; CURRENT APPLICATION NUMBER: US/09/938,744  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: PCT/CN00/00036  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: CN 99102450.8  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Oligonucleotide primer  
US-09-938-744-2

Query Match 36.7%; Score 11; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TTCCTGCGGCC 19  
Db 11 TTCCTGCGGCC 1

RESULT 11  
US-09-969-373-1923/c  
; Sequence 1923, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Effertz, Roger J.  
; TITLE OF INVENTION: Soybean SSR and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 1923  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-1923

Query Match 36.7%; Score 11; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCTCTCCTGC 15  
Db 14 CCTCTCCTGC 4

RESULT 12  
US-09-879-389B-4/c

; Sequence 4, Application US/09879389B  
; Publication No. US20030032165A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20030032165A1  
; APPLICANT: Wu, Wendeng, Peter Rahbek  
; APPLICANT: Ostergaard, Peter Rahbek  
; APPLICANT: Kauppinen, Markus Sakari  
; TITLE OF INVENTION: ASPARTIC ACID PROTEASES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 6123.200-US  
; CURRENT APPLICATION NUMBER: US/09/879,389B  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-879-389B-4

Query Match 36.7%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TTCCTGCGGCC 19  
Db 11 TTCCTGCGGCC 1

RESULT 13  
US-09-902-563-38/c  
; Sequence 38, Application US/09902563  
; Publication No. US2003009654A1  
; GENERAL INFORMATION:  
; APPLICANT: Levy, Gary  
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation  
; FILE REFERENCE: 9579-37  
; CURRENT APPLICATION NUMBER: US/09/902,563  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 09/442,143  
; PRIOR FILING DATE: 1999-11-15  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-902-563-38

Query Match 36.7%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCCTCTCTCG 14  
Db 17 TCCTCTCTCG 7

RESULT 14  
US-09-902-563-41  
; Sequence 41, Application US/09902563  
; Publication No. US2003009654A1  
; GENERAL INFORMATION:  
; APPLICANT: Levy, Gary  
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation  
; FILE REFERENCE: 9579-37  
; CURRENT APPLICATION NUMBER: US/09/902,563  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 09/442,143  
; PRIOR FILING DATE: 1999-11-15



NUMBER OF SEQ ID NOS: 53  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 41  
 LENGTH: 19  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Primer  
 US-09-902-563-41

Query Match 36.7%; Score 11; DB 9; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 5e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTG 14  
 |||||  
 DB 8 TCCTCTTCTG 18

RESULT 15  
 US-10-096-255-38/c  
 ; Sequence 38, Application US/10096255  
 ; Publication No. US20030103974A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Levy, Gary  
 ; APPLICANT: Clark, David A.  
 ; TITLE OF INVENTION: Methods of Modulating Immune Coagulation  
 ; FILE REFERENCE: 9579-52  
 ; CURRENT APPLICATION NUMBER: US/10/096,255  
 ; CURRENT FILING DATE: 2002-03-13  
 ; PRIOR APPLICATION NUMBER: US 60/046,537  
 ; PRIOR FILING DATE: 1997-05-17  
 ; PRIOR APPLICATION NUMBER: US 60/061,684  
 ; PRIOR FILING DATE: 1997-10-10  
 ; NUMBER OF SEQ ID NOS: 53  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 38  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 ; US-10-096-255-38

Query Match 36.7%; Score 11; DB 9; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 5e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTG 14  
 |||||  
 DB 17 TCCTCTTCTG 7

Search completed: June 23, 2003, 20:01:28  
 Job time : 244.076 secs



Query Match 51.3%; Score 15.4; DB 8; Length 39;  
Best Local Similarity 76.0%; Pred. No. 9.5e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 TCCTCTTCTGCGGCTGAACGCT 28  
DB 15 TCCTCTTCTGCGGCTGAACGCT 39

RESULT 12  
US-10-287-787-22949/C  
; Sequence 22949, Application US/10287787

; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Caulobacter crescentus complete genome.  
; FILE REFERENCE: Jim Zegeer law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/287,787  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 27958  
; SOFTWARE: Proprietary  
; SEQ ID NO 22949  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Caulobacter crescentus complete genome.  
; FEATURE:  
; LOCATION: (3315887)...(3315934)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 25340  
US-10-287-787-22949

Query Match 51.3%; Score 15.4; DB 10; Length 48;  
Best Local Similarity 76.0%; Pred. No. 9.7e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTTCCCTTCTGCGGCTGAACG 26  
DB 48 GTTCCCTTCTGCGGCTGAACG 24

RESULT 13  
US-60-427-808-174226/C  
; Sequence 174226, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 174226  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-174226

Query Match 50.7%; Score 15.2; DB 12; Length 25;  
Best Local Similarity 85.0%; Pred. No. 1.1e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CTTCCTGCGGCTGAACG 27  
DB 22 CTTCCTGCGGCTGAACG 3

RESULT 14  
US-60-427-808-358682  
; Sequence 358682, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808

; CURRENT FILING DATE: 2002-11-20

; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 358682  
; LENGTH: 25

; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-358682

Query Match 50.7%; Score 15.2; DB 12; Length 25;  
Best Local Similarity 85.0%; Pred. No. 1.1e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 CTTCGCGGCTGAACGCTGA 30  
DB 2 CTTCGCGGCTGAACGCTGA 21

RESULT 15  
US-60-427-808-829890  
; Sequence 829890, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 829890  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-829890

Query Match 50.7%; Score 15.2; DB 12; Length 25;  
Best Local Similarity 85.0%; Pred. No. 1.1e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCCTCTTCTGCGGCTGA 23  
DB 3 TCCTCTTCTGCGGCTGA 22

Search completed: June 26, 2003, 04:14:59  
Job time : 757.961 secs

RESULT 8  
US-60-427-808-739619, Application US/60427808  
; Sequence 739619, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 739619  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus

Query Match 52.7%; Score 15.8; DB 12; Length 25;  
Best Local Similarity 89.5%; Pred. No. 6.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCTCTCTGCGGCGCTGAAA 24  
DB 6 CTCTCTCTGCGGCGCAAGAA 24

RESULT 7  
US-60-427-808-551160/C  
; Sequence 551160, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 551160  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus

Query Match 52.0%; Score 15.6; DB 12; Length 25;  
Best Local Similarity 81.8%; Pred. No. 7.4e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTCTCTCTGCGGCGCTGAAA 27  
DB 24 CTCTCTCTGCGGCGCTGAAA 3

RESULT 8  
US-60-427-808-739619  
; Sequence 739619, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 739619  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus

Query Match 51.3%; Score 15.4; DB 12; Length 25;  
Best Local Similarity 76.0%; Pred. No. 9.1e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTGCGGCGCTGAAA 26  
DB 1 GTTCTTCTGCTGCTGCTGAAA 25

RESULT 9  
US-60-427-836-669241  
; Sequence 669241, Application US/60427836  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527  
; CURRENT APPLICATION NUMBER: US/60/427,836  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 669241  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus

Query Match 51.3%; Score 15.4; DB 12; Length 25;  
Best Local Similarity 76.0%; Pred. No. 9.1e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TTCTCTTCTGCGGCGCTGAAA 27  
DB 1 TTCTCTTCTGCGGCGCTGAAA 25

RESULT 10  
US-60-427-836-669242  
; Sequence 669242, Application US/60427836  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527  
; CURRENT APPLICATION NUMBER: US/60/427,836  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 669242  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus

Query Match 51.3%; Score 15.4; DB 12; Length 25;  
Best Local Similarity 76.0%; Pred. No. 9.1e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TTCTCTTCTGCGGCGCTGAAA 27  
DB 1 TTCTCTTCTGCGGCGCTGAAA 25

RESULT 11  
US-10-447-242-23365  
; Sequence 23365, Application US/10447242  
; GENERAL INFORMATION:  
; APPLICANT: Havukkala, Ilkka  
; TITLE OF INVENTION: Polynucleotide, Materials Incorporating  
; FILE REFERENCE: 11000.1049AU.C1  
; CURRENT APPLICATION NUMBER: US/10/447,242  
; CURRENT FILING DATE: 2003-05-27  
; PRIOR APPLICATION NUMBER: 09/724,750  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/171,431  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 25203  
; SOFTWARE: PaatSeq for Windows Version 4.0  
; SEQ ID NO 23365  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Pinus radiata

US-10-447-242-23365

QY 7 TCTTCCTGGGCGCTGAAA 24  
Db 19 TCTTCCTGGGCGCTGAAA 2

## RESULT 2

PCT-US03-04088-290  
; Sequence 290, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; PRIOR FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 290  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense  
; OTHER INFORMATION: region  
PCT-US03-04088-290

Query Match 60.0%; Score 18; DB 1; Length 19;  
Best Local Similarity 72.2%; Pred. No. 6.6e+02;  
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCCTGGGCGCTGAAA 24  
Db 1 UCUUCUGCGCGCCUGAAA 18

## RESULT 3

US-60-427-808-174225/c  
; Sequence 174225, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 174225  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-174225

Query Match 56.0%; Score 16.8; DB 12; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTTCCTGGGCGCTGAAACGG 27  
Db 22 CTTCCTGGGCGAGCAAAACGG 3

## RESULT 4

US-10-325-899-304/c  
; Sequence 304, Application US/10325899  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Woodward, Robert  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT  
; FILE REFERENCE: 506612000122  
; CURRENT APPLICATION NUMBER: US/10/325,899  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; NUMBER OF SEQ ID NOS: 9966  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 304  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-325-899-304

Query Match 55.3%; Score 16.6; DB 9; Length 50;  
Best Local Similarity 82.6%; Pred. No. 2.9e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 TCTTCCTGGGCGCTGAAACGG 29  
Db 46 TCTTTTGTGGCTGAAACGATG 24

## RESULT 5

US-60-427-808-324892  
; Sequence 324892, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 324892  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-324892

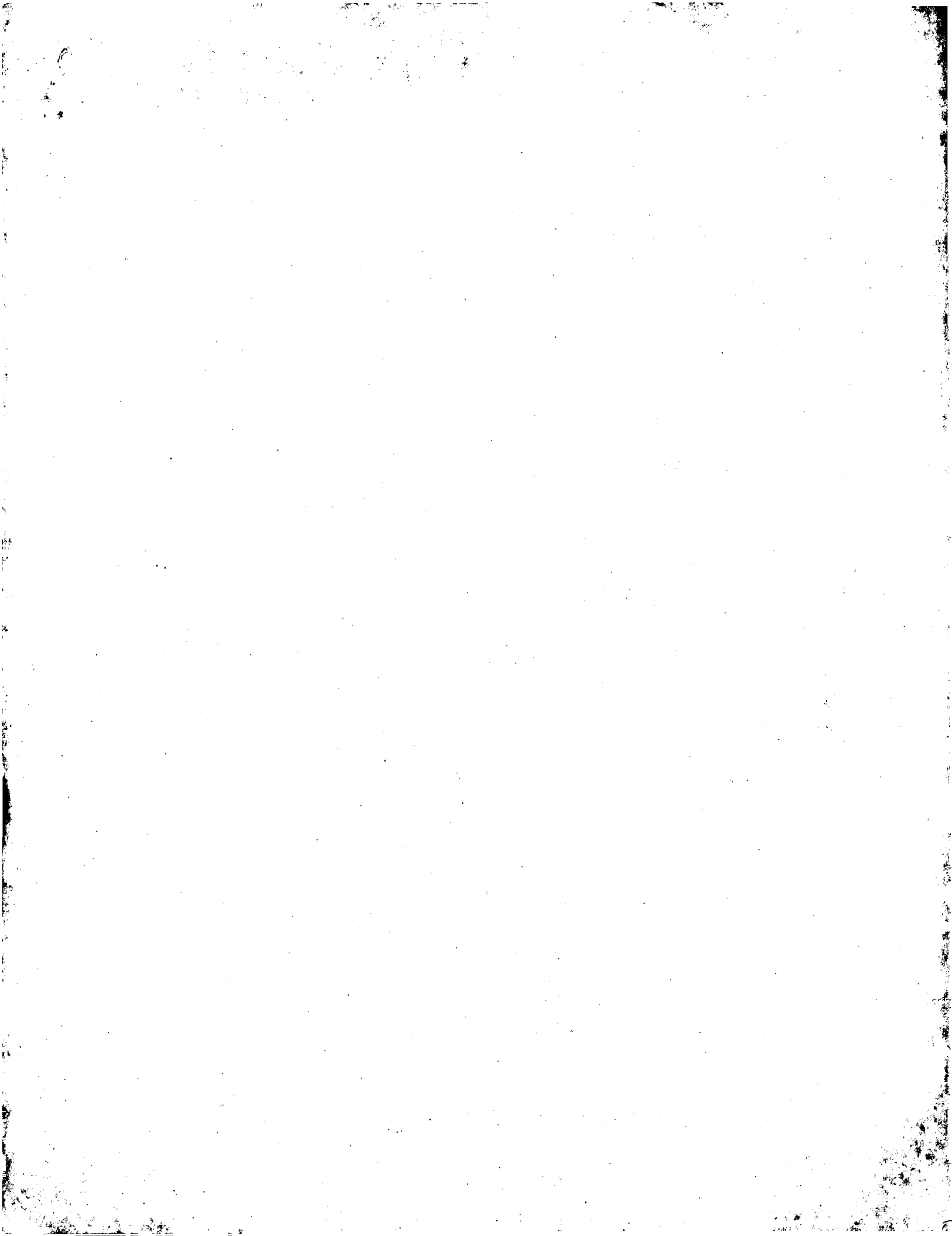
Query Match 54.0%; Score 16.2; DB 12; Length 25;  
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Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTGGGCGCTGA 22  
Db 3 GTTCATCTTCAGCAGCCTGA 23

## RESULT 6

US-60-427-836-549003  
; Sequence 549003, Application US/60427836  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou





Fri Jun 27 07:41:44 2003

us-08-770-564a-1\_copy\_137\_196.01go.rge

Page 5

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source location/Qualifiers  
1..16  
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BASE COUNT 5 a 5 c 3 g 3 t  
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Best Local Similarity 100.0%; Fred.No.3.1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTGAAGCTCT 45  
|||  
16 GAGAGTGAAGCTCT 5

RESULT 15  
AR009327/c 17 bp DNA linear PAT 04-DEC-1998  
LOCUS AR009327  
DEFINITION Sequence 95 from patent US 5756291.  
ACCESSION AR009327  
VERSION AR009327.1 GI:3968132  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Griffin,L., Albrecht,G., Latham,J., Leung,L., Vermaas,E. and  
Toole,J.J.  
TITLE Apatemers specific for biomolecules and methods of making  
JOURNAL Patent: US 5756291-A 95 26-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..17  
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BASE COUNT 1 a 1 c 10 g 5 t  
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QY 16 CCCAACGAGCCC 27  
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17 CCCAACGAGCCC 6

Search completed: June 23, 2003, 20:29:39  
Job time : 601.016 secs



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ORIGIN				

BASE COUNT	6 a	9 c	11 g	5 t
ORIGIN				

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Best Local Similarity	100.0%;	Pred. No. 7.5e+03;		

Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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48 CGAGAGCCGCGAG 60

14 CGAGAGCCGCCGAG 26

RESULT 11  
AR043925/c  
100000  
40 lbs  
DWT  
14-0000  
DATE 20 APR 1990

LOCUS	AK043925	40 bp
DEFINITION	Sequence 1 from patent US 5817310.	

ACCESSION AR043925

AR043925.1 GI:5965390

KEYWORDS : AR043923.1 GI:59653590

**KEYWORDS** :  
**SOURCE** :  
inkknown

SOURCE	Unknown.
ORGANISM	Unknown.

ORGANISM	Unknown.
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Unclassified.

Db 18 AGAGAGTGACTCT 6

RESULT 6  
LOCUS AX038445/c  
DEFINITION Sequence 202 from Patent WO0061795.  
ACCESSION AX038445  
VERSION AX038445.1 GI:11227793  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
De Canck, I.D., Rossau, R. and Rombout, A.  
Method for the amplification of hla class I alleles  
Patent: WO 0061795-A 202 19-OCT-2000;  
CANCER IL28 DB (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);  
ROMBOUT ANNEBILIS (BE)  
FEATURES  
source Location/Qualifiers  
1..24  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 6 a 8 c 4 g 6 t  
ORIGIN

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 33 AGAGAGTGACTCT 45  
19 AGAGAGTGACTCT 7

RESULT 7  
LOCUS AX038446/c  
DEFINITION Sequence 203 from Patent WO0061795.  
ACCESSION AX038446  
VERSION AX038446.1 GI:11227794  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
De Canck, I.D., Rossau, R. and Rombout, A.  
Method for the amplification of hla class I alleles  
Patent: WO 0061795-A 203 19-OCT-2000;  
CANCER IL28 DB (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);  
ROMBOUT ANNEBILIS (BE)  
FEATURES  
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1..25  
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BASE COUNT 6 a 8 c 5 g 6 t  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 33 AGAGAGTGACTCT 45  
20 AGAGAGTGACTCT 8

RESULT 8  
LOCUS AX428325/c  
25 bp DNA 11near PAT 20-JUN-2002

DEFINITION Sequence 37 from Patent EP1199356.  
ACCESSION AX428325  
VERSION AX428325.1 GI:21538283  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE  
AUTHORS Araki, H.C., Hagihara, H.C., Hayashi, Y.C., Endo, K.C., Igarashi, K.C.  
TITLE Highly productive alpha-amylases  
JOURNAL Patent: EP 1199356-A 37 24-APR-2002;  
Kao Corporation (JP)  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 6 a 2 c 10 g 7 t  
ORIGIN

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 TTCCCCCAACCA 23  
15 TTCCCCCAACCA 3

RESULT 9  
LOCUS AR088753/c  
DEFINITION Sequence 8 from patent US 5990092.  
ACCESSION AR088753  
VERSION AR088753.1 GI:10015516  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Walsh, K.  
TITLE GATA-6 transcription factor: compositions and methods  
JOURNAL Patent: US 5990092-A 8 23-NOV-1999;  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 2 a 11 c 8 g 6 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 48 CGAGAGCCCGGAG 60  
15 CGAGAGCCCGGAG 3

RESULT 10  
LOCUS AR088752  
DEFINITION Sequence 7 from patent US 5990092.  
ACCESSION AR088752  
VERSION AR088752.1 GI:10015515  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Walsh, K.  
TITLE GATA-6 transcription factor: compositions and methods  
JOURNAL Patent: US 5990092-A 7 23-NOV-1999;  
FEATURES  
source Location/Qualifiers

1 (bases 1 to 31)  
Unclasseified.

## KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)

FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
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QY 20 ACCAGCCCCCGAGAGT 39  
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AX038441/c 20 bp DNA linear PAT 16-NOV-2000  
LOCUS AX038441  
DEFINITION Sequence 198 from Patent WO0061795.  
ACCESSION AX038441  
VERSION AX038441.1 GI:11227789  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS De Canck,I.D., Rossau,R. and Rombout,A.  
TITLE 1 (bases 1 to 20)  
JOURNAL Method for the amplification of hla class I alleles  
Patent: WO 0061795-A 198-19-OCT-2000;  
CANCK ILSB DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);  
ROMBOUT ANNEBELIES (BE)

FEATURES  
source Location/Qualifiers  
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BASE COUNT  
4 a 6 c 4 g 6 t

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QY 33 AGAGAGTGACTCT 45  
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RESULT 3  
AX038442/c 21 bp DNA linear PAT 16-NOV-2000  
LOCUS AX038442  
DEFINITION Sequence 199 from Patent WO0061795.  
ACCESSION AX038442  
VERSION AX038442.1 GI:11227790  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS De Canck,I.D., Rossau,R. and Rombout,A.  
TITLE 1 (bases 1 to 21)  
JOURNAL Method for the amplification of hla class I alleles  
Patent: WO 0061795-A 199-19-OCT-2000;  
CANCK ILSB DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);  
ROMBOUT ANNEBELIES (BE)

FEATURES  
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BASE COUNT  
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## ORIGIN

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AX038443/c 22 bp DNA linear PAT 16-NOV-2000  
LOCUS AX038443  
DEFINITION Sequence 200 from Patent WO0061795.  
ACCESSION AX038443  
VERSION AX038443.1 GI:11227791  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS De Canck,I.D., Rossau,R. and Rombout,A.  
TITLE 1 (bases 1 to 22)  
JOURNAL Method for the amplification of hla class I alleles  
Patent: WO 0061795-A 200-19-OCT-2000;  
CANCK ILSB DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);  
ROMBOUT ANNEBELIES (BE)

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTGACTCT 45  
|||||  
17 AGAGAGTGACTCT 5

RESULT 5  
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LOCUS AX038444  
DEFINITION Sequence 201 from Patent WO0061795.  
ACCESSION AX038444  
VERSION AX038444.1 GI:11227792  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS De Canck,I.D., Rossau,R. and Rombout,A.  
TITLE 1 (bases 1 to 23)  
JOURNAL Method for the amplification of hla class I alleles  
Patent: WO 0061795-A 201-19-OCT-2000;  
CANCK ILSB DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);  
ROMBOUT ANNEBELIES (BE)

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTGACTCT 45

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:17:23 ; Search time 598.016 Seconds

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Title: US-08-770-564A-1\_Copy\_137\_196

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Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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1: gb\_ba:\*  
2: gb\_hg:\*  
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5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
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10: gb\_ro:\*  
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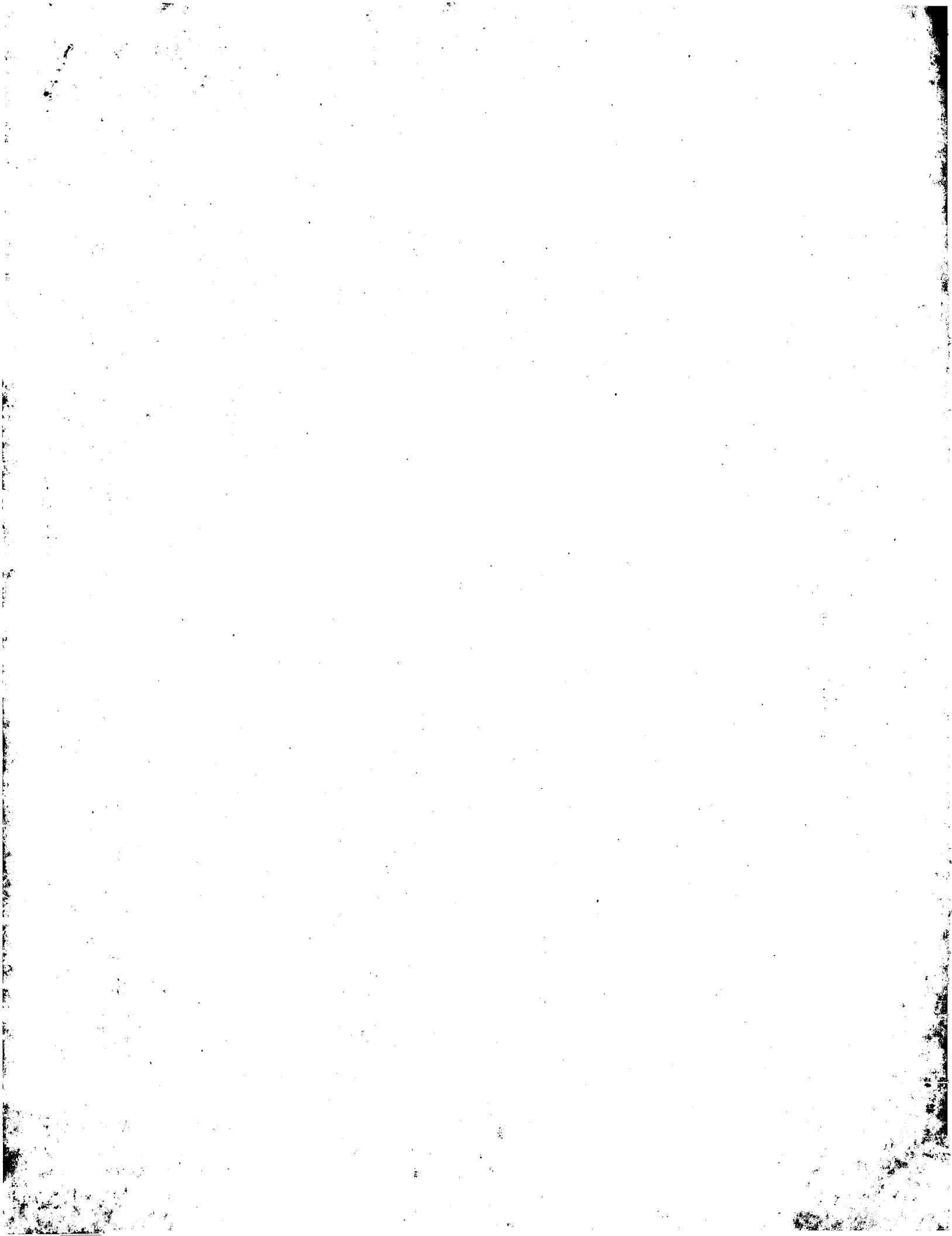
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2	13	21.7	20	6	AX038441
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4	13	21.7	22	6	AX038443
5	13	21.7	23	6	AX038444
6	13	21.7	24	6	AX038445
7	13	21.7	25	6	AX038446
8	13	21.7	25	6	AX428325
9	13	21.7	27	6	AR088753
10	13	21.7	31	6	AR088752
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13	13	21.7	40	6	BD000716
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15	12	20.0	17	6	AR009327
16	12	20.0	17	6	AR060792
17	12	20.0	17	6	131571
18	12	20.0	20	6	AR000220
19	12	20.0	20	6	AR105633
20	12	20.0	20	6	AR167446
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25	12	20.0	21	6	AR009315
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32	12	20.0	33	6	AX397889
33	12	20.0	39	6	AX230498
34	12	20.0	45	6	AX085874
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36	11	18.3	15	6	152251
37	11	18.3	17	6	188902
38	11	18.3	17	6	AR045419
39	11	18.3	17	6	AR125598
40	11	18.3	17	6	AR197489
41	11	18.3	17	6	AX214835
42	11	18.3	17	6	AX215708
43	11	18.3	17	6	AX215709
44	11	18.3	17	6	AX216493
45	11	18.3	17	6	AX440600

## ALIGNMENTS

RESULT 1  
AX019608  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX019608  
Sequence 62 from Patent WO938964.  
AX019608  
AX019608.1 GI:10043522  
20 bp  
DNA  
linear  
PAT 07-SEP-2000  
synthetic construct.  
artificial sequences.  
1 (pages 1 to 20)  
Keith W.N.  
Promoter regions of the mouse and human telomerase rna component  
genes  
Patent: WO 938964-A 62 05-AUG-1999;



```

PI De Canck I, Rombout A, Rousseau R;
XX
XX WPI; 2000-647426/62.
XX
XX Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using
PT defined primer sets, useful for subtyping or typing of HLA Class I
PT alleles -
XX
XX Claim 4; Page 40; 128bp; English.
XX
XX The present invention relates to a method for the locus-specific,
CC separate amplification of exon 2, exon 3, and/or exon 4 of human
CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
CC for subtyping or typing of HLA class I alleles. The present sequence is
CC an amplification primer used in the method.
XX
XX Sequence 22 BP; 4 A; 8 C; 4 G; 6 T; 0 other;
SQ
Query Match 21.7%; Score 13; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 AGAGAGTGAAGTCT 45
DB 17 AGAGAGTGAAGTCT 5
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ID AAC80283 standard; DNA; 23 BP.
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XX AAC80283;
XX
XX 03-MAY-2001 (first entry)
XX
XX Reverse primer #11 used for amplification of HLA-A exon 3.
XX
XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200061795-A2.
XX
XX 19-OCT-2000.
XX
XX 05-APR-2000; 2000WO-EP02998.
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XX 09-APR-1999; 99EP-0870068.
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XX 11-JUN-1999; 99US-0138614.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX De Canck I, Rombout A, Rousseau R;
XX
XX WPI; 2000-647426/62.
XX
XX Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using
PT defined primer sets, useful for subtyping or typing of HLA Class I
PT alleles -
XX
XX Claim 4; Page 40; 128bp; English.
XX
XX The present invention relates to a method for the locus-specific,
CC separate amplification of exon 2, exon 3, and/or exon 4 of human
CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
CC for subtyping or typing of HLA class I alleles. The present sequence is
CC an amplification primer used in the method.
XX
XX Sequence 23 BP; 5 A; 8 C; 4 G; 6 T; 0 other;
SQ

```

```

Query Match 21.7%; Score 13; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 AGAGAGTGAAGTCT 45
DB 18 AGAGAGTGAAGTCT 6
RESULT 15
AAC80284/C
ID AAC80284 standard; DNA; 24 BP.
XX
XX AAC80284;
XX
XX 03-MAY-2001 (first entry)
XX
XX Reverse primer #12 used for amplification of HLA-A exon 3.
XX
XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200061795-A2.
XX
XX 19-OCT-2000.
XX
XX 05-APR-2000; 2000WO-EP02998.
XX
XX 09-APR-1999; 99EP-0870068.
XX
XX 11-JUN-1999; 99US-0138614.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX De Canck I, Rombout A, Rousseau R;
XX
XX WPI; 2000-647426/62.
XX
XX Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using
PT defined primer sets, useful for subtyping or typing of HLA Class I
PT alleles -
XX
XX Claim 4; Page 40; 128bp; English.
XX
XX The present invention relates to a method for the locus-specific,
CC separate amplification of exon 2, exon 3, and/or exon 4 of human
CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
CC for subtyping or typing of HLA class I alleles. The present sequence is
CC an amplification primer used in the method.
XX
XX Sequence 24 BP; 6 A; 8 C; 4 G; 6 T; 0 other;
SQ
Query Match 21.7%; Score 13; DB 21; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 AGAGAGTGAAGTCT 45
DB 19 AGAGAGTGAAGTCT 7
Search completed: June 23, 2003, 20:09:18
Job time : 229.107 secs

```

Db 14 AGAGAGTACTCT 2

RESULT 11

AAx38046/c  
ID AAX38046 standard; DNA; 21 BP.

AC AAX38046;

DT 04-JUN-1999 (first entry)

DE HLA-A untranslated region primer SEQ ID NO:202.

KM Human; histocompatibility locus antigen; HLA; determination; allele;

XX HLA-B typing; PCR, HLA class I; cis/trans linkage resolution; ss.

OS Synthetic.

OS Homo sapiens.

PN WO907883-A1.

PD 18-FEB-1999.

PF 11-AUG-1998; 98WO-CM00768.

PR 11-AUG-1997; 97US-0909290.

PA (BLAS/) BLASZYK R H.

PA (VISI-) VISIBLE GENETICS INC.

PI Blaszyk RH, Leushner J;

DR WPI; 1999-167446/14.

PT Determination of HLA class I group type of a subject - using group

PT specific untranslated region primer pair

PS Disclosure; Page 19; 195pp; English.

CC The present invention describes a method using novel primers involving  
CC the PCR-based determination of histocompatibility locus antigen B  
CC (HLA-B) Class I group type. Determining the HLA-B Class I group type of  
CC a subject comprises: (i) combining a group-specific untranslated region  
CC primer pair with a target DNA sample from the subject under conditions  
CC such that primer-based amplification of the target DNA may occur; and  
CC (ii) determining whether a nucleic acid product is produced by the  
CC amplification; where the ability of the primer pair to produce a nucleic  
CC acid product is associated with a particular HLA group type. The method  
CC can be used for HLA-B typing. In the method, the initial group specific  
CC amplification allows a PCR based separation of haplotypes in 95% of  
CC patient samples. It permits the resolution of cis/trans linkages of  
CC heterozygote sequencing results which cannot be achieved with other  
CC protocols. AAX37845 to AAX38286 represent DNA sequence used in the  
CC exemplification of the present invention.

SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 other;

Query Match 21.7%; Score 13; DB 20; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45

DB 13 AGAGAGTACTCT 1

RESULT 12

AAc80281/c

ID AAC80281 standard; DNA; 21 BP.

AC AAC80281;

DT 03-MAY-2001 (first entry)

XX Reverse primer #109 used for amplification of HLA-A exon 3.

DE HLA-A; HLA-B; HLA-C; typing; primer; human; ss.

XX Homo sapiens.

OS Synthetic.

PN WO200061795-A2.

PD 19-OCT-2000.

PF 05-APR-2000; 2000WO-EP02998.

PR 09-APR-1999; 99EP-0870068.

PR 11-JUN-1999; 99US-0138614.

PA (INNO-) INNOGENETICS NV.

PI De Canck I, Rombout A, Rossau R;

DR WPI; 2000-647426/62.

PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4

PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using

PT defined primer sets, useful for subtyping or typing of HLA Class I

PT alleles -

PS Claim 4; Page 40; 128pp; English.

CC The present invention relates to a method for the locus-specific,  
CC separate amplification of exon 2, exon 3, and/or exon 4 of human  
CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful  
CC for subtyping or typing of HLA class I alleles. The present sequence is  
CC an amplification primer used in the method.

SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;

Query Match 21.7%; Score 13; DB 21; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45

DB 16 AGAGAGTACTCT 4

RESULT 13

AAc80282/c

ID AAC80282 standard; DNA; 22 BP.

AC AAC80282;

DT 03-MAY-2001 (first entry)

DE Reverse primer #110 used for amplification of HLA-A exon 3.

XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.

OS Homo sapiens.

OS Synthetic.

PN WO200061795-A2.

PD 19-OCT-2000.

PF 05-APR-2000; 2000WO-EP02998.

PR 09-APR-1999; 99EP-0870068.

PR 11-JUN-1999; 99US-0138614.

PA (INNO-) INNOGENETICS NV.

XX AAV46054 and AAV46200-V46264 are primers used in isolating human  
 CC histocompatibility locus antigen (HLA-A) Class I alleles which are used  
 CC in a novel method of HLA Class I typing. The method involves combining  
 CC a group-specific untranslated region primer pair with a target DNA to  
 CC allow primer-based amplification of the DNA, and determining whether a  
 CC nucleic acid product is produced by the amplification. The ability of  
 CC the primer pair to produce a product is associated with a particular  
 CC HLA group type. The methods can be used for typing the 3 classical HLA  
 CC Class I genes (comprising the loci HLA-A, HLA-B, and HLA-C) in e.g.  
 CC donors and hosts for tissue transplantation. The initial group specific  
 CC amplification allows a PCR based separation of haplotypes in 95% of  
 CC patient samples. The subsequent sequencing can provide for  
 CC high-resolution typing.

XX Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 other;  
 SQ

Query Match 21.7%; Score 13; DB 19; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45  
 |||||  
 DB 14 AGAGAGTACTCT 2

RESULT 9  
 AAV46221/c  
 ID AAV46221 standard; DNA; 21 BP.  
 XX  
 XX AAV46221;  
 AC  
 XX 16-OCT-1998 (first entry)  
 DT  
 XX Human HLA-A primer 13-282.  
 DE  
 XX Histocompatibility locus antigen; HLA-A class I; human; class typing;  
 KW donor; host; tissue transplantation; primer; ss.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX W09826091-A2.  
 PN  
 XX 18-JUN-1998.  
 PD  
 XX 12-DEC-1997; 97WO-CA00955.  
 PF  
 XX 12-DEC-1996; 96US-076189.  
 PR  
 XX (VISI-) VISIBLE GENETICS INC.  
 PA  
 XX Blaesczyk RH, Leushner J;  
 PI WPI; 1998-348544/30.  
 XX  
 XX HLA Class I typing - by primer-based amplification of target DNA.  
 PT using group-specific untranslated region primer pair  
 PS Claim 4; Page 128; 185pp; English.

CC AAV46054 and AAV46200-V46264 are primers used in isolating human  
 CC histocompatibility locus antigen (HLA-A) Class I alleles which are used  
 CC in a novel method of HLA Class I typing. The method involves combining  
 CC a group-specific untranslated region primer pair with a target DNA to  
 CC allow primer-based amplification of the DNA, and determining whether a  
 CC nucleic acid product is produced by the amplification. The ability of  
 CC the primer pair to produce a product is associated with a particular  
 CC HLA group type. The methods can be used for typing the 3 classical HLA  
 CC Class I genes (comprising the loci HLA-A, HLA-B, and HLA-C) in e.g.  
 CC donors and hosts for tissue transplantation. The initial group specific  
 CC amplification allows a PCR based separation of haplotypes in 95% of  
 CC patient samples. The subsequent sequencing can provide for

CC high-resolution typing.  
 XX Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 other;  
 SQ

Query Match 21.7%; Score 13; DB 19; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45  
 |||||  
 DB 13 AGAGAGTACTCT 1

RESULT 10  
 AAX38044/c  
 ID AAX38044 standard; DNA; 21 BP.  
 XX  
 XX AAX38044;  
 AC  
 XX 04-JUN-1999 (first entry)  
 DT  
 XX HLA-A untranslated region primer SEQ ID NO:200.  
 DE  
 XX Human; histocompatibility locus antigen; HLA; determination; allele;  
 KW HLA-B typing; PCR; HLA class I; cis/trans linkage resolution; ss.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX W09907883-A1.  
 PN  
 XX 18-FEB-1999.  
 PD  
 XX 11-AUG-1998; 98WO-CA00768.  
 PF  
 XX 11-AUG-1997; 97US-090290.  
 PR  
 XX (BLAS/) BLASZCYK R H.  
 PA (VISI-) VISIBLE GENETICS INC.  
 XX  
 XX Blaesczyk RH, Leushner J;  
 PI WPI; 1999-167446/14.  
 DR  
 XX Determination of HLA class I group type of a subject - using group  
 PT specific untranslated region primer pair  
 PS Disclosure; Page 19; 195pp; English.

CC The present invention describes a method using novel primers involving  
 CC the PCR-based determination of histocompatibility locus antigen B  
 CC (HLA-B) Class I group type. Determining the HLA-B class I group type of  
 CC a subject comprises: (i) combining a group-specific untranslated region  
 CC primer pair with a target DNA sample from the subject under conditions  
 CC such that primer-based amplification of the target DNA may occur; and  
 CC (ii) determining whether a nucleic acid product is produced by the  
 CC amplification; where the ability of the primer pair to produce a nucleic  
 CC acid product is associated with a particular HLA group type. The method  
 CC can be used for HLA-B typing. In the method, of haplotypes in 95% of  
 CC patient samples. It permits the resolution of cis/trans linkages of  
 CC heterozygote sequencing results which cannot be achieved with other  
 CC protocols. AAX37845 to AAX38286 represent DNA sequence used in the  
 CC exemplification of the present invention.

XX Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 other;  
 SQ

Query Match 21.7%; Score 13; DB 20; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45  
 |||||



DT	09-MAR-1999	(first entry)
XX		
DE	Antisense primer for intron boundary mapping of DNA Metase exon 38-39.	
XX		
KW	DNA methyltransferase; DNA Metase; antisense oligonucleotide; human;	
KW	cellular growth; tumour growth inhibition; silenced gene activation;	
KW	beta thalassemia; sickle cell anemia; PCR primer; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
FN	WO9854313-A2.	
XX		
ED	03-DEC-1998.	
XX		
PF	29-MAY-1998; 98WO-IB01107.	
XX		
PR	17-DEC-1997; 97US-0069865.	
PR	30-MAY-1997; 97US-0866340.	
XX		
PA	(UTWC-) UNIV MCGILL.	
XX		
PI	Bigey P, Ramchandani S, Szyf M;	
XX		
DR	WPI, 1999-059833/05.	
XX		
XX	New DNA methyltransferase nucleotide sequences - used particularly	
PT	to develop antisense oligonucleotides for diagnostic and therapeutic	
PT	purposes, particularly for inhibiting tumour growth	
XX		
PS	Example 8; Page 32; 108pp; English.	
XX		
CC	PCR primers AAV9163-220 were used to map the intron boundaries of	
CC	the exons of DNA methyltransferase (DNA Metase) genomic sequence.	
CC	Antisense oligonucleotides which inhibit inhibit DNA Metase expression	
CC	can be derived from the genomic DNA Metase sequence. The antisense	
CC	oligonucleotides can be used in investigating the role of DNA Metase	
CC	in cellular growth. They can be administered at different points in	
CC	the cell cycle, or in conjugation with promoters or inhibitors of cell	
CC	growth to determine the role of DNA Metase in the growth of the cell	
CC	type of interest. The antisense oligonucleotides can also be used for	
CC	inhibiting tumour growth in a mammal, or to activate silenced genes to	
CC	provide a missing gene function. This ameliorates disease symptoms,	
CC	e.g. in beta thalassemia and sickle cell anemia. The antisense	
CC	oligonucleotides can also be used an analytical and diagnostic tools	
CC	and a potentiators of transgenic plant and animal studies.	
XX		
SO	Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 other;	
	Query Match	21.7%; Score 13; DB 20; Length 20;
	Best Local Similarity	100.0%; Pred. No. 1.7e+03;
	Matches 13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	28 GCCCGAGAGATG 40	
DB	15 GCCCGAGAGATG 3	
RESULT 7		
XX	AAC80280/c	
XX	ID AAC80280 standard, DNA; 20 BP.	
XX		
AC	AAC80280;	
XX		
DT	03-MAY-2001 (first entry)	
XX		
DB	Reverse primer #108 used for amplification of HLA-A exon 3.	
XX		
XX	HLA-A; HLA-B; HLA-C; typing; primer; human; ss.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		

PN WO200061795-A2.  
XX 19-OCT-2000.  
PD  
XX 05-APR-2000; 2000WO-EP02998.  
XX  
XX 09-APR-1999; 99EP-0870068.  
PR 11-JUN-1999; 99US-0138614.  
XX  
XX (INNO-) INNOGENETICS NV.  
PA  
XX De Canck I, Rombout A, Rossau R;  
XX  
XX WPI; 2000-647426/62.  
DR  
XX locus-specific, separate amplification of exon 2, exon 3, and/or exon 4  
XX of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using  
XX defined primer sets, useful for subtyping or typing of HLA Class I  
XX alleles.  
XX  
XX Claim 4; Page 40; 128pp; English.  
PS  
XX The present invention relates to a method for the locus-specific,  
XX separate amplification of exon 2, exon 3, and/or exon 4 of human  
XX leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful  
XX for subtyping or typing of HLA class I alleles. The present sequence is  
XX an amplification primer used in the method.  
XX  
XX Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 other;  
SQ  
XX  
XX Query Match 21.7%; Score 13; DB 21; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 33 AGAGAGTGACTCT 45  
DB 15 AGAGAGTGACTCT 3

CC (AA129513-AA13114) from the human genome which include polymorphic sites  
 CC which can predispose individuals to disease. Various genes from a number  
 CC of individuals were resequenced and single nucleotide polymorphisms  
 CC (SNPs) in these genes discovered. The method is useful for predicting the  
 CC presence, absence or severity of a particular phenotype or disorder (e.g.  
 CC diabetes), associated with a particular genotype. The nucleic acids  
 CC containing the polymorphic sites may be useful in forensic and paternity  
 CC testing.

CC Sequence 31 BP; 2 A; 11 C; 16 G; 2 T; 0 other;

Query Match 23.3%; Score 14; DB 22; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCAGCCGCCCGAG 34  
 DB 19 CCAGCCGCCCGAG 6

#### RESULT 4

AAFP2154/C  
 ID AAFP2154 standard; DNA; 15 BP.

AC AAFP2154;

XX 15-MAY-2001 (first entry)

DE Human IGERB allele specific probe SEQ ID NO: 12.

KW Human; immunoglobulin E receptor beta chain; IGERB; chromosome 11q13;  
 KM allergy; asthma; rhinitis; eczema; single nucleotide polymorphism; SNP;

XX atcopy; probe; PCR primer; ss.

OS Homo sapiens.

XX WO200114588-A1.

XX 01-MAR-2001.

XX 11-AUG-2000; 2000WO-US22175.

XX 24-AUG-1999; 99US-0150423.

XX (GENA-) GENAISANCE PHARM INC.

XX (NAND/) NANDABALAN K.

XX Denton RR, Klem SE, Stephens JC;

XX WPI; 2001-226623/23.

XX Novel polynucleotide useful for therapeutic purposes, comprises  
 PT nucleotide polymorphisms in immunoglobulin E receptor beta chain gene

XX Claim 15; Page 61; 88pp; English.

XX The present invention provides the protein and coding sequences of  
 CC several polymorphic variants of the human immunoglobulin E receptor beta  
 CC chain (IGERB). These contain single nucleotide polymorphisms (SNPs) which  
 CC may be indicative of a predisposition to atopy, allergy, asthma, rhinitis  
 CC and eczema. Also provided are the sequences of probes and primers for use  
 CC in identifying the genotype of an individual with regards to the IGERB  
 CC gene. The IGERB gene is found at human chromosome 11q13. The sequences  
 CC are all useful in therapeutics. The present sequence was used to isolate  
 CC the IGERB gene.

XX Sequence 15 BP; 4 A; 1 C; 8 G; 2 T; 0 other;

Query Match 21.7%; Score 13; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTCCCGTTCCCC 17  
 DB 13 TTCCCGTTCCCC 1

#### RESULT 5

AAQ10624  
 ID AAQ10624 standard; DNA; 19 BP.

AC AAQ10624;

XX 29-APR-1991 (first entry)

DE HLA Class I locus-specific primer A2.2.

KW Human leukocyte antigen; major histocompatibility complex; MHC;  
 KM restriction fragment length polymorphic analysis; RFLP;

XX tissue typing; allele; PCR; ss.

OS Synthetic.

XX EP414469-A.

XX 27-FEB-1991.

XX 20-AUG-1990; 90EP-0309107.

XX 11-JUL-1990; 90US-0551239.

XX 25-AUG-1989; 89US-0398217.

XX 11-SEP-1989; 89US-0405499.

XX 16-JAN-1990; 90US-0465863.

XX (GENE-) GENETYPIC AG.

XX Simons MJ;

XX WPI; 1991-059664/09.

XX Detection of adjacent and non-adjacent locus, e.g. HLA alleles -  
 PT by amplifying genomic DNA, for direct determination of haplotype

XX Claim 29; Page 49; 53pp; English.

XX The primer is specific for nt 1667-1685 of HLA Class I A2 locus.  
 CC It is used in a method for the prodn. of RFLP fragments for an HLA  
 CC locus, together with a second primer making up a locus-specific  
 CC primer (LSP) pair. It is pref. used with a Class I-specific  
 CC primer which hybridises with at least two different Class I loci,  
 CC pref. at least one of each of A, B, and C, and most pref. all of  
 CC these. The Class I primer esp. hybridises with intervening  
 CC sequence (IVS) III or IVS I sequences. Direct determination of  
 CC the haplotype is possible, providing useful information for  
 CC identity of individuals for e.g. paternity case and forensic  
 CC investigations.  
 CC See also AAQ10621-Q10669.

XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 other;

Query Match 21.7%; Score 13; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45  
 DB 3 AGAGAGTACTCT 15

#### RESULT 6

AAV9218/C  
 ID AAV9218 standard; DNA; 20 BP.

XX AAV9218;

XX Disclosure; Fig 15; 109pp; English.

PS The invention relates to promoter regions from mouse and human telomerase

CC RNA (TR) component genes. The TR gene promoter can be linked to a

CC heterologous gene, especially a gene encoding a cytotoxin, for therapy

CC of cancer, especially neoplasias. The telomerase is necessary for the

CC unrestricted proliferative capacity of many human cancers. Mutation or

CC dysregulation of the telomerase repression pathway may cause reactivation

CC or upregulation of telomerase expression in cancer. Substances,

CC identified in the methods, can be used to block transcription from the TR

CC gene promoter through interaction of the 5' regulatory sequences. These

CC substances, e.g. antisense oligonucleotides, transcription factors, are

CC peptide nucleic acids and factors that disrupt signal transduction, are

CC useful for cancer therapy. In particular, gene therapy vectors

CC (especially pG162-codupp) comprising the promoter and a viral thymidine

CC kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that

CC neoplasia can be controlled or treated. Direct down-regulation of

CC telomerase RNA gene through manipulation of transcription factors may be

CC effective anticancer therapy and the cloning of the hTR gene promoter

CC allows the analysis of therapeutic molecules which modulate hTR promoter

CC activity. The present sequence represents an oligo comprising a Sp1 site.

XX

SQ Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 other;

Query Match 33.3%; Score 20; DB 20; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCAGCCCCGCCGAGAGT 39

DB 1 ACCAGCCCCGCCGAGAGT 20

RESULT 2

AA207318

ID AA207318 standard; DNA; 20 BP.

XX

AC AA207318;

XX

DT 22-OCT-1999 (first entry)

XX

DE Human telomerase RNA gene (hTR) promoter specific primer h4.

XX

KM Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;

KW gene therapy; thymidine kinase gene; anticancer therapy; human;

KW mutagenesis; PCR primer; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9938964-A2.

XX

PD 05-AUG-1999.

XX

PF 29-JAN-1999; 99WO-GB00308.

XX

PR 29-JAN-1998; 98GB-0001902.

XX

PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX

PI Keith MN;

XX

DR WPI; 1999-479183/40.

XX

PT Mouse and human telomerase RNA gene promoters, useful for tumor

PT specific gene therapy

XX

PS Disclosure; Fig 12; 109pp; English.

XX

CC The invention relates to promoter regions from mouse and human

CC telomerase RNA (TR) component genes. The TR gene promoter can be linked

CC to a heterologous gene, especially a gene encoding a cytotoxin, for

CC therapy of cancer, especially neoplasias. The telomerase is necessary for

CC the unrestricted proliferative capacity of many human cancers. Mutation

CC or dysregulation of the telomerase repression pathway may cause

CC reactivation or upregulation of telomerase expression in cancer.

CC Substances, identified in the methods, can be used to block transcription

CC from the TR gene promoter through interaction of the 5' regulatory

CC sequences. These substances, e.g. antisense oligonucleotides,

CC transcription factors, peptide nucleic acids and factors that disrupt

CC signal transduction, are useful for cancer therapy. In particular, gene

CC therapy vectors (especially pG162-codupp) comprising the promoter and a

CC viral thymidine kinase gene can be used to convert a prodrug, e.g.

CC gancyclovir, so that neoplasia can be controlled or treated. Direct

CC down-regulation of telomerase RNA gene through manipulation of

CC transcription factors may be effective anticancer therapy and the cloning

CC of the hTR gene promoter allows the analysis of therapeutic molecules

CC which modulate hTR promoter activity. Sequences AA207626-321 represent

CC PCR primers used in cloning and mutagenesis of human TR gene (hTR)

CC promoter region

XX

SQ Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 other;

Query Match 33.3%; Score 20; DB 20; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCAGCCCCGCCGAGAGT 39

DB 1 ACCAGCCCCGCCGAGAGT 20

RESULT 3

AA13062/c

ID AA13062 standard; DNA; 31 BP.

XX

AC AA13062;

XX

DT 18-OCT-2001 (first entry)

XX

DE Human single nucleotide polymorphism (SNP) 74.

XX

KM Human; ressequence; genotype; disease; forensic; paternity testing;

KW single nucleotide polymorphism; SNP; ss.

XX

OS Homo sapiens.

XX

FH Key

FT Variation

FT Location/Qualifiers

FT /\*tag= a

FT /standard\_name= "single nucleotide polymorphism"

XX

PN WO200166800-A2.

XX

PD 13-SEP-2001.

XX

PF 07-MAR-2001; 2001WO-US07268.

XX

PR 07-MAR-2000; 2000US-0187510.

XX

PR 22-MAY-2000; 2000US-0206129.

XX

PA (WHEED ) WHITEHEAD INST BIOMEDICAL RES.

XX

PI Cargill M, Ireland JS, Lander ES;

XX

DR WPI; 2001-522952/57.

XX

PT Nucleic acid molecules from the human genome which include polymorphic

PT sites, useful in methods for predicting the presence, absence or

PT severity of a particular phenotype or disorder (e.g. diabetes)

PT associated with a particular genotype -

XX

PS Claim 1; Page 65; 145pp; English.

XX

CC The invention relates to the identification of nucleic acid molecules

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:14:29 ; Search time 227.107 Seconds  
(without 315 minutes)

(without alignments)  
594.960 Million cell updates/sec

Title: US-08-770-564A-1\_COPY\_137\_196  
Perfect score: 60

Sequence: 1 TAAATTTCCCGTCCCCCA...ACTCTACGAGAGCCGGAG 60

Scoring table: OLIGO\_NUC  
Gapop\_60

Searched: 2185239 seqs, 1125999159 residues

**Word size :**

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

**Book no. \_\_\_\_\_ Title**

Post-processing: Listing first 45 summaries

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Database : N_Geneseq_101002:*
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21	/SIDS/gcgatg/genseeg/genseeqn-emb1/NA2000.DAT *
22	/SIDS/gcgatg/genseeg/genseeqn-emb1/NA2001A.DAT *
23	/SIDS/gcgatg/genseeg/genseeqn-emb1/NA2001B.DAT *
24	/SIDS/gcgatg/genseeg/genseeqn-emb1/NA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

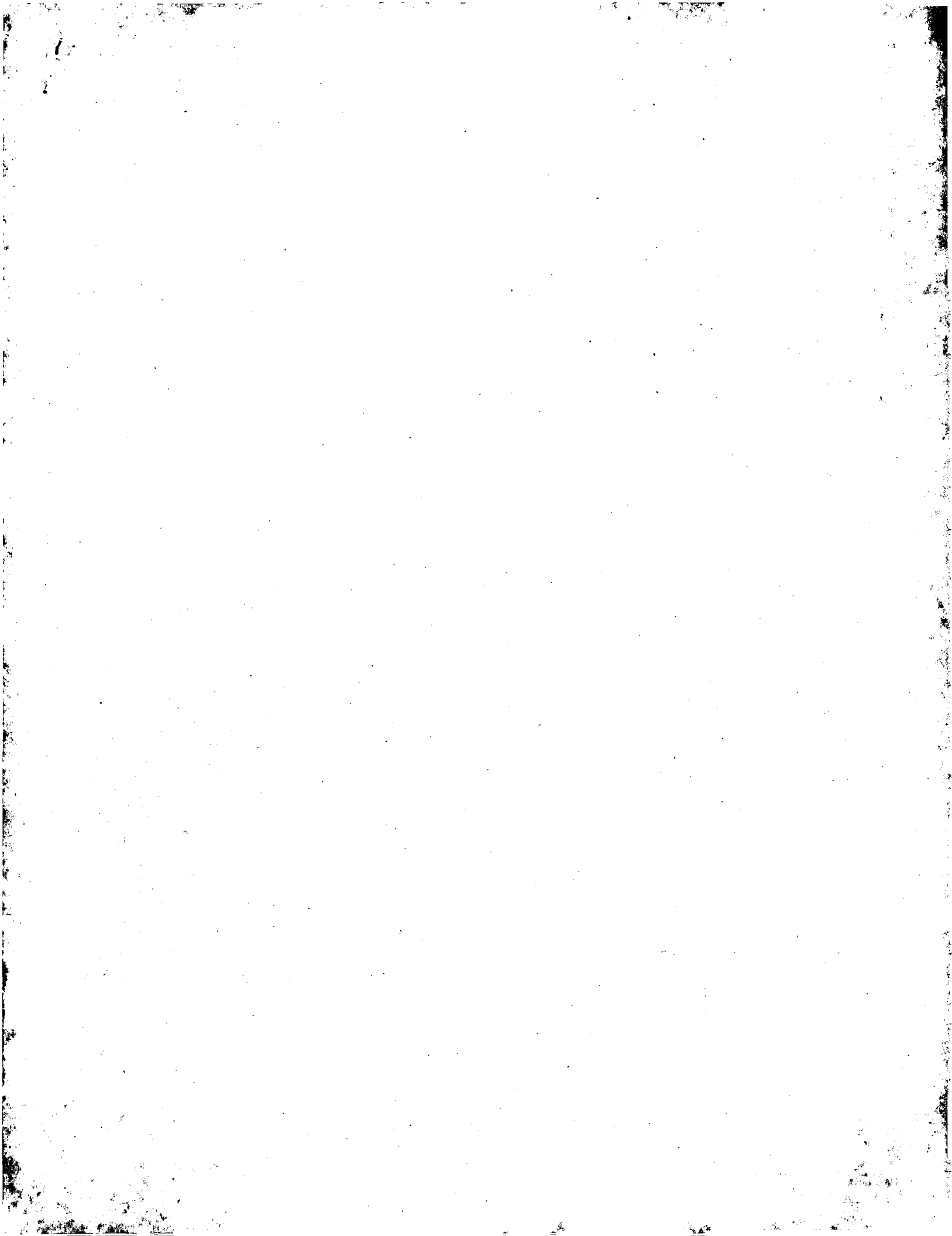
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Result No.	Score	Query Match	Length	DB	ID	Description
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2	20	33.3	20	20	AA07318	Human telomerase R
3	14	23.3	31	22	AA13062	Human single nucleic
4	13	21.7	15	22	AA92154	Human IGBR allele
5	13	21.7	19	12	AA010624	H1A Class I locus
6	13	21.7	20	20	AA92918	Antisense primer K
7	13	21.7	20	21	AA080280	Reverse primer #10
8	13	21.7	21	19	AA46219	Human H1A-A primer
9	13	21.7	21	19	AA46221	Human H1A-A primer

C	10	AAK38046	21	20	H1A-A untranslated
C	11	AAK38046	21	21	H1A-A untranslated
C	12	AAK80281	21	21	H1A-A untranslated
C	13	AAK80281	22	21	Reverse primer #10
C	14	AAK80283	23	21	Reverse primer #11
C	15	AAK80284	24	21	Reverse primer #11
C	16	AAK80285	25	21	Reverse primer #11
C	17	AAK99915	25	24	Reverse primer #11
C	18	AAQ42939	39	19	Alpha-amylase delta
C	19	AAV57697	40	19	3'-5' sequence of
C	20	ABEC88498	13	23	Human POGF receptor
C	21	ABEC88498	13	23	Oligonucleotide SE
C	22	ABEC90072	13	23	Oligonucleotide SE
C	23	ABEC90072	13	23	Oligonucleotide SE
C	24	AAQ48328	16	14	Oligonucleotide SE
C	25	AAQ98837	16	16	Mb 25D2 primer B1
C	26	AAV60461	17	19	Anti-human IL-4 MA
C	27	AAQ95327	20	16	Thrombin-binding a
C	28	AAV80030	20	18	Primer A (Group 1,
C	29	AAV11202	20	19	Alphal integrin pr
C	30	AAZ17949	20	20	peptide nucleic ac
C	31	AAK09080	20	20	HOX gene specific
C	32	AAK26173	20	20	Mouse necrosis fa
C	33	AAV99432	20	20	Fah05 exon 1 ampli
C	34	AAV72640	20	20	Antisense oligonuc
C	35	AAZ96658	20	21	Antisense oligonuc
C	36	AAZ48967	20	21	Mouse protein kina
C	37	AAZ48967	20	21	Murine PKC-alpha t
C	38	AAZ38001	20	24	Human ICM-1 antise
C	39	AAZ27794	20	24	Antisense oligonuc
C	40	AAZ28562	21	13	Human PKC-alpha an
C	41	AAV60445	21	13	Ancored aptamer.
C	42	AAV798137	21	18	Fibrinogen-cleavin
C	43	AAK85980	24	18	Primogen-9
C	44	AAK88156	24	20	PCR primer used to
C	45	AAK99908	25	24	T cell receptor al
C	46	AAZ45027	28	21	Alpha-amylase delt
C	47	AAZ45027	28	21	PCR primer for OSM

## ALIGNMENTS

RESULT 1	
AAZ07255	
ID	AAZ07255 etandard; DNA; 20 BP.
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AC	AAZ07255;
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DT	22-OCT-1999 (first entry)
XX	
DE	Wld-type oligo h41 comprising Sp1 site.
XX	
XX	Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
KM	gene therapy; thymidine kinase gene; anticancer therapy; human; ss
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	W09938964-A2.
XX	
PD	05-AUG-1999.
XX	
PF	29-JAN-1999; 99MO-GB00308.
XX	
PR	29-JAN-1998; 98GB-0001902.
XX	
PA	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX	
PT	Keith MN;
XX	
DR	WPI; 1999-479183/40.
XX	
PT	Mouse and human telomerase RNA gene promoters, useful for tumor specific gene therapy



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/ SOFTWARE: WordPerfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/685,484
/ FILING DATE: 24-JUL-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/108,591
/ FILING DATE: 22-NOV-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Michael P. Straher
/ REGISTRATION NUMBER: 38,325
/ REFERENCE/DOCKET NUMBER: ISIS-2270
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 3
/ OTHER INFORMATION: guanine attached to aminoethyl-lysine
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 7
/ OTHER INFORMATION: thymine attached to aminoethyl-lysine
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 11
/ OTHER INFORMATION: thymine attached to aminoethyl-lysine
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 16
/ OTHER INFORMATION: cytosine attached to aminoethyl-lysine
/ OTHER INFORMATION: backbone
/ US-08-685-484-18
/
/ Query Match
/ Best Local Similarity 20.0%; Score 12; DB 1; Length 20;
/ Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ QY 10 GTTCCCCCAAC 21
/ DB 9 GTTCCCCCAAC 20
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/ RESULT 15
/ US-08-847-108-18
/ Sequence 18, Application US/0847108
/ Patent No. 5736336
/ GENERAL INFORMATION:
/ APPLICANT: Buchardt et al.
/ TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
/ TITLE OF INVENTION: Binding Affinity, Sequence Specificity
/ Patent No. 5736336
/ TITLE OF INVENTION: and Solubility
/ NUMBER OF SEQUENCES: 53
/ CORRESPONDENCE ADDRESSES:
/ ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5736336r18 LLP
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: U.S.A.
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch disk, 1.44 MB
/ COMPUTER: IBM PC compatible
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 6.1
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/ APPLICATION NUMBER: US/08/847,108
/ FILING DATE: 01-MAY-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/686,116
/ FILING DATE: JULY 24, 1996
/ APPLICATION NUMBER: 08/108,591
/ FILING DATE: 22-NOV-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Michael P. Straher
/ REGISTRATION NUMBER: 38,325
/ REFERENCE/DOCKET NUMBER: ISIS-2271
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 3
/ OTHER INFORMATION: guanine attached to aminoethyl-lysine
/ FEATURE:
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/ OTHER INFORMATION: thymine attached to aminoethyl-lysine
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/ OTHER INFORMATION: thymine attached to aminoethyl-lysine
/ FEATURE:
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/ LOCATION: 16
/ OTHER INFORMATION: cytosine attached to aminoethyl-lysine
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/ US-08-847-108-18
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/ Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ DB 9 GTTCCCCCAAC 20
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GENERAL INFORMATION:  
APPLICANT: TOOLE, JOHN J.  
APPLICANT: LATNAM, JOHN  
APPLICANT: BOCK, LOUIS C.  
APPLICANT: GRIFFIN, LINDA C.  
TITLE OF INVENTION: APTAMER ANALOGS SPECIFIC FOR  
TITLE OF INVENTION: BIOMOLECULES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/237,973  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,921  
FILING DATE: 06-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28,216  
REFERENCE/DOCKET NUMBER: 24610-20032.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO.: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-237-973-36

Query Match 20.0%; Score 12; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCCAACCAGCCC 27  
DB 17 CCCAACCAGCCC 6

RESULT 13  
US-08-686-116A-18  
Sequence 18, Application US/08686116A  
Patent No. 5714331  
GENERAL INFORMATION:  
APPLICANT: Buchardt et al.  
TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced  
TITLE OF INVENTION: Binding Affinity, Sequence Specificity  
Patent No. 5714331  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5714331ris LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 1.44 MB  
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OPERATING SYSTEM: PC-DOS/MS-DOS  
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FILING DATE: July 24, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/108,591  
FILING DATE: 22-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael P. Straher  
REGISTRATION NUMBER: 38,325  
REFERENCE/DOCKET NUMBER: ISIS-2271  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO.: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: guanine attached to aminoethyl-lysine  
OTHER INFORMATION: backbone  
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LOCATION: 16  
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US-08-686-116A-18

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Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCCCCCACC 21  
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RESULT 14  
US-08-685-484-18  
Sequence 18, Application US/08685484  
Patent No. 5719262  
GENERAL INFORMATION:  
APPLICANT: Buchardt et al.  
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid  
TITLE OF INVENTION: Side Chains  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5719262ris LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 1.44 MB  
OPERATING SYSTEM: PC-DOS/MS-DOS

Filing Date: 03-JUL-1986  
Application Number: US 06/843,958  
Filing Date: 25-MAR-1986  
Application Number: US 06/799,668  
Filing Date: 19-NOV-1985  
Attorney/Agent Information:  
Name: Foulke, Cynthia L.  
Registration Number: 32,364  
Reference/Docket Number: 2409K7  
Telecommunication Information:  
Telephone: 908-298-5388  
Telefax: 908-298-2987  
Information for SEQ ID NO: 10:  
Sequence Characteristics:  
Length: 16 base pairs  
Type: nucleic acid  
Strandedness: single  
Topology: linear  
US-08-290-793B-10

Query Match 20.0%; Score 12; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTACTCT 45  
DB 16 GAGAGTACTCT 5

RESULT 10  
US-08-234-613-23/c  
Sequence 23, Application US/08234613  
Patent No. 5582381  
GENERAL INFORMATION:  
APPLICANT: TOOLE, JOHN J.  
APPLICANT: LATHAM, JOHN  
APPLICANT: BOCK, LOUIS C.  
APPLICANT: GRIFFIN, LINDA C.  
TITLE OF INVENTION: APTAMER TARGET ELUTION METHOD  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,613  
Filing Date:  
Classification: 435  
Prior Application Data:  
Application Number: US/07/744,870  
Filing Date:  
Attorney/Agent Information:  
Name: GRACEY, NANCEY J.  
Registration Number: 28,216  
Reference/Docket Number: 24610-20030.00  
Telecommunication Information:  
Telephone: (415) 813-5600  
Telefax: (415) 494-0792  
TeleX: 706141  
Information for SEQ ID NO: 23:  
Sequence Characteristics:  
Length: 17 base pairs  
Type: nucleic acid  
Strandedness: single  
Topology: linear

US-08-234-613-23

Query Match 20.0%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCCAACCGCC 27  
DB 17 CCCAACCGCC 6

RESULT 11  
US-08-484-192-95/c  
Sequence 95, Application US/08484192  
Patent No. 575291  
GENERAL INFORMATION:  
APPLICANT: GRIFFIN, LINDA C.  
APPLICANT: ALBRECHT, GLENN  
APPLICANT: LATHAM, JOHN  
APPLICANT: LEUNG, LAWRENCE  
APPLICANT: VERMAAS, ERIC  
APPLICANT: TOOLE, JOHN J.  
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND  
NUMBER OF SEQUENCES: 181  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,192  
Filing Date:  
Classification: 435  
Prior Application Data:  
Application Number: US 07/934,387  
Filing Date: 21-AUG-1992  
Attorney/Agent Information:  
Name: GRACEY, NANCEY J.  
Registration Number: 28,216  
Reference/Docket Number: 246102002221  
Telecommunication Information:  
Telephone: 415-813-5600  
Telefax: 415-494-0792  
TeleX: 706141  
Information for SEQ ID NO: 95:  
Sequence Characteristics:  
Length: 17 base pairs  
Type: nucleic acid  
Strandedness: single  
Topology: linear  
US-08-484-192-95

Query Match 20.0%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCCAACCGCC 27  
DB 17 CCCAACCGCC 6

RESULT 12  
US-08-237-973-36/c  
Sequence 36, Application US/08237973  
Patent No. 5640867



TELEPHONE: (908) 298-2987  
TELEFAX: (908) 298-5388  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-704-744-10

Query Match 20.0%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTACTCT 45  
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Db 16 GAGAGTACTCT 5

RESULT 8  
US-08-469-557-10/c  
Sequence 10, Application US/08469557  
Patent No. 5770403  
GENERAL INFORMATION:  
APPLICANT: Dalie, Barbara  
APPLICANT: Le, Hung, Kenneth  
APPLICANT: Miller, Kenneth  
APPLICANT: Murgolo, Nicholas  
APPLICANT: Nguyen, Hanh  
APPLICANT: Tindall, Stephen  
APPLICANT: Zavodny, Paul  
TITLE OF INVENTION: Cloning and Expression of  
TITLE OF INVENTION: Humanized Monoclonal Antibodies  
TITLE OF INVENTION: Against Human Interleukin-4  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation  
STREET: 2000 Galloping Hill Road  
CITY: Kenilworth  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07033-0530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.5  
SOFTWARE: Microsoft Word 5.1A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,557  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/290,793  
FILING DATE: August 16, 1994  
APPLICATION NUMBER: PCT/US93/01301  
FILING DATE: 19-FEB-1992  
APPLICATION NUMBER: US 07/841,659  
FILING DATE: 19-FEB-1992  
APPLICATION NUMBER: US 07/782,784  
FILING DATE: 24-OCT-1991  
APPLICATION NUMBER: US 07/499,327  
FILING DATE: 21-MAY-1990  
APPLICATION NUMBER: PCT/US88/03631  
FILING DATE: 21-OCT-1988  
APPLICATION NUMBER: US 07/655,966  
FILING DATE: 14-FEB-1991  
APPLICATION NUMBER: US 07/113,623  
FILING DATE: 26-OCT-1987  
APPLICATION NUMBER: US 06/881,553  
FILING DATE: 03-JUL-1986  
APPLICATION NUMBER: US 06/843,958  
FILING DATE: 25-MAR-1986

APPLICATION NUMBER: US 06/799,668  
FILING DATE: 19-NOV-1985  
ATTORNEY/AGENT INFORMATION:  
NAME: Foulke, Cynthia L.  
REGISTRATION NUMBER: 32,364  
REFERENCE/DOCKET NUMBER: 2409K7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-298-2987  
TELEFAX: 908-298-5388  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-469-557-10

Query Match 20.0%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTACTCT 45  
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Db 16 GAGAGTACTCT 5

RESULT 9  
US-08-290-793B-10/c  
Sequence 10, Application US/08290793B  
Patent No. 5863537  
GENERAL INFORMATION:  
APPLICANT: Dalie, Barbara  
APPLICANT: Le, Hung, Kenneth  
APPLICANT: Miller, Kenneth  
APPLICANT: Murgolo, Nicholas  
APPLICANT: Nguyen, Hanh  
APPLICANT: Tindall, Stephen  
APPLICANT: Zavodny, Paul  
TITLE OF INVENTION: Cloning and Expression of  
TITLE OF INVENTION: Humanized Monoclonal Antibodies  
TITLE OF INVENTION: Against Human Interleukin-4  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation  
STREET: 2000 Galloping Hill Road  
CITY: Kenilworth  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07033-0530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.5  
SOFTWARE: Microsoft Word 5.1A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,793B  
FILING DATE: August 16, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/01301  
FILING DATE: 19-FEB-1992  
APPLICATION NUMBER: US 07/841,659  
FILING DATE: 19-FEB-1992  
APPLICATION NUMBER: US 07/782,784  
FILING DATE: 24-OCT-1991  
APPLICATION NUMBER: US 07/499,327  
FILING DATE: 21-MAY-1990  
APPLICATION NUMBER: PCT/US88/03631  
FILING DATE: 21-OCT-1988  
APPLICATION NUMBER: US 07/655,966  
FILING DATE: 14-FEB-1991  
APPLICATION NUMBER: US 07/113,623  
FILING DATE: 26-OCT-1987  
APPLICATION NUMBER: US 06/881,553  
FILING DATE: 25-MAR-1986

```

RESULT 5
PCT-US92-10359-1/c
; Sequence 1, Application PC/US9210359
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Vanicha
; APPLICANT: Escobedo, Maria A.
; APPLICANT: Preeto, Larry J.
; TITLE OF INVENTION: Inhibitory Immunoglobulin Polypeptides
; TITLE OF INVENTION: to Human PDGF Beta Receptor
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10359
; FILING DATE: 19921201
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,795
; FILING DATE: 02-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 12418-18
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2420
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US92-10359-1

Query Match          21.7%; Score 13; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AATTCCCGTTCC 14
DB      19 AATTCCCGTTCC 7

RESULT 6
US-08-208-886C-10/c
; Sequence 10, Application US/0820886C
; Patent No. 5597710
; GENERAL INFORMATION:
; APPLICANT: Dalle, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,886C
; FILING DATE: March 10, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298 2987
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-208-886C-10

Query Match          20.0%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      34 GAGAGTACTCT 45
DB      16 GAGAGTACTCT 5

RESULT 7
US-08-704-744-10/c
; Sequence 10, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalle, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:

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COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,394  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/025,574  
FILING DATE: 06-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: S1237/7005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-927-394-8

Query Match 21.7%; Score 13; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 CGAGAGCCGCGAG 60  
Db 15 CGAGAGCCGCGAG 3

RESULT 3  
US-08-927-394-7  
Sequence 7, Application US/08927394  
Patent No. 5990092  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: GATA-6 TRANSCRIPTION FACTOR: COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield, & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,394  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/025,574  
FILING DATE: 06-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: S1237/7005  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-927-394-7

Query Match 21.7%; Score 13; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 CGAGAGCCGCGAG 60  
Db 14 CGAGAGCCGCGAG 26

RESULT 4  
US-08-258-283-1/c  
Sequence 1, Application US/08258283  
Patent No. 5817310  
GENERAL INFORMATION:  
APPLICANT: Ramakrishnan, Vanitha  
APPLICANT: Escobedo, Maria A.  
TITLE OF INVENTION: INHIBITORY IMMUNOGLOBULIN POLYPEPTIDES  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/258,283  
FILING DATE: 10 JUN 1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Karen B. Dow  
REGISTRATION NUMBER: 29,684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-08-258-283-1

Query Match 21.7%; Score 13; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AATTCCCGTTCC 14  
Db 19 AATTCCCGTTCC 7





QY 42 CTCTCAGCAGAG 53  
|||  
Db 25 CTCTCAGCAGAG 14

RESULT 15  
US-10-098-263B-24180/c  
; Sequence 24180, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Miltman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO: 24180  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-24180

Query Match 20.0%; Score 12; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 42 CTCTCAGCAGAG 53  
|||  
Db 25 CTCTCAGCAGAG 14

Search completed: June 24, 2003, 20:39:34  
Job time : 733.909 secs

MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-003-810-1

Query Match 21.7%; Score 13; DB 9; Length 40;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTCCCGTTC 14  
Db 19 AATTCCCGTTC 7

RESULT 11  
US-09-419-076-1/c  
Sequence 1, Application US/09419076  
Patent No. US2002009443A1  
GENERAL INFORMATION:  
APPLICANT: Ramakrishnan, Vanitha  
APPLICANT: Pectro, Larry U.  
TITLE OF INVENTION: Inhibitory Immunoglobulin Polypeptides to Human PDGF  
FILE REFERENCE: 44481-5017-04-US  
CURRENT APPLICATION NUMBER: US/09/419,076  
PRIOR FILING DATE: 1999-10-15/801,795  
PRIOR APPLICATION NUMBER: US 07/801,795  
PRIOR FILING DATE: 1991-12-02  
PRIOR APPLICATION NUMBER: US 08/253,440  
PRIOR FILING DATE: 1994-06-07  
PRIOR APPLICATION NUMBER: US 08/258,263  
PRIOR FILING DATE: 1994-06-10  
PRIOR APPLICATION NUMBER: US 09/003,810  
PRIOR FILING DATE: 1998-01-07  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 1  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide for creating PDGF beta receptor  
US-09-419-076-1

Query Match 21.7%; Score 13; DB 10; Length 40;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTCCCGTTC 14  
Db 19 AATTCCCGTTC 7

RESULT 12  
US-09-932-300-66  
Sequence 66, Application US/09932300  
Publication No. US20030032788A1  
GENERAL INFORMATION:  
APPLICANT: GARNER, Eric  
APPLICANT: TU, Quang-Chou  
APPLICANT: ISRAEL, Yedy  
TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION  
FILE REFERENCE: 9855-3U2  
CURRENT APPLICATION NUMBER: US/09/932,300  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: US 60/051,705  
PRIOR FILING DATE: 1997-07-03  
PRIOR APPLICATION NUMBER: US 09/109,663  
PRIOR FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 111

SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 66  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Known  
OTHER INFORMATION: effective ASO  
US-09-932-300-66

Query Match 20.0%; Score 12; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCCCCCAAC 21  
Db 9 GTTCCCCCAAC 20

RESULT 13  
US-10-016-149-62/c  
Sequence 62, Application US/10016149  
Publication No. US20030100524A1  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Jacqueline Wyatt  
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP V (CA2+-DEPENDENT) EXPRESSION  
FILE REFERENCE: RTS-0325  
CURRENT APPLICATION NUMBER: US/10/016,149  
CURRENT FILING DATE: 2001-11-01  
NUMBER OF SEQ ID NOS: 84  
SEQ ID NO 62  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-016-149-62

Query Match 20.0%; Score 12; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTGACTCT 45  
Db 12 GAGAGTGACTCT 1

RESULT 14  
US-10-098-263B-24179/c  
Sequence 24179, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 24179  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-24179

Query Match 20.0%; Score 12; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 21.7%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45  
 |||||  
 DB 20 AGAGAGTACTCT 8

RESULT 7  
 US-10-098-263B-8500  
 ; Sequence 8500, Application US/10098263B  
 ; Publication No. US20030104410A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mitterman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; PRIOR FILING DATE: 2003-01-08  
 ; PRIOR APPLICATION NUMBER: 60/276,759  
 ; NUMBER OF SEQ ID NOS: 131066  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 8500  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-8500

Query Match 21.7%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTCACGAGAGCCG 56  
 |||||  
 DB 12 CTCACGAGAGCCG 24

RESULT 8  
 US-10-098-263B-24815/C  
 ; Sequence 24815, Application US/10098263B  
 ; Publication No. US20030104410A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mitterman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; PRIOR FILING DATE: 2003-01-08  
 ; PRIOR APPLICATION NUMBER: 60/276,759  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 131066  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 24815  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-24815

Query Match 21.7%; Score 13; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 ACTCTCAGAGAG 53  
 |||||  
 DB 25 ACTCTCAGAGAG 13

RESULT 9  
 US-09-971-611-37/C  
 ; Sequence 37, Application US/09971611  
 ; Patent No. US20020123124A1  
 ; GENERAL INFORMATION:

APPLICANT: ARAKI, HIROYUKI  
 ; APPLICANT: ENDO, KEIJI  
 ; APPLICANT: HASEGAWA, HIROSHI  
 ; APPLICANT: IGARASHI, KAZUAKI  
 ; APPLICANT: HAYASHI, YASUHIRO  
 ; APPLICANT: OZAKI, KATSUYA  
 ; TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES  
 ; FILE REFERENCE: 214377USO  
 ; CURRENT APPLICATION NUMBER: US/09/971,611  
 ; PRIOR FILING DATE: 2001-10-09  
 ; PRIOR APPLICATION NUMBER: JP 2000/310605  
 ; NUMBER OF SEQ ID NOS: 51  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 37  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic DNA  
 US-09-971-611-37

Query Match 21.7%; Score 13; DB 10; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCCCCCAACCA 23  
 |||||  
 DB 15 TTCCCCCAACCA 3

RESULT 10  
 US-09-003-810-1/C  
 ; Sequence 1, Application US/09003810  
 ; Publication No. US20030059425A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ramakrishnan, Vanitha  
 ; TITLE OF INVENTION: INHIBITORY IMMUNOGLOBULIN POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Knourle and Crew  
 ; STREET: 379 Lytton Avenue  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/003,810  
 ; FILING DATE: 07-Jan-1998  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/258,283  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Karen B. Dow  
 ; REGISTRATION NUMBER: 29,684  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 326-2400  
 ; TELEFAX: (415) 326-2422  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 40 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear



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FILE REFERENCE: IGT-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-199

Query Match      21.7%; Score 13; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTGACTCT 45
Db      16 AGAGAGTGACTCT 4

RESULT 3
US-09-964-261-200/c
; Sequence 200, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGT-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 200
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-200

Query Match      21.7%; Score 13; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTGACTCT 45
Db      17 AGAGAGTGACTCT 5

RESULT 4
US-09-964-261-201/c
; Sequence 201, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGT-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
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NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 201
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-201

Query Match      21.7%; Score 13; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTGACTCT 45
Db      18 AGAGAGTGACTCT 6

RESULT 5
US-09-964-261-202/c
; Sequence 202, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGT-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 202
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-202

Query Match      21.7%; Score 13; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTGACTCT 45
Db      19 AGAGAGTGACTCT 7

RESULT 6
US-09-964-261-203/c
; Sequence 203, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGT-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-203
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using bw model

Run on: June 23, 2003, 20:29:49 ; Search time 730.909 Seconds  
(without alignments)  
120.460 Million cell updates/sec

Title: US-08-770-564a-1\_COPY\_137\_196  
Perfect score: 60  
Sequence: 1 TAAATTCCTCCGTTCCGCCCA.....ACTCTCAGAGAGCCGCGAG 60

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Published Applications\_NA.\*  
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10: /cgn2\_6/ptodaca/2/pubpna/US05\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodaca/2/pubpna/US10\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodaca/2/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodaca/2/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodaca/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13	21.7	20	9 US-09-964-261-198	Sequence 198, App
C 2	13	21.7	21	9 US-09-964-261-199	Sequence 199, App
C 3	13	21.7	22	9 US-09-964-261-200	Sequence 200, App
C 4	13	21.7	23	9 US-09-964-261-201	Sequence 201, App
C 5	13	21.7	24	9 US-09-964-261-202	Sequence 202, App
C 6	13	21.7	25	9 US-09-964-261-203	Sequence 203, App
C 7	13	21.7	25	9 US-10-098-263B-8500	Sequence 8500, App
C 8	13	21.7	25	9 US-10-098-263B-8500	Sequence 8500, App
C 9	13	21.7	25	10 US-09-971-611-37	Sequence 37, Appl
C 10	13	21.7	40	9 US-09-003-810-1	Sequence 1, Appl
C 11	13	21.7	40	10 US-09-419-076-1	Sequence 1, Appl
C 12	13	20.0	20	9 US-09-932-300-66	Sequence 66, Appl
C 13	13	20.0	20	9 US-10-016-149-62	Sequence 62, Appl
C 14	13	20.0	25	9 US-10-098-263B-41179	Sequence 24180, A
C 15	13	20.0	25	9 US-10-098-263B-41179	Sequence 24180, A
C 16	13	20.0	25	9 US-10-098-263B-42816	Sequence 24816, A
C 17	13	20.0	25	9 US-10-098-263B-42816	Sequence 24816, A
C 18	13	20.0	25	9 US-10-098-263B-40334	Sequence 40334, A
C 19	13	20.0	25	9 US-10-098-263B-40334	Sequence 40334, A

C 20	12	20.0	25	9 US-10-098-263B-48690	Sequence 48690, A
C 21	12	20.0	25	9 US-10-098-263B-49760	Sequence 49760, A
C 22	12	20.0	25	9 US-10-098-263B-75176	Sequence 75176, A
C 23	12	20.0	25	9 US-10-098-263B-86702	Sequence 86702, A
C 24	12	20.0	25	9 US-10-098-263B-99417	Sequence 99417, A
C 25	12	20.0	25	9 US-10-098-263B-110168	Sequence 110168, A
C 26	12	20.0	25	9 US-10-098-263B-110168	Sequence 110168, A
C 27	12	20.0	25	10 US-09-971-611-30	Sequence 30, Appl
C 28	12	20.0	31	9 US-10-163-552-1392	Sequence 1392, App
C 29	11	18.3	17	9 US-09-904-968A-104	Sequence 104, App
C 30	11	18.3	17	9 US-09-780-533A-277	Sequence 277, App
C 31	11	18.3	17	9 US-09-780-533A-1150	Sequence 1150, App
C 32	11	18.3	17	9 US-09-780-533A-1151	Sequence 1151, App
C 33	11	18.3	17	9 US-09-780-533A-1935	Sequence 1935, App
C 34	11	18.3	17	9 US-09-930-423-287	Sequence 287, App
C 35	11	18.3	17	9 US-09-930-423-288	Sequence 288, App
C 36	11	18.3	17	9 US-09-930-423-289	Sequence 289, App
C 37	11	18.3	17	9 US-09-930-423-291	Sequence 291, App
C 38	11	18.3	17	9 US-09-930-423-1146	Sequence 1146, App
C 39	11	18.3	18	9 US-09-853-526-387	Sequence 387, App
C 40	11	18.3	18	10 US-09-901-484A-1387	Sequence 121, App
C 41	11	18.3	20	9 US-09-824-322B-121	Sequence 688, App
C 42	11	18.3	20	9 US-09-888-326-688	Sequence 312, App
C 43	11	18.3	20	9 US-10-112-653-112	Sequence 323, App
C 44	11	18.3	20	9 US-10-017-995-323	Sequence 323, App
C 45	11	18.3	20	9 US-09-776-479-323	Sequence 323, App

#### ALIGNMENTS

RESULT 1  
US-09-964-261-198/c  
; Sequence 198, Application US/09964261  
; Publication No. US20020197613A1  
; GENERAL INFORMATION:  
; APPLICANT: De Canck, Ilse  
; APPLICANT: Rombout, Annelies  
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES  
; FILE REFERENCE: 163-002  
; CURRENT APPLICATION NUMBER: US/09/964,261  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: EP 99870068.6  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 60/138,614  
; NUMBER OF SEQ ID NOS: 446  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 198  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-964-261-198

Query Match 21.7%; Score 13; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45  
DB 15 AGAGAGTACTCT 3

RESULT 2  
US-09-964-261-199/c  
; Sequence 199, Application US/09964261  
; Publication No. US20020197613A1  
; GENERAL INFORMATION:  
; APPLICANT: De Canck, Ilse  
; APPLICANT: Rombout, Annelies  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES

```

; SOFTWARE: Proprietary
; SEQ ID NO 15330
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, plasmid
; FEATURE:
; LOCATION: (1850407)..(1850421)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 17904
PCT-US02-25940-15330

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Query Match      21.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

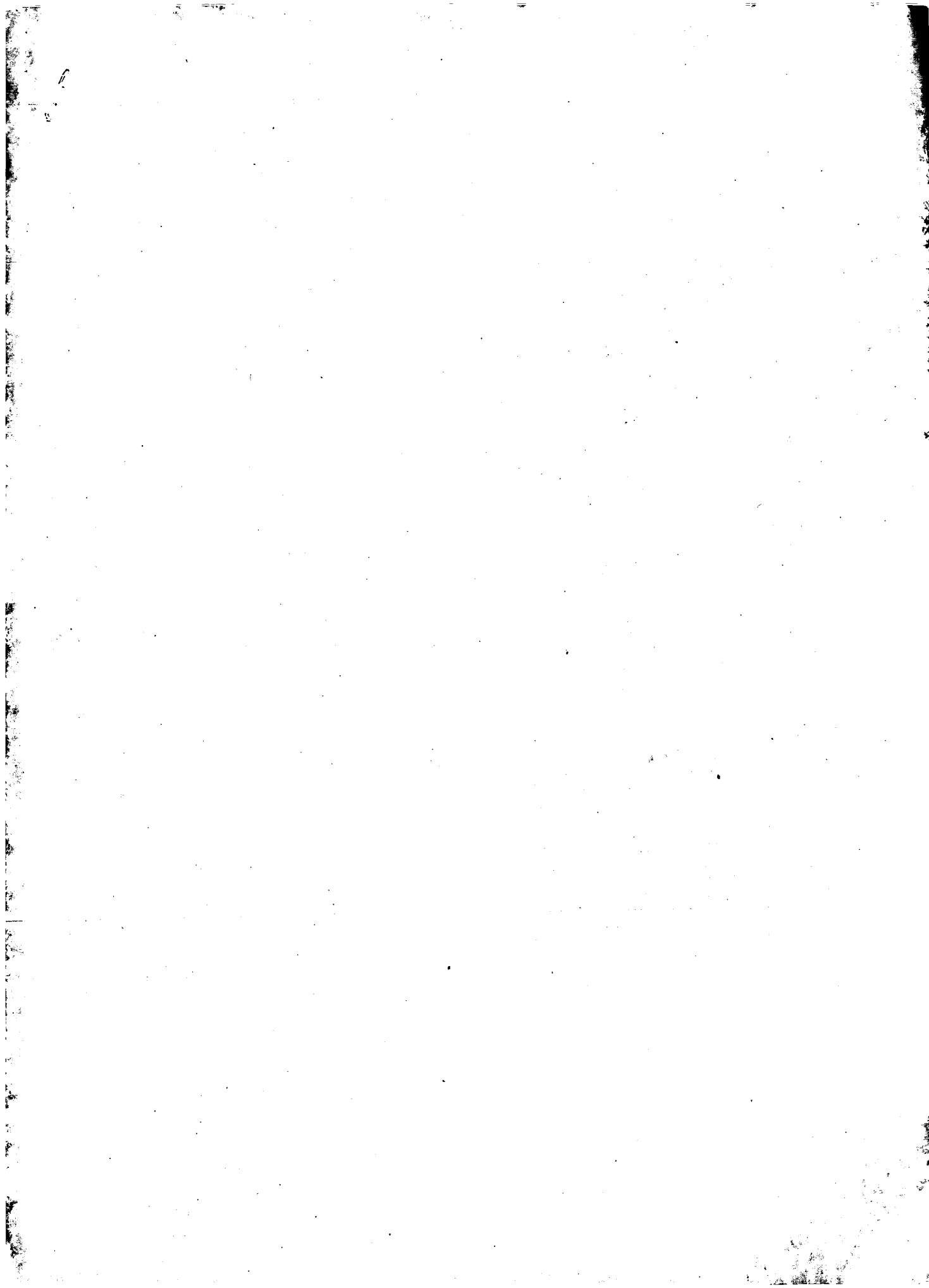
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Qy      24  GCCCGCCCGAGAG 36
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Db      1  GCCCGCCCGAGAG 13

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Search completed: June 24, 2003, 18:22:27  
 Job time : 2598.88 secs



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APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196F
CURRENT FILING DATE: 2001-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41222
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196F-41222

Query Match      23.3%; Score 14; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 GCCCGAGAGAGTGA 41
DB      9 GCCCGAGAGAGTGA 22

RESULT 11
US-09-396-196G-41222
Sequence 41222, Application US/09396196G
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41222
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-41222

Query Match      23.3%; Score 14; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 GCCCGAGAGAGTGA 41
DB      9 GCCCGAGAGAGTGA 22

RESULT 12
US-60-353-987-314865
Sequence 314865, Application US/60353987
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 314865
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
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```
US-60-353-987-314865

Query Match      23.3%; Score 14; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      47 ACGAGAGCCCGCAG 60
DB      12 ACGAGAGCCCGCAG 25

RESULT 13
US-60-353-987-847501
Sequence 847501, Application US/60353987
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 847501
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-60-353-987-847501

Query Match      23.3%; Score 14; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      47 ACGAGAGCCCGCAG 60
DB      10 ACGAGAGCCCGCAG 23

RESULT 14
US-60-353-987-952021/c
Sequence 952021, Application US/60353987
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 952021
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-60-353-987-952021

Query Match      23.3%; Score 14; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 CGAGAGAGTGATC 44
DB      21 CGAGAGAGTGATC 8

RESULT 15
PCT-US02-25940-15330
Sequence 15330, Application PCT/US0225940
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25940
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 25502
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RESULT 5
US-60-234-017-339051
; Sequence 339051, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 339051
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA982370
US-60-234-017-339051

Query Match      28.3%; Score 17; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTACTCTCAGC 49
DB      4 AGAGAGTACTCTCAGC 20

RESULT 6
US-60-353-987-351034/c
; Sequence 351034, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 351034
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-351034

Query Match      26.7%; Score 16; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      36 GAGTGACTCTCAGCAG 51
DB      18 GAGTGACTCTCAGCAG 3

RESULT 7
US-09-956-584-328898
; Sequence 328898, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 328898
; LENGTH: 25

; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-328898

Query Match      25.0%; Score 15; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTACTCTCA 47
DB      11 AGAGAGTACTCTCA 25

RESULT 8
US-60-234-017-339061
; Sequence 339061, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 339061
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA982370
US-60-234-017-339061

Query Match      25.0%; Score 15; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTACTCTCA 47
DB      11 AGAGAGTACTCTCA 25

RESULT 9
US-60-353-987-448107
; Sequence 448107, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 448107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-448107

Query Match      25.0%; Score 15; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 GCCCGAGAGAGTGAC 42
DB      8 GCCCGAGAGAGTGAC 22

RESULT 10
US-09-396-196F-41222
; Sequence 41222, Application US/09396196F
; GENERAL INFORMATION:
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22 13 21.7 16 1 PCT-US02-25940-18174 Sequence 18174, A
23 13 21.7 16 1 PCT-US02-25940-22043 Sequence 22043, A
24 13 21.7 16 42 US-10-327-563-18174 Sequence 18174, A
25 13 21.7 16 42 US-10-327-563-22043 Sequence 22043, A
26 13 21.7 18 1 PCT-US02-25940-17148 Sequence 17148, A
27 13 21.7 18 1 PCT-US02-25940-17149 Sequence 17149, A
28 13 21.7 18 1 PCT-US02-25940-18156 Sequence 18156, A
29 13 21.7 18 42 US-10-327-563-17148 Sequence 17148, A
30 13 21.7 18 42 US-10-327-563-17149 Sequence 17149, A
31 13 21.7 19 38 US-10-327-563-18156 Sequence 18156, A
32 13 21.7 19 38 US-10-005-626A-33 Sequence 33, Appl
33 13 21.7 20 30 US-09-777-525-129 Sequence 129, App
34 13 21.7 20 36 US-09-964-261-198 Sequence 198, App
35 13 21.7 21 11 US-08-766-1898-200 Sequence 200, App
36 13 21.7 21 11 US-08-766-1898-202 Sequence 202, App
37 13 21.7 21 11 US-08-766-189C-200 Sequence 200, App
38 13 21.7 21 11 US-08-766-189C-202 Sequence 202, App
39 13 21.7 21 13 US-08-909-290-200 Sequence 200, App
40 13 21.7 21 13 US-08-909-290-202 Sequence 202, App
41 13 21.7 21 36 US-09-964-261-199 Sequence 199, App
42 13 21.7 22 8 US-08-472-801-625 Sequence 625, App
43 13 21.7 22 10 US-08-668-235-626 Sequence 626, App
44 13 21.7 22 36 US-09-964-261-200 Sequence 200, App
45 13 21.7 23 1 PCT-US00-35593A-61 Sequence 61, Appl

```

## ALIGNMENTS

## RESULT 1

```

US-09-601-267-62
; Sequence 62, Application US/09601267
; GENERAL INFORMATION:
; APPLICANT: William Nicol KEITH
; TITLE OF INVENTION: Promoter Regions of the Mouse and Human Telomerase RNA Component
; FILE REFERENCE: 9013.18
; CURRENT APPLICATION NUMBER: US/09/601.267
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/GB99/00308
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: GB 9801902.9
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-09-601-267-62

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Query Match 33.3%; Score 20; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 20 ACCGAGCCCGCCGAGAGT 39
Db 1 ACCGAGCCCGCCGAGAGT 20

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## RESULT 2

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US-09-956-584-328887
; Sequence 328887, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956.584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20

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; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 328887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-328887

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```

Query Match 28.3%; Score 17; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 AGAGAGTGACTCTCAG 49
Db 4 AGAGAGTGACTCTCAG 20

```

## RESULT 3

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US-09-956-584-328890
; Sequence 328890, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956.584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 328890
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-328890

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Query Match 28.3%; Score 17; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 AGAGAGTGACTCTCAG 49
Db 9 AGAGAGTGACTCTCAG 25

```

## RESULT 4

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US-60-234-017-339049
; Sequence 339049, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltman, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339049
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA982370
US-60-234-017-339049

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Query Match 28.3%; Score 17; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 33 AGAGAGTGACTCTCAG 49
Db 9 AGAGAGTGACTCTCAG 25

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:01:44 ; Search time 2594.88 Seconds  
(Without alignments)  
581.357 Million cell updates/sec

Title: US-08-770-564a-1\_COPY\_137\_196

Sequence: 1 TAAATCCCGTCCCGCCCA.....ACTCTCAGAGAGCGCGAG 60

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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1	20	33.3	20	US-09-601-267-62	Sequence 62, Appl
2	17	28.3	25	US-09-956-584-328887	Sequence 328887,
3	17	28.3	25	US-09-956-584-328890	Sequence 328890,
4	17	28.3	25	US-60-234-017-339049	Sequence 339049,
5	17	28.3	25	US-60-234-017-339051	Sequence 339051,
6	16	26.7	25	US-60-353-987-314655	Sequence 314655,
7	15	25.0	25	US-09-956-584-328898	Sequence 328898,
8	15	25.0	25	US-60-353-987-314655	Sequence 314655,
9	15	25.0	25	US-09-396-196F-41222	Sequence 41222, A
10	14	23.3	25	US-09-396-196F-41222	Sequence 41222, A
11	14	23.3	25	US-60-353-987-314655	Sequence 314655,
12	14	23.3	25	US-60-353-987-314655	Sequence 314655,
13	14	23.3	25	US-60-353-987-314655	Sequence 314655,
14	14	23.3	25	US-60-353-987-314655	Sequence 314655,
15	14	23.3	25	US-60-353-987-314655	Sequence 314655,
16	13	21.7	15	PCT-US02-25940-15330	Sequence 15330, A
17	13	21.7	15	PCT-US02-25940-15330	Sequence 15330, A
18	13	21.7	15	US-09-889-866A-12	Sequence 12, Appl
19	13	21.7	15	US-10-227-563-15330	Sequence 15330, A
20	13	21.7	15	US-10-227-563-15330	Sequence 15330, A
21	13	21.7	15	US-10-227-563-15330	Sequence 15330, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES



QY 36 GAGTGACTCTCAG 49  
 |||||  
 Db 25 GAGTGACTCTCAG 12

RESULT 12  
 US-60-417-190-41679/c  
 ; Sequence 41679, Application US/60417190  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Giulia Kennedy  
 ; APPLICANT: Hajime Matsuzaki  
 ; APPLICANT: Mei-Mei Shen  
 ; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans  
 ; FILE REFERENCE: 3522  
 ; CURRENT APPLICATION NUMBER: US/60/417,190  
 ; CURRENT FILING DATE: 2002-10-02  
 ; NUMBER OF SEQ ID NOS: 122930  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 41679  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-60-417-190-41679

Query Match 23.3%; Score 14; DB 12; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAG 48  
 |||||  
 Db 24 AGAGTGACTCTCAG 11

RESULT 13  
 US-60-417-190-41680/c  
 ; Sequence 41680, Application US/60417190  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Giulia Kennedy  
 ; APPLICANT: Hajime Matsuzaki  
 ; APPLICANT: Mei-Mei Shen  
 ; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans  
 ; FILE REFERENCE: 3522  
 ; CURRENT APPLICATION NUMBER: US/60/417,190  
 ; CURRENT FILING DATE: 2002-10-02  
 ; NUMBER OF SEQ ID NOS: 122930  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 41680  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-60-417-190-41680

Query Match 23.3%; Score 14; DB 12; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAG 48  
 |||||  
 Db 23 AGAGTGACTCTCAG 10

RESULT 14  
 US-60-427-808-34731/c  
 ; Sequence 34731, Application US/60427808  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528  
 ; CURRENT APPLICATION NUMBER: US/60/427,808  
 ; CURRENT FILING DATE: 2002-11-20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 34731

; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-60-427-808-34731

Query Match 23.3%; Score 14; DB 12; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTGACTCTCA 47  
 |||||  
 Db 22 GAGAGTGACTCTCA 9

RESULT 15  
 US-60-427-808-709610  
 ; Sequence 709610, Application US/60427808  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528  
 ; CURRENT APPLICATION NUMBER: US/60/427,808  
 ; CURRENT FILING DATE: 2002-11-20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 709610  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-60-427-808-709610

Query Match 23.3%; Score 14; DB 12; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 CTCTCAGAGAGCC 55  
 |||||  
 Db 8 CTCTCAGAGAGCC 21

Search completed: June 24, 2003, 20:14:42  
 Job time : 3335.23 secs

SEQ ID NO 41675  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-60-417-190-41675

Query Match  
Best Local Similarity 100.0%; Score 15; DB 12; Length 25;  
Pred. No. 7.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAGC 49  
|||||  
Db 23 AGAGTGACTCTCAGC 9

RESULT 7  
US-60-470-475-42235/c  
Sequence 42235, Application US/60470475  
GENERAL INFORMATION:  
APPLICANT: Matsuzaki, Hajime  
APPLICANT: Shen, Mei-Mei  
APPLICANT: Kennedy, Giulia  
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans  
FILE REFERENCE: 3522.1  
CURRENT APPLICATION NUMBER: US/60/470,475  
CURRENT FILING DATE: 2003-05-14  
PRIOR APPLICATION NUMBER: 60/417,190  
NUMBER OF SEQ ID NOS: 124031  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 42235  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-60-470-475-42235

Query Match  
Best Local Similarity 100.0%; Score 15; DB 13; Length 25;  
Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAGC 49  
|||||  
Db 23 AGAGTGACTCTCAGC 9

RESULT 8  
US-10-355-577-314865  
Sequence 314865, Application US/10355577  
GENERAL INFORMATION:  
APPLICANT: Miltmann, Michael  
APPLICANT: Miltmann, Michael  
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
FILE REFERENCE: 3121  
CURRENT APPLICATION NUMBER: US/10/355,577  
CURRENT FILING DATE: 2003-01-31  
NUMBER OF SEQ ID NOS: 997516  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 314865  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-355-577-314865

Query Match  
Best Local Similarity 100.0%; Score 14; DB 9; Length 25;  
Pred. No. 7.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 ACGAGAGCCGCGAG 60  
|||||  
Db 12 ACGAGAGCCGCGAG 25

RESULT 9  
US-10-355-577-847501

Sequence 847501, Application US/10355577  
GENERAL INFORMATION:  
APPLICANT: Miltmann, Michael  
APPLICANT: Miltmann, Michael  
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
FILE REFERENCE: 3121  
CURRENT APPLICATION NUMBER: US/10/355,577  
CURRENT FILING DATE: 2003-01-31  
NUMBER OF SEQ ID NOS: 997516  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 847501  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-355-577-847501

Query Match  
Best Local Similarity 100.0%; Score 14; DB 9; Length 25;  
Pred. No. 7.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 ACGAGAGCCGCGAG 60  
|||||  
Db 10 ACGAGAGCCGCGAG 23

RESULT 10  
US-10-355-577-952021/c  
Sequence 952021, Application US/10355577  
GENERAL INFORMATION:  
APPLICANT: Miltmann, Michael  
APPLICANT: Miltmann, Michael  
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
FILE REFERENCE: 3121  
CURRENT APPLICATION NUMBER: US/10/355,577  
CURRENT FILING DATE: 2003-01-31  
NUMBER OF SEQ ID NOS: 997516  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 952021  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-355-577-952021

Query Match  
Best Local Similarity 100.0%; Score 14; DB 9; Length 25;  
Pred. No. 7.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CGAGAGTGACTC 44  
|||||  
Db 21 CGAGAGTGACTC 8

RESULT 11  
US-60-417-190-41673/c  
Sequence 41673, Application US/60417190  
GENERAL INFORMATION:  
APPLICANT: Matsuzaki, Hajime  
APPLICANT: Matsuzaki, Hajime  
APPLICANT: Shen, Mei-Mei  
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans  
FILE REFERENCE: 3522  
CURRENT APPLICATION NUMBER: US/60/417,190  
CURRENT FILING DATE: 2002-10-02  
NUMBER OF SEQ ID NOS: 122930  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 41673  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-60-417-190-41673

Query Match  
Best Local Similarity 100.0%; Score 14; DB 12; Length 25;  
Pred. No. 7.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAGAGAG 53  
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Db 1 AGAGTGACTCTCAGAGAG 19

## RESULT 2

PCT-US03-04088-265/c  
; Sequence 265, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 265  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense  
PCT-US03-04088-265

Query Match 31.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAGAGAG 53  
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Db 19 AGAGTGACTCTCAGAGAG 1

## RESULT 3

US-10-355-577-351034/c  
; Sequence 351034, Application US/10355577  
; GENERAL INFORMATION:  
; APPLICANT: Miltmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
; FILE REFERENCE: 3121  
; CURRENT APPLICATION NUMBER: US/10/355,577  
; CURRENT FILING DATE: 2003-01-31  
; NUMBER OF SEQ ID NOS: 997516  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 351034  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-355-577-351034

Query Match 26.7%; Score 16; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAGTGACTCTCAGAG 51  
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Db 18 GAGTGACTCTCAGAG 3

## RESULT 4

US-10-355-577-448107  
; Sequence 448107, Application US/10355577  
; GENERAL INFORMATION:  
; APPLICANT: Miltmann, Michael  
; APPLICANT: Hajime Matsuzaki  
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
; FILE REFERENCE: 3121  
; CURRENT APPLICATION NUMBER: US/10/355,577  
; CURRENT FILING DATE: 2003-01-31  
; NUMBER OF SEQ ID NOS: 997516  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 448107  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-355-577-448107

Query Match 25.0%; Score 15; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GCCCGAGAGAGTGAC 42  
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Db 8 GCCCGAGAGAGTGAC 22

## RESULT 5

US-60-417-190-41674/c  
; Sequence 41674, Application US/60417190  
; GENERAL INFORMATION:  
; APPLICANT: Giulia Kennedy  
; APPLICANT: Hajime Matsuzaki  
; APPLICANT: Mei-Mei Shen  
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans  
; FILE REFERENCE: 3522  
; CURRENT APPLICATION NUMBER: US/60/417,190  
; CURRENT FILING DATE: 2002-10-02  
; NUMBER OF SEQ ID NOS: 122930  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 41674  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-60-417-190-41674

Query Match 25.0%; Score 15; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAGC 49  
|||||:|||||  
Db 24 AGAGTGACTCTCAGC 10

## RESULT 6

US-60-417-190-41675/c  
; Sequence 41675, Application US/60417190  
; GENERAL INFORMATION:  
; APPLICANT: Giulia Kennedy  
; APPLICANT: Hajime Matsuzaki  
; APPLICANT: Mei-Mei Shen  
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans  
; FILE REFERENCE: 3522  
; CURRENT APPLICATION NUMBER: US/60/417,190  
; CURRENT FILING DATE: 2002-10-02  
; NUMBER OF SEQ ID NOS: 122930  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

GenCore version 5.1.6  
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OW nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:09:29 ; Search time 3332.23 Seconds  
(without alignments)  
125.426 Million cell updates/sec

Title: US-08-770-564a-1\_COPY\_137\_196

Perfect score: 60  
Sequence: 1 TAAATCCCGTCCCGCCCA.....ACTCTCAGAGCGCGGAG 60

Scoring table: OLIGO.MNC  
Gapop 60.0, Gapext 60.0

Searched: 7821610 seqs, 3482903955 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8654690

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

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12: /cgn2\_6/pdata/2/pna/US60 NEW COMB. seq.\*  
13: /cgn2\_6/pdata/2/pna/US60 NEW COMB. seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	15	25.0	25	12	US-10-355-577-448107
5	15	25.0	25	12	US-10-355-577-448107
6	15	25.0	25	12	US-10-355-577-448107
7	15	25.0	25	12	US-10-355-577-448107
8	15	25.0	25	12	US-10-355-577-448107
9	15	25.0	25	12	US-10-355-577-448107
10	15	25.0	25	12	US-10-355-577-448107
11	15	25.0	25	12	US-10-355-577-448107
12	15	25.0	25	12	US-10-355-577-448107
13	15	25.0	25	12	US-10-355-577-448107
14	15	25.0	25	12	US-10-355-577-448107
15	15	25.0	25	12	US-10-355-577-448107
16	15	25.0	25	12	US-10-355-577-448107
17	15	25.0	25	12	US-10-355-577-448107
18	15	25.0	25	12	US-10-355-577-448107
19	15	25.0	25	12	US-10-355-577-448107
20	15	25.0	25	12	US-10-355-577-448107

21	13	21.7	16	10	US-10-367-892-18174	Sequence 18174, A
22	13	21.7	16	10	US-10-367-892-22043	Sequence 22043, A
23	13	21.7	18	10	US-10-367-892-17148	Sequence 17148, A
24	13	21.7	18	10	US-10-367-892-17148	Sequence 17148, A
25	13	21.7	18	10	US-10-367-892-18156	Sequence 18156, A
26	13	21.7	19	5	US-09-935-9984-33	Sequence 33, Appl
27	13	21.7	23	10	US-10-367-892-17147	Sequence 17147, A
28	13	21.7	25	9	US-10-098-262B-5500	Sequence 8500, Ap
29	13	21.7	25	9	US-10-098-262B-5500	Sequence 24815, A
30	13	21.7	25	9	US-10-355-577-104028	Sequence 104028, A
31	13	21.7	25	9	US-10-355-577-165154	Sequence 165154, A
32	13	21.7	25	9	US-10-355-577-178327	Sequence 178327, A
33	13	21.7	25	9	US-10-355-577-180701	Sequence 180701, A
34	13	21.7	25	9	US-10-355-577-364135	Sequence 364135, A
35	13	21.7	25	9	US-10-355-577-404368	Sequence 404368, A
36	13	21.7	25	9	US-10-355-577-517364	Sequence 517364, A
37	13	21.7	25	9	US-10-355-577-561143	Sequence 561143, A
38	13	21.7	25	9	US-10-355-577-627414	Sequence 627414, A
39	13	21.7	25	9	US-10-355-577-665858	Sequence 665858, A
40	13	21.7	25	12	US-60-417-180-41672	Sequence 41672, A
41	13	21.7	25	12	US-60-417-180-41672	Sequence 41672, A
42	13	21.7	25	12	US-60-417-180-41672	Sequence 41672, A
43	13	21.7	25	12	US-60-427-808-157066	Sequence 157066, A
44	13	21.7	25	12	US-60-427-808-255259	Sequence 255259, A
45	13	21.7	25	12	US-60-427-808-473800	Sequence 473800, A

#### ALIGNMENTS

RESULT 1  
PCT-US03-04088-1  
Sequence 1, Application PC/TUS0304088  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Beigelsen, James  
TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene  
FILE REFERENCE: 02-708-A (400/080)  
CURRENT APPLICATION NUMBER: PCT/US03/04088  
CURRENT FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: US 60/396,600  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense  
OTHER INFORMATION: region  
PCT-US03-04088-1  
Query Match 31.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 1; Indels 0; Gaps 0;  
Matches 16; Conservative 3; Mismatches 0;

DIFFUSION ;, mRNA sequence.

ACCESSION H27426

VERSION H27426.1 GI:897416

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 34)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulman, M., Kucada, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

Unpublished (1995)

COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 735

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LIND

This clone is available royalty-free through LIND; contact the

IMAGE Consortium (info@image.lind.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 735 Std Error: 0.00

Seq primer: M13Rev

High quality sequence stop: 1.

location/Qualifiers

source

1..34 /organism="Homo sapiens"

/db\_xref="GDB:575254"

/db\_xref="taxon:9606"

/clone="IMAGE:161139"

/clone\_lib="Soares breast 3NBH8t"

/sex="Female"

/dev\_stage="adult"

/lab\_host="DH10B (ampicillin resistant)"

/note="Organ: breast; Vector: pT73D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of a modified pT73 vector (Pharmacia).

Library went through one round of normalization to a Cot =

20. Library constructed by Bento Soares and M.Fatima

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Bonaldi."

Search completed: June 24, 2003, 16:52:41

Job time : 1575.41 secs

BASE COUNT 6 a 10 c 8 g 10 t

ORIGIN

Query Match 18.3%; Score 11; DB 14; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCCCAACCAGC 25

DB 30 CCCCAACCAGC 20

LOCUS A0025148 30 bp DNA linear GSS 23-AUG-2000  
 DEFINITION EP(3)1001 Drosophila melanogaster EP line Drosophila melanogaster  
 genomic sequence recovered from 5' end of P element, DNA sequence.  
 ACCESSION A0025148  
 VERSION A0025148.1 GI:3265500  
 KEYWORDS GSS.  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 30)  
 Liao,G.-C., Rehm,E.J. and Rubin,G.M.  
 Insertion site preferences of the P transposable element in  
 Drosophila melanogaster  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)  
 JOURNAL 20202638  
 MEDLINE  
 COMMENT Contact: Gerald Rubin  
 Berkeley Drosophila Genome Project  
 University of California, Berkeley  
 LSA Building Berkeley, CA 94720-3200, USA  
 Fax: 5106433947  
 Email: ger@fruitfly.berkeley.edu  
 Sequence recovery method was inverse PCR.  
 Sequence orientation is forward strand relative to 5' end of P  
 element  
 The P element insertion position is base 23 in the 30 bases. This  
 insertion position refers to the first base of the 8 base target  
 recognition sequence.  
 Class: transposon-tagged.  
 Location/Qualifiers  
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 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_1ib="Drosophila melanogaster EP line"  
 /note="Inverse PCR was performed on Drosophila  
 melanogaster strains each of which contains a single EP  
 transposable element insertion. (The generation of these  
 insertion strains is described in Roth P, Szabo K, Bailey  
 A, Laverdy T, Rehm J, Rubin GM, Weigman K, Milan M, Benes  
 V, Laverdy W, Cohen SM, 1998. Systematic gain-of-function  
 genetics in Drosophila. Development 6:1049-1057.) The  
 resultant fragment for each strain was directly sequenced  
 to determine the genomic sequence at the site of  
 insertion. Details of the protocols used can be found at  
 http://fruitfly.berkeley.edu/p\_disrupt/inverse\_pcr.html."  
 BASE COUNT 0 a 11 c 10 g 9 t  
 ORIGIN  
 Query Match 18.3%; Score 11; DB 17; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 46 CACGAGAGCCG 56  
 DB 16 CACGAGAGCCG 6  
 RESULT 14  
 LOCUS A1793967 31 bp mRNA linear EST 07-JUN-2001  
 DEFINITION f56604.x1 zebrafish Mashu MPing EST Danio rerio cDNA clone  
 IMAGE3725430.3 similar to TR061888 Q61888 PROLINE RICH PROTEIN.  
 COMMENT element MSRI repetitive element; mRNA sequence.  
 ACCESSION A1793967  
 VERSION A1793967.1 GI:5341683  
 KEYWORDS EST.  
 SOURCE zebrafish.  
 ORGANISM Danio rerio.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

REFERENCE 1 (bases 1 to 31)  
 AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy  
 S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood  
 K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,  
 Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,  
 Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.  
 and Wilson,R.  
 TITLE Mashu Zebrafish EST Project 1998  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Stephen L. Johnson  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: zbrafish@wustl.edu  
 CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:  
 Matthew Clark. DNA Sequencing by: Washington University Genome  
 Sequencing Center Clone distribution: Genome Systems, St. Louis,  
 Missouri (web address: www.genomesystems.com) (email contact:  
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama  
 (web address: www.resgen.com) (email contact: info@resgen.com) and  
 ResourcenzentrumPrimatendatenbank, Berlin, Germany (web address:  
 www.rzp.dn.de)  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: T7 ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
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 /db\_xref="taxon:7955"  
 /clone="IMAGE:3725430"  
 /clone\_1ib="zebrafish Mashu MPing EST"  
 /sex="mixed"  
 /tissue\_type="26 somite embryos, adult livers, shield  
 stage embryos"  
 /lab\_host="X11-blue MPF"  
 /note="Vector: pSPORT1, Site 1: NotI, Site 2: SalI; 1st  
 strand cDNA was primed with a NotI oligo(dT)15 primer  
 (5'-GACATGTTTAAATCGACGAGCGCGCTTTTATTTTT3');  
 double-stranded cDNA was ligated to SalI adaptor (BRL),  
 digested with NotI and cloned into the NotI and SalI  
 sites of the pSPORT1 vector (BRL). Library was constructed  
 by Matthew Clark (Lehrach lab), ICRF, London and Max Planck  
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST  
 analysis were selected following oligonucleotide  
 hybridization fingerprinting of arrayed clones from  
 zebrafish late somitogenesis (26 ss), adult liver or  
 embryonic shield stage (5.6 h) libraries. Fingerprint  
 data were used to computationally cluster cDNAs, and a  
 single cDNA from each cluster was chosen for sequencing.  
 In some cases multiple members of the same cluster were  
 sequenced to assess clustering parameters or single clones  
 were sequenced additional times to assess quality  
 control."  
 BASE COUNT 9 a 20 c 2 g 0 t  
 ORIGIN  
 Query Match 18.3%; Score 11; DB 9; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 CCCCCCAACA 23  
 DB 15 CCCCCCAACA 25  
 RESULT 15  
 LOCUS H27426/c 34 bp mRNA linear EST 12-JUN-1995  
 DEFINITION Y14402.x1 Soares breast 3MBHst Homo sapiens cDNA clone  
 IMAGE:161139.5 similar to SP:PDUF\_SALTY P37451 PROPANEDIOL

LOCUS AZ809974 27 bp DNA linear GSS 20-FEB-2001  
 DEFINITION 2M0074C18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0074C18 F, DNA sequence.  
 ACCESSION AZ809974  
 VERSION AZ809974.1 GI:12976775  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 27)  
 REFERENCE 1  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0074 row: C column: 18  
 Seq primer: CGTTGTAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0074C18"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 8 a 6 c 11 g 2 t  
 ORIGIN  
 Query Match 18.3%; Score 11; DB 17; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CCGTTCCCCC 18  
 |||||  
 Db 21 CCGTTCCCCC 11

RESULT 12  
 AZ307173

LOCUS AZ307173 28 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1M0008N03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0008N03 R, DNA sequence.  
 ACCESSION AZ307173  
 VERSION AZ307173.1 GI:10345909  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 28)  
 REFERENCE 1  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0008 row: N column: 03  
 Seq primer: CACACGAGAAACGATATGACC  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 2 a 13 c 5 g 8 t  
 ORIGIN  
 Query Match 18.3%; Score 11; DB 17; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 CCAGCCCGCCC 31  
 |||||  
 Db 4 CCAGCCCGCCC 14

RESULT 13  
 AQ025148/c

LOCUS A2653028 22 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M0218003F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0218003 F, DNA sequence.  
 ACCESSION A2653028  
 VERSION A2653028.1 GI:13824255  
 KEYWORDS GSS  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 REFERENCE 1  
 Dunham, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunham@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0218 row: 0 column: 03  
 Seq primer: CGTGTGTAACGACGCGCAGCT  
 Class: plasmid ends  
 High quality sequence stop: 22.  
 Location/Qualifiers  
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 /db\_xref="taxon:10090"  
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 /clone\_1fb="Mouse 10kb plasmid UUGC2M library"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/shares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g1473214|9b|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."  
 BASE COUNT 1 a 0 c 14 g 7 t  
 ORIGIN  
 Query Match 18.3%; Score 11; DB 17; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 CCCCCCAACCA 23  
 DB 12 CCCCCCAACCA 2

LOCUS A2653869 23 bp DNA linear GSS 14-DEC-2000  
 DEFINITION 1M0527D14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0527D14 R, DNA sequence.  
 ACCESSION A2653869  
 VERSION A2653869.1 GI:11791015  
 KEYWORDS GSS  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 23)  
 REFERENCE 1  
 Dunham, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunham@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0527 row: D column: 14  
 Seq primer: CACACGAGAAACGCTATACAC  
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 /clone\_1fb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/shares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g1473214|9b|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."  
 BASE COUNT 4 a 1 c 13 g 5 t  
 ORIGIN  
 Query Match 18.3%; Score 11; DB 17; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 CCGTCCCCCCC 18  
 DB 11 CCGTCCCCCCC 1

RESULT 10  
 A2653869/c

RESULT 11  
 A2609974/c



Query Match 20.0%; Score 12; DB 9; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCAGCCGCCGCCG 32  
 DB 25 CCAGCCGCCGCCG 14

RESULT 7  
 AZ921814/c 50 bp DNA linear GSS 17-DEC-2001  
 LOCUS 1006032PF07.xl 1006 - Rescemu Grid G Zea mays genomic, DNA  
 DEFINITION sequence.

ACCESSION A2921814  
 VERSION A2921814.1 GI:13393834  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.

REFERENCE 1 (bases 1 to 50)  
 AUTHORS Walbot, V.  
 TITLE Maize genomic sequences found using engineered Rescemu transposon  
 JOURNAL Unpublished. (2001)  
 COMMENT Contact: Walbot, V.  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave,  
 Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 1006032 row: 45  
 Class: transposon-tagged.

FEATURES  
 source location/Qualifiers

1..50  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /clone\_lib="1006 - Rescemu Grid G"  
 /issue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: leaf; Vector: Rescemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 13 c 18 g 8 t  
 ORIGIN

Query Match 20.0%; Score 12; DB 17; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CACGAGAGCCGC 57  
 DB 15 CACGAGAGCCGC 4

RESULT 8  
 AZ769086/c

LOCUS AZ769086 21 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 1M0569G22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0569G22 F, DNA sequence.

ACCESSION AZ769086  
 VERSION AZ769086.1 GI:12888857  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0569 row: G column: 22  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 21.

FEATURES  
 source location/Qualifiers

1..21  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_lib="UUGC1M0569G22"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|9d|AT12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E.coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 1 c 14 g 4 t  
 ORIGIN

Query Match 18.3%; Score 11; DB 17; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCCCCCAACC 22  
 DB 17 TCCCCCAACC 7

RESULT 9  
 AZ953028/c

Query Match 21.7%; Score 13; DB 13; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CACCAAGCCCGCC 30  
 |||||  
 29 CACCAAGCCCGCC 17

DB

RESULT 4  
 BJ048330/c 49 bp mRNA linear EST 07-DEC-2001  
 LOCUS  
 DEFINITION BJ048330 NIBB Mochii normalized Xenopus neurula library Xenopus laevis cDNA clone X1019110 3', mRNA sequence.  
 ACCESSION BJ048330  
 VERSION BJ048330.1 GI:17408746  
 KEYWORDS EST.  
 SOURCE African clawed frog.  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.

REFERENCE  
 AUTHORS Kikuyama, A., Teraoka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara, I.  
 TITLE Expressed genes in X. laevis embryo  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Tadao Shin-I  
 Center for Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tehin@genes.nig.ac.jp.

FEATURES  
 source location/Qualifiers

1. .49  
 /organism="Xenopus laevis"  
 /db\_xref="taxon:8355"  
 /clone="X1019110"  
 /clone\_1lb="NIBB Mochii normalized Xenopus neurula library"  
 /issue\_type="whole embryo"  
 /dev\_stage="stage 15"  
 /note="vector: pBSR3; Site 1: NotI; Site 2: EcoRI; CDNA5 were oligo-dT primed and directionally cloned. Stegging according to Nieukoop and Faber. Library is substracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT 15 a 16 c 12 g 4 t 2 others

ORIGIN

Query Match 20.0%; Score 12; DB 13; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGTCCCCCA 19  
 |||||  
 44 CCGTCCCCCA 33

DB

RESULT 5  
 AU102328/c 50 bp mRNA linear EST 30-AUG-2001  
 LOCUS  
 DEFINITION AU102328 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone K1006002, mRNA sequence.  
 ACCESSION AU102328  
 VERSION AU102328.1 GI:13551848  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 MEDLINE 21270072  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
 source location/Qualifiers

1. .50  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_1lb="Sugano Homo sapiens cDNA library"  
 /note="Differential display comparison of untreated and dimethylumate treated U937 cells"

BASE COUNT 2 a 18 c 15 g 15 t

ORIGIN

Query Match 20.0%; Score 12; DB 9; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCCCCACGCGC 25  
 |||||  
 45 CCCCCACGCGC 34

DB

RESULT 6  
 AU105457/c 50 bp mRNA linear EST 30-AUG-2001  
 LOCUS  
 DEFINITION AU105457 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone ADSU02120, mRNA sequence.  
 ACCESSION AU105457  
 VERSION AU105457.1 GI:13554978  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 MEDLINE 21270072  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
 source location/Qualifiers

1. .50  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_1lb="Sugano Homo sapiens cDNA library"  
 /note="Differential display comparison of untreated and dimethylumate treated U937 cells"

BASE COUNT 5 a 10 c 24 g 11 t

ORIGIN

Insert Length: 1209 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers

# FEATURES

Source

1. 49  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2187223"  
 /tissue\_type="poorly differentiated adenocarcinoma with  
 signed ring cell features"  
 /lab\_host="DH10B"  
 /note="Organ: stomach; Vector: PCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

BASE COUNT 18 a 4 c 25 g 2 t

# ORIGIN

Query Match 23.3%; Score 14; DB 9; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTCCCGTTCCCGCC 18  
 |||||  
 Db 49 TTCCCGTTCCCGCC 36

# RESULT 2

AZ444521

LOCUS 47 bp DNA linear GSS 04-OCT-2000  
 DEFINITION 1M0239F13R Mouse 10kb plasmid UNGC1M library Mus musculus genomic  
 clone UNGC1M0239F13 R, DNA sequence.

ACCESSION AZ444521 GI:10593472  
 VERSION  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 47)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weise, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0239 row: P column: 13  
 Seq primer: CACACAGGAACACCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 47.  
 Location/Qualifiers

# FEATURES

Source

1. 47  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UNG1M0239F13"  
 /clone\_1b="Mouse 10kb plasmid UNGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 12 a 10 c 11 g 14 t

# ORIGIN

Query Match 21.7%; Score 13; DB 17; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 GAGAGAGTACTC 44  
 |||||  
 Db 12 GAGAGAGTACTC 24

# RESULT 3

B1526845/c

LOCUS 50 bp mRNA linear EST 29-AUG-2001  
 DEFINITION 602927364F1 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5059839 5',  
 mRNA sequence.

ACCESSION B1526845 GI:15351637  
 VERSION  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 50)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L1M1161 row: P column: 16  
 High quality sequence start: 2  
 High quality sequence stop: 4.  
 Location/Qualifiers

# FEATURES

Source

1. 50  
 /organism="Mus musculus"  
 /strain="FVB/N-3"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5059839"  
 /clone\_1b="NCI CGAP Mam2"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH"

BASE COUNT 9 a 11 c 19 g 11 t

# ORIGIN

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 16:08:34 ; Search time 1570.41 Seconds  
(without alignments)  
618.773 Million cell updates/sec

Title: US-08-770-564A-1\_COPY\_137\_196

Perfect score: 60  
Sequence: 1 TAAATTCCTCCGTTCCGCCCA.....ACTCTCAGAGAGCGCGAG 60

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

EST:  
1: em\_estbda:\*  
2: em\_estbda:\*  
3: em\_estbda:\*  
4: em\_estbda:\*  
5: em\_estbda:\*  
6: em\_estbda:\*  
7: em\_estbda:\*  
8: em\_estbda:\*  
9: gb\_estbda:\*  
10: gb\_estbda:\*  
11: gb\_estbda:\*  
12: gb\_estbda:\*  
13: gb\_estbda:\*  
14: gb\_estbda:\*  
15: em\_estbda:\*  
16: em\_estbda:\*  
17: gb\_estbda:\*  
18: em\_estbda:\*  
19: em\_estbda:\*  
20: em\_estbda:\*  
21: em\_estbda:\*  
22: em\_estbda:\*  
23: em\_estbda:\*  
24: em\_estbda:\*  
25: em\_estbda:\*  
26: em\_estbda:\*  
27: em\_estbda:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	14	23.3	49	A1802512
2	13	21.7	17	A2444521
3	13	21.7	50	B1526845
4	12	20.0	49	B048330
5	12	20.0	50	AU102328
6	12	20.0	50	AU105457

C	7	12	20.0	50	17	A2921814	A2921814
C	8	11	18.3	21	17	A2769086	A2769086
C	9	11	18.3	22	17	A2953028	A2953028
C	10	11	18.3	23	17	A2653869	A2653869
C	11	11	18.3	27	17	A2809974	A2809974
C	12	11	18.3	28	17	A2307173	A2307173
C	13	11	18.3	30	17	AQ025148	AQ025148
C	14	11	18.3	31	17	A1793967	A1793967
C	15	11	18.3	34	14	H27426	H27426
C	16	11	18.3	36	17	BH862765	BH862765
C	17	11	18.3	37	9	AA912047	AA912047
C	18	11	18.3	37	13	B1549647	B1549647
C	19	11	18.3	37	13	B1550102	B1550102
C	20	11	18.3	37	13	B1552796	B1552796
C	21	11	18.3	40	17	AL766731	AL766731
C	22	11	18.3	42	10	AM250581	AM250581
C	23	11	18.3	42	13	B1546340	B1546340
C	24	11	18.3	43	17	HSWC37D09	HSWC37D09
C	25	11	18.3	44	13	B1825899	B1825899
C	26	11	18.3	46	9	AA969300	AA969300
C	27	11	18.3	46	9	A1544460	A1544460
C	28	11	18.3	46	9	A1591356	A1591356
C	29	11	18.3	47	17	AA072343	AA072343
C	30	11	18.3	49	9	A1733140	A1733140
C	31	11	18.3	50	9	AU102860	AU102860
C	32	11	18.3	50	9	AU104726	AU104726
C	33	11	18.3	50	9	AU105456	AU105456
C	34	11	18.3	50	9	AU105456	AU105456
C	35	11	18.3	50	9	AU105772	AU105772
C	36	11	18.3	50	9	AU105772	AU105772
C	37	11	18.3	50	9	AU105843	AU105843
C	38	11	18.3	50	17	A2351333	A2351333
C	39	11	18.3	50	17	A2318120	A2318120
C	40	11	16.7	21	17	A2645749	A2645749
C	41	10	16.7	22	10	AM247820	AM247820
C	42	10	16.7	22	17	A2454940	A2454940
C	43	10	16.7	24	17	A2836988	A2836988
C	44	10	16.7	25	9	AA931385	AA931385
C	45	10	16.7	25	9	A1474586	A1474586

#### ALIGNMENTS

RESULT 1  
LOCUS A1802512/c 49 bp mRNA linear EST 14-DEC-1999  
DEFINITION tp08h04.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2187223 3'  
similar to TR:048805 O48809 F2401.18. ; mRNA sequence.

ACCESSION A1802512  
VERSION A1802512.1 GI:5367984

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 49)

NCI-CCAF http://www.nci.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Unpublished (1997)

JOURNAL

COMMENT

Email: CGAP@femail.nih.gov  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution: NCI-CCAF clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINM at:  
www-bio.lim.gov/btrp/image/image.html

Trace considered overall poor quality



Fri Jun 27 07:41:55 2003

us-08-770-564a-1\_copy\_290\_319.oligo.rge

Page 5

ACCESSION AX019586  
VERSION AX019586.1 GI:10043500  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE artificial sequences.  
1 (bases 1 to 38)  
AUTHORS Keith, W.N.  
TITLE Promoter regions of the mouse and human telomerase rna component  
genes  
JOURNAL Patent: WO 938964-A 40 05-AUG-1999;  
KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)  
FEATURES  
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/note="Oligonucleotide"  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Search completed: June 23, 2003, 20:29:41  
Job time : 301.008 secs

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Db 23 GGTGGTGGCCAT 12

RESULT 11  
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DEFINITION Sequence 2 from patent US 5968506.  
ACCESSION AR079889  
VERSION AR079889.1 GI:10006642  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)  
AUTHORS Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vassero,A.P.,  
Pruzan,R.A. and Kealey,J.T.  
TITLE Purified telomerase  
JOURNAL Patent: US 5968506-A 2 19-OCT-1999;  
FEATURES Location/Qualifiers  
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RESULT 12  
LOCUS A84592 31 bp DNA linear PAT 21-JAN-2000  
DEFINITION Sequence 2 from Patent WO9845450.  
ACCESSION A84592  
VERSION A84592.1 GI:6733508  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Atkinson,E.M. and Kealey,J.T.  
TITLE PURIFIED TELOMERASE  
JOURNAL Patent: WO 9845450-A 2 15-OCT-1998;  
FEATURES Location/Qualifiers  
source 1..31  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 TGTCTAACCTA 30

Db 30 TGTCTAACCTA 19  
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RESULT 13  
LOCUS AX268979 31 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 60 from Patent WO0175165.  
ACCESSION AX268979  
VERSION AX268979.1 GI:16541998  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Mcconlogue,L.C., Games,K.D., Yednock,T.A., Hua,T., Messersmith,E.  
and Baird,F.  
TITLE Screening markers and methods for neurodegenerative disorders  
JOURNAL Patent: WO 0175165-A 60 11-OCT-2001;  
FEATURES Location/Qualifiers  
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RESULT 14  
LOCUS A76106 33 bp DNA linear PAT 19-OCT-1999  
DEFINITION Sequence 45 from Patent WO9320210.  
ACCESSION A76106  
VERSION A76106.1 GI:6088247  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Taylor,G. and Stott,E.J.  
TITLE ANTIBODIES FOR TREATMENT AND PREVENTION OF RESPIRATORY SYNCYTIAL  
VIRUS INFECTION  
JOURNAL Patent: WO 9320210-A 45 14-OCT-1993;  
FEATURES Location/Qualifiers  
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Qy 3 GGTGGTGGCCAT 14  
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Db 28 GGTGGTGGCCAT 17

RESULT 15  
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DEFINITION Sequence 40 from Patent WO9338964.

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DEFINITION Sequence 45 from Patent. WO9318964.
ACCESSION AX019591.1 GI:10043505
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Keith, W.N.
TITLE Promoter regions of the mouse and human telomerase rna component
JOURNAL Patent: WO 9318964-A 45 05-AUG-1993;
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RESULT 7
LOCUS AR067095 22 bp DNA linear PAT 29-SEP-1999
DEFINITION AR067095
ACCESSION AR067095
VERSION AR067095.1 GI:598317
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Evans, G.A. and Smith, M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 443 22-DEC-1998;
FEATURES
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 8
LOCUS AX037834 26 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 185 from Patent WO0059917.
ACCESSION AX037834
VERSION AX037834.1 GI:11227216
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Howard, J.C., Feldkamp, U., Rauhe, H. and Banzhaf, W.
TITLE Information-carrying and information-processing polymers
JOURNAL Patent: WO 0059917-A 185 12-OCT-2000;

```

```

HOWARD JONATHAN C (DE) ; FELDKAMP UDO (DE) ; RAUHE HILMAR (DE) ;
BANZHAF WOLFGANG (DE)
FEATURES
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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        |||||
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LOCUS AX037835 26 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 186 from Patent WO0059917.
ACCESSION AX037835
VERSION AX037835.1 GI:11227217
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Howard, J.C., Feldkamp, U., Rauhe, H. and Banzhaf, W.
TITLE Information-carrying and information-processing polymers
JOURNAL Patent: WO 0059917-A 186 12-OCT-2000;
        HOWARD JONATHAN C (DE) ; FELDKAMP UDO (DE) ; RAUHE HILMAR (DE) ;
        BANZHAF WOLFGANG (DE)
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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        20 TTGTCTAACCT 9
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DB
RESULT 10
LOCUS ARI45878 29 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 22 from patent US 6218131.
ACCESSION ARI45878
VERSION ARI45878.1 GI:15109067
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Keesee, S.K., Ober, R. and Wu, Y.-J.
TITLE Materials and methods for detection of breast cancer
JOURNAL Patent: US 6218131-A 22 17-APR-2001;
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source 1. .20

/organism="unknown"

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ORIGIN

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Db 20 TTTGCTAACCTA 7

RESULT 2

AR075544/c

LOCUS AR075544 20 bp DNA linear PAT 30-AUG-2000

DEFINITION Sequence 41 from patent US 5958680.

ACCESSION AR075544

VERSION AR075544.1 GI:10002290

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Valleponteau,B., Feng,J., Funk,W. and Andrews,W.H.

TITLE Mammalian telomerase

JOURNAL Patent: US 5958680-A 41 28-SEP-1999;

FEATURES Location/Qualifiers

source 1. .20

BASE COUNT 7 a 3 c 5 g 5 t

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Db 20 TTTGCTAACCTA 7

RESULT 3

I31751/c

LOCUS I31751 20 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 4 from patent US 5583016.

ACCESSION I31751

VERSION I31751.1 GI:1822542

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Valleponteau,B., Feng,J., Funk,W. and Andrews,W.H.

TITLE Mammalian telomerase

JOURNAL Patent: US 5583016-A 4 10-DEC-1996;

FEATURES Location/Qualifiers

source 1. .20

BASE COUNT 7 a 3 c 5 g 5 t

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Db 20 TTTGCTAACCTA 7

RESULT 4

AX471972/c

LOCUS AX471972 29 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 3 from Patent WO02054073.

ACCESSION AX471972

VERSION AX471972.1 GI:22207029

KEYWORDS

SOURCE Synthetic construct.

ORGANISM Synthetic construct.

REFERENCE 1 Deslauriers,M., Quinn,F.D., Beall,D.S., King,P. and Birkeness,K.A.

AUTHORS Latent human tuberculosis model, diagnostic antigens, and methods

TITLE of use

JOURNAL Patent: WO 02054073-A 3 11-JUL-2002;

FEATURES The Secretary, Department of Health and Human Services (US)

source 1. .29

/organism="synthetic construct"

/db\_xref="taxon:32630"

/note="Synthetic Oligonucleotide"

BASE COUNT 5 a 14 c 6 g 4 t

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Oy 2 GGGTGGTGGCCATT 15

Db 23 GGGTGGTGGCCATT 10

RESULT 5

AX405383

LOCUS AX405383 44 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 77 from Patent WO0222830.

ACCESSION AX405383

VERSION AX405383.1 GI:21438478

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE Aeschlimann,D.P. and Grenard,P.M.

JOURNAL Transglutaminase gene products

PATENT: WO 0222830-A 77 21-MAR-2002;

FEATURES UNIVERSITY COLLEGE CARDIFF CONSULTANTS LTD. (GB)

source 1. .44

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Oy 16 TTTGCTAACCTT 29

Db 1 TTTGCTAACCTT 14

RESULT 6

AX019591

LOCUS AX019591 20 bp DNA linear PAT 07-SEP-2000

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:17:23 ; Search time 299.008 Seconds

(without alignment)  
2919.933 Million cell updates/sec

Title: US-08-770-564A-1\_COPY\_290\_319

Perfect score: 30  
Sequence: 1 GGGGTGGTGGCCATTCTTTGTCTAACCCCTA 30Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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33: em_hlg_mus:.*
34: em_hlg_pln:.*
35: em_hlg_rtd:.*
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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

## SUMMARIES

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C 2	14	46.7	20	6 AR075544	AR075544 Sequence
C 3	14	46.7	20	6 AR11751	AR11751 Sequence 4
C 4	14	46.7	29	6 AX471972	AX471972 Sequence
C 5	14	46.7	44	6 AX405383	AX405383 Sequence
C 6	12	40.0	20	6 AX019591	AX019591 Sequence
C 7	12	40.0	22	6 AR067095	AR067095 Sequence
C 8	12	40.0	26	6 AX037834	AX037834 Sequence
C 9	12	40.0	26	6 AX037835	AX037835 Sequence
C 10	12	40.0	29	6 AR145878	AR145878 Sequence
C 11	12	40.0	30	6 AR079889	AR079889 Sequence
C 12	12	40.0	31	6 AR4592	AR4592 Sequence 2
C 13	12	40.0	31	6 AR268979	AR268979 Sequence
C 14	12	40.0	33	6 A76106	A76106 Sequence 45
C 15	12	40.0	38	6 AX019586	AX019586 Sequence
C 16	12	40.0	38	6 AX019587	AX019587 Sequence
C 17	12	40.0	43	6 AR009856	AR009856 Sequence
C 18	12	40.0	50	6 AR121268	AR121268 Sequence 12
C 19	12	40.0	50	6 AR121268	AR121268 Sequence
C 20	11	36.7	18	6 AR17823	AR17823 Sequence
C 21	11	36.7	18	6 AR17823	AR17823 Sequence
C 22	11	36.7	18	6 AR08945	AR08945 Sequence
C 23	11	36.7	18	6 AR08945	AR08945 Sequence
C 24	11	36.7	18	6 AR08945	AR08945 Sequence
C 25	11	36.7	18	6 AR08945	AR08945 Sequence
C 26	11	36.7	20	6 AR208778	AR208778 Sequence
C 27	11	36.7	20	6 AR208778	AR208778 Sequence
C 28	11	36.7	20	6 AR208778	AR208778 Sequence
C 29	11	36.7	21	6 AR384817	AR384817 Sequence
C 30	11	36.7	24	6 AR444256	AR444256 Sequence
C 31	11	36.7	25	6 AR146639	AR146639 Sequence
C 32	11	36.7	25	6 AR448222	AR448222 Sequence
C 33	11	36.7	27	6 AR199694	AR199694 Sequence
C 34	11	36.7	28	6 AR016063	AR016063 Sequence
C 35	11	36.7	28	6 AR016072	AR016072 Sequence
C 36	11	36.7	28	6 AR075541	AR075541 Sequence
C 37	11	36.7	29	6 AR172342	AR172342 Sequence
C 38	11	36.7	30	6 AR188726	AR188726 Sequence
C 39	11	36.7	31	6 AR196022	AR196022 Sequence
C 40	11	36.7	33	6 AR048520	AR048520 Sequence
C 41	11	36.7	33	6 AR058297	AR058297 Sequence
C 42	11	36.7	34	11 C75757	C75757 Homo sapien
C 43	11	36.7	36	6 AR087533	AR087533 Sequence
C 44	11	36.7	36	6 AR19352	AR19352 Sequence 2
C 45	11	36.7	40	6 AR172313	AR172313 Sequence

## ALIGNMENTS

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AR059219/c  
LOCUS AR059219 20 bp DNA linear PAT 29-SEP-1993  
DEFINITION Sequence 26 from patent US 5837857.  
ACCESSION AR059219  
VERSION AR059219.1 GI:5984796  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Villaponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 5837857-A 26 17-NOV-1998;  
FEATURES Location/Qualifiers

XX Andrews WH, Avillon AA, Feng J, Funk W, Greider C;  
 PI Marhenda MA, Villeponteau B;  
 XX WPI; 1996-097428/10.  
 XX RNA components of (non)human mammalian telomerase(s) - useful in  
 PT studying cell senescence and immortalisation  
 XX  
 PS Disclosure; Page 23; 85pp; English.  
 XX The RNA components of (non) human mammalian telomerase(s) especially  
 CC from mouse, rat and chinese hamster are all claimed. Antisense  
 CC oligonucleotides can be used to block the activity of the  
 CC telomerase; probes and primers can be used in detection; vectors and  
 CC host cells transformed with the isolated telomerase genes can be  
 CC used for production of telomerases; RNA and DNA ribozymes and triplex  
 CC forming oligonucleotides directed against the telomerase genes can  
 CC be used therapeutically as can plasmids. A mouse which lacks the  
 CC telomerase gene (also claimed) can be used for study of telomere  
 CC regulation in vivo, and the role it plays in immortalisation. The  
 CC antisense oligonucleotide is synthesised as a 2-O-methyl RNA  
 CC oligonucleotide and is more resistant to hydrolysis than unmodified  
 CC RNA oligonucleotides (See AAT1032-35).  
 CC  
 SQ Sequence 20 BP; 7 A; 3 C; 5 G; 5 U; 0 other;

Query Match 46.7%; Score 14; DB 17; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 TTTGTTACCCCTA 30  
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 Db 20 TTTGTTACCCCTA 7

RESULT 15  
 AAT89245  
 ID AAT89245 standard; DNA; 24 BP.  
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 AC AAT89245;  
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 DT 12-MAY-1998 (first entry)  
 XX  
 DE DNA oligonucleotide 1, used in the measurement of Tm values.  
 XX  
 KM Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;  
 KW inhibitor; human telomerase RNA; htr; PCR; oligonucleotide; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9738013-A1.  
 PD 16-OCT-1997.  
 XX  
 PF 09-APR-1997; 97WO-US05931.  
 XX  
 PR 09-APR-1996; 96US-0630019.  
 XX  
 PA (GERO-) GERON CORP.  
 XX  
 PI Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;  
 XX WPI; 1997-512647/47.  
 DR  
 PT New peptide nucleic acids hybridising to mammalian telomerase RNA -  
 PT used to inhibit telomerase, for treating tumours and other  
 XX proliferative diseases, also for diagnosis  
 XX  
 PS Example 2; Page 49; 76pp; English.  
 CC This is an oligonucleotide used in the measurement of Tm values and  
 CC their complementary peptide nucleic acids (PNAs), (e.g. AAT89228-T89233,  
 23

CC AAT89243-T89244). PNAs hybridise specifically to an RNA component of  
 CC mammalian telomerase, and include the sequence GGG for specific  
 CC hybridisation to the template region of this component. PNAs can be  
 CC used as probes to detect the RNA component of mammalian telomerase and  
 CC as inhibitors of telomerase activity, especially in the treatment of  
 CC cancer.  
 CC  
 SQ Sequence 24 BP; 7 A; 5 C; 5 G; 7 T; 0 other;

Query Match 46.7%; Score 14; DB 18; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 TTTGTTACCCCTA 30  
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 Db 1 TTTGTTACCCCTA 14

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 Job time : 113.554 secs



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OS Synthetic.
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XX PN W0938964-A2.
XX
XX PD 05-AUG-1999.
XX
XX PF 29-JAN-1999; 99MO-GB00308.
XX
XX PR 29-JAN-1998; 98GB-0001902.
XX
XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX PI Keith MN;
XX
XX DR WPI; 1999-479183/40.
XX
XX PT Mouse and human telomerase RNA gene promoters, useful for tumor
XX specific gene therapy
XX
XX PS Disclosure; Fig 19; 109pp; English.
XX
XX CC The invention relates to promoter regions from mouse and human
XX telomerase RNA (TR) component genes. The TR gene promoter can be linked
XX to a heterologous gene, especially a gene encoding a cytotoxin, for
XX therapy of cancer, especially neoplasias. The telomerase is necessary for
XX the unrestricted proliferative capacity of many human cancers. Mutation
XX or dysregulation of the telomerase repression pathway may cause
XX reactivation or upregulation of telomerase expression in cancer.
XX Substances, identified in the methods, can be used to block transcription
XX from the TR gene promoter through interaction of the 5' regulatory
XX sequences. These substances, e.g. antisense oligonucleotides,
XX transcription factors, peptide nucleic acids and factors that disrupt
XX signal transduction, are useful for cancer therapy. In particular, gene
XX therapy vectors (especially p6762-codapp) comprising the promoter and a
XX viral thymidine kinase gene can be used to convert a prodrug, e.g.
XX gancyclovir, so that neoplasia can be controlled or treated. Direct
XX down-regulation of telomerase RNA gene through manipulation of
XX transcription factors may be effective anticancer therapy and the cloning
XX of the hTR gene promoter allows the analysis of therapeutic molecules
XX which modulate hTR promoter activity. Sequences AA207324-332 and
XX CA400332-340 represent constructs with hTR promoter sequence element
XX mutations.
XX
XX SQ Sequence 47 BP; 11 A; 7 C; 15 G; 14 T; 0 other;
XX
XX Query Match 66.7%; Score 20; DB 20; Length 47;
XX Best Local Similarity 100.0%; Pred. No. 0.1;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 TGGCCATTTTGTCTAACC 27
XX Db 28 TGGCCATTTTGTCTAACC 47
XX
XX RESULT 11
XX ID AAA37591 standard; RNA; 31 BP.
XX
XX AC AAA37591;
XX
XX DT 15-AUG-2000 (first entry)
XX
XX DE Telomerase target sequence.
XX
XX KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
XX inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
XX AIDS; HIV; fungal infection; forensic identification; detect; tumour;
XX paternity testing; ss.
XX
XX OS Synthetic.
XX
XX PN US6046307-A.
XX

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PD 04-APR-2000.
XX
XX PP 09-APR-1997; 97US-0836545.
XX
XX PR 09-APR-1996; 96US-0630019.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Wright WE, Piatydzek MA, Shay JW, Norton JC, Corey DR;
XX
XX DR WPI; 2000-292432/25.
XX
XX PT New peptide nucleic acid (PNA) compounds that inhibit telomerase
XX activity in mammalian cells is useful as probes to detect the RNA
XX component of a mammalian telomerase
XX
XX PS Example 2; Column 37; 45pp; English.
XX
XX CC The present sequence represents a telomerase target sequence. The
XX invention relates to an antisense oligonucleotide used as a control
XX sequence alongside a peptide nucleic acid molecule which hybridises to
XX the mRNA component of mammalian telomerase, and inhibits telomerase
XX activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one
XX strand of the telomeric DNA, using as a template an 11 nucleotide
XX sequence contained within the RNA component of the enzyme. The invention
XX relates to PNA molecules having a sequence of no more than 25 bases,
XX which include the sequence GTTAGG. The unchanged nature of the PNA
XX backbone increases the melting temperature of associating strands,
XX increases the rate of association with targeted nucleic acids, and
XX affords greater resistance of degradation by proteases or nucleases. The
XX therapeutic PNAs may be used for treating disease conditions such as
XX cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
XX immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
XX syndrome) and associated pathologies, fungal infections, and other
XX diseases characterized by abnormal telomere metabolism or telomerase
XX activity, in combination with antineoplastic and other cytotoxic or
XX cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
XX used for molecular diagnostics. Labelled PNAs are used as hybridization
XX probes to detect or quantitate polynucleotides having a human telomerase
XX RNA (hTR) sequence. PNA probes are also used for forensic identification
XX of individuals, e.g. paternity testing, based on hTR gene restriction
XX fragment length polymorphism (RFLP) pattern. PNAs are also useful as
XX probes to detect the RNA component of a mammalian telomerase and as
XX inhibitors of telomerase activity. The method of the present invention
XX allows cancerous conditions to be detected with increased confidence and
XX possibly at an earlier stage, before cells are detected as cancerous
XX based on pathological characteristics. The diagnostic and prognostic
XX methods of the present invention can be used to detect an immortal or
XX neoplastic cell or tumour tissue or cancer of any origin, provided the
XX cell expresses telomerase activity and its RNA component.
XX
XX SQ Sequence 31 BP; 8 A; 6 C; 8 G; 9 U; 0 other;
XX
XX Query Match 50.0%; Score 15; DB 21; Length 31;
XX Best Local Similarity 53.3%; Pred. No. 55;
XX Matches 8; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 16 TTTTGTCTAACCCTA 30
XX Db 1 UUUUGUCUAAACCCTA 15
XX
XX RESULT 12
XX ID AAS15462 standard; RNA; 31 BP.
XX
XX AC AAS15462;
XX
XX DT 14-FEB-2002 (first entry)
XX
XX DE Human telomerase RNA (hTR) strand #2.
XX
XX KW Mammalian; forensic; paternity testing; human telomerase RNA component;
XX

```

CC screening a genomic library of mouse D3 embryonic stem cells.  
XX Sequence 27 BP; 2 A; 4 C; 12 G; 9 T; 0 other;

Query Match 66.7%; Score 20; DB 17; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGTTGGCCATTCTTTTG 20  
DB 8 GGGGTGTTGGCCATTCTTTTG 27

RESULT 8  
AAZ0787  
ID AAZ0787 standard; DNA; 28 BP.

AC AAZ0787;  
XX 13-JAN-2000 (first entry)

DE Human telomerase RNA specific PCR primer-1.  
XX PCR primer; human telomerase RNA; hTR; amplify; human strafen cDNA;  
XX hstraf; synthesized; random hexamer primer;  
XX Superscript II reverse transcriptase; ss.

OS Synthetic.  
OS Homo sapiens.

XX WO951255-A1.

XX 14-OCT-1999.

XX 06-APR-1999; 99WO-US07533.

XX 06-APR-1998; 98US-0080783.

XX (UNJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Greider CM, Le S;

XX WPI; 1999-620168/53.

XX Human strafen polypeptide useful in methods for identifying telomerase  
XX inhibitors

XX Disclosure; Page 15; 50pp; English.

CC The present sequence is a PCR primer specific to human telomerase  
CC RNA (hTR). It is used to amplify human strafen (hstraf) cDNA synthesized  
CC using random hexamer primers and Superscript II reverse transcriptase.

XX Sequence 28 BP; 2 A; 4 C; 13 G; 9 T; 0 other;

Query Match 66.7%; Score 20; DB 20; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGTTGGCCATTCTTTTG 20  
DB 9 GGGGTGTTGGCCATTCTTTTG 28

RESULT 9  
AAZ00339  
ID AAZ00339 standard; DNA; 47 BP.

AC AAZ00339;

XX 22-OCT-1999 (first entry)

DE Mutated hTR promoter fragment containing construct 115.

XX Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;  
XX gene therapy; thymidine kinase gene; anticancer therapy; human; ss.

OS Homo sapiens.  
OS Synthetic.

XX WO938964-A2.

XX 05-AUG-1999.

XX 23-JAN-1999; 99WO-GB00308.

XX 23-JAN-1998; 98GB-0001902.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Keith MN;

XX WPI; 1999-479183/40.

PT Mouse and human telomerase RNA gene promoters, useful for tumor  
XX specific gene therapy  
XX Disclosure; Fig 19; 109pp; English.

CC The invention relates to promoter regions from mouse and human  
CC telomerase RNA (TR) component genes. The TR gene promoter can be linked  
CC to a heterologous gene, especially a gene encoding a cytotoxin, for  
CC therapy of cancer, especially neoplasia. The telomerase is necessary for  
CC the unrestricted proliferative capacity of many human cancers. Mutation  
CC or dysregulation of the telomerase repression pathway may cause  
CC reactivation or upregulation of telomerase expression in cancer.  
CC Substances, identified in the methods, can be used to block transcription  
CC from the TR gene promoter through interaction of the 5' regulatory  
CC sequences. These substances, e.g. antisense oligonucleotides,  
CC transcription factors, peptide nucleic acids and factors that disrupt  
CC signal transduction, are useful for cancer therapy. In particular, gene  
CC therapy vectors (especially pGT62-codrup) comprising the promoter and a  
CC viral thymidine kinase gene can be used to convert a produg, e.g.  
CC gancyclovir, so that neoplasia can be controlled or treated. Direct  
CC down-regulation of telomerase RNA gene through manipulation of  
CC transcription factors may be effective anticancer therapy and the cloning  
CC of the hTR gene promoter allows the analysis of therapeutic molecules  
CC which modulate hTR promoter activity. Sequences AAZ07324-332 and  
CC AAZ00332-340 represent constructs with hTR promoter sequence element  
CC mutations.

XX Sequence 47 BP; 8 A; 7 C; 18 G; 14 T; 0 other;

Query Match 66.7%; Score 20; DB 20; Length 47;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGCCATTCTTTGCTAAC 27  
DB 28 TGGCCATTCTTTGCTAAC 47

RESULT 10  
AAZ00340  
ID AAZ00340 standard; DNA; 47 BP.

AC AAZ00340;

XX 22-OCT-1999 (first entry)

DE Mutated hTR promoter fragment containing construct 114.

XX Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;  
XX gene therapy; thymidine kinase gene; anticancer therapy; human; ss.

OS Homo sapiens.

CC of individuals, e.g. paternity testing, based on htr gene restriction  
 CC fragment length polymorphism (RFLP) pattern. PNA's are also useful as  
 CC probes to detect the RNA component of a mammalian telomerase and as  
 CC inhibitors of telomerase activity. The method of the present invention  
 CC allows cancerous conditions to be detected with increased confidence and  
 CC possibly at an earlier stage, before cells are detected as cancerous  
 CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component.

SQ Sequence 23 BP; 5 A; 7 C; 1 G; 10 T; 0 other;

Query Match 66.7%; Score 20; DB 21; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Gaps 0;

Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 11 CCATTTTGTCTAACCTTA 30  
 Db 1 CCATTTTGTCTAACCTTA 20

RESULT 6  
 AAS15446

ID AAS15446 standard; DNA; 23 BP.

XX AAS15446;

XX 14-FEB-2002 (first entry)

XX Oligonucleotide #2 used in melting temperature studies of PNA's.

DE Mammalian; paternity testing; human telomerase RNA component;  
 KW htr gene RFLP pattern; cancer; inflammation; forensic;  
 KW lymphoproliferative disease; autoimmune disease; hyperplasia;  
 KW neurodegenerative disease; neoplasia; HIV; AIDS; cytostatic;  
 KW human immunodeficiency virus; acquired immunodeficiency syndrome;  
 KW telomere metabolism; anti-inflammatory; immunosuppressive; ss.

OS Homo sapiens.  
 OS Synthetic.

PN US6294650-B1.

PD 25-SEP-2001.

XX 08-JUL-1999; 99US-0349532.

XX 09-APR-1997; 97US-0838545.

PR 09-APR-1996; 96US-0630019.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;

DR WPI; 2001-638024/73.

PT New peptide nucleic acids that hybridizes to the RNA component of  
 PT mammalian telomerase, useful for treating or preventing cancer,  
 PT inflammation, lymphoproliferative diseases, autoimmune disease, or  
 PT neurodegenerative diseases -

PS Example 2; Column 34; 46pp; English.

XX The present invention relates to peptide nucleic acids (PNAs), comprising  
 CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in  
 CC mammalian cells by hybridising to the RNA component of mammalian  
 CC telomerase. The PNAs are useful as probes to detect the RNA component  
 CC of mammalian telomerase and as inhibitors of telomerase activity, or to  
 CC detect and/or quantitate polynucleotide having the human telomerase  
 CC RNA component (htr) sequence, as well as in forensic identification of  
 CC individuals, such as paternity testing or identification of criminal  
 CC suspects or unknown descendants based on the htr gene RFLP pattern. The

CC PNA can be further used for treating or preventing cancer, inflammation,  
 CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative  
 CC diseases. The PNAs in combination with other pharmaceuticals (such as  
 CC antineoplastic or cytostatic agents) can be used for treating neoplasia,  
 CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired  
 CC immunodeficiency syndrome (AIDS) and associated pathologies, and other  
 CC diseases characterised by abnormal telomere metabolism or telomerase  
 CC activity. The present sequence representing a DNA oligonucleotide is  
 CC complementary to some of the PNAs of the present invention, and is  
 CC used in melting temperature studies.

SQ Sequence 23 BP; 5 A; 7 C; 1 G; 10 T; 0 other;

Query Match 66.7%; Score 20; DB 23; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Gaps 0;

Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 11 CCATTTTGTCTAACCTTA 30  
 Db 1 CCATTTTGTCTAACCTTA 20

RESULT 7  
 AAT11045

ID AAT11045 standard; DNA; 27 BP.

XX AAT11045;

XX 02-JUL-1996 (first entry)

XX Primer used for producing telomerase probe.

DE Telomerase; mammal; antisense; triplex forming oligonucleotide;  
 KW plasmid; probe; primer; ribozyme; ss.

OS Synthetic.

PN WO9601614-A2.

PD 25-JUN-1996.

XX 07-JUL-1995; 95WO-US08620.

XX 07-JUN-1995; 95US-0485778.

PR 27-JUL-1994; 94US-0272102.

PR 27-OCT-1994; 94US-0330123.

PR 13-FEB-1995; 95US-0387524.

XX (COLD-) COLD SPRING HARBOR LAB.

PA (GERO-) GERON CORP.

PI Andrews WH, Avillion AA, Feng J, Funk W, Greider C;

PI Marhunda MA, Villeponteau B;

DR WPI; 1996-097428/10.

PT RNA components of (non)human mammalian telomerase(s) - useful in

PT studying cell senescence and immortalisation

PS Example 10; Page 55; 85pp; English.

XX The RNA components of (non) human mammalian telomerase(s) especially  
 CC from mouse, rat and chinese hamster are all claimed. Antisense  
 CC oligonucleotides can be used to block the activity of the  
 CC telomerase; probes and primers can be used in detection; vectors and  
 CC host cells transformed with the isolated telomerase genes can be  
 CC used for production of telomerases; RNA and DNA ribozymes and triplex  
 CC forming oligonucleotides directed against the telomerase genes can  
 CC be used therapeutically as can plasmids. A mouse which lacks the  
 CC telomerase gene (also claimed) can be used for study of telomere  
 CC regulation in vivo, and the role it plays in immortalisation.  
 CC Two primers (AAT11045, AAT11046) were used to amplify a fragment of the  
 CC human telomerase encoding enzyme for its use as a probe in

CC Substances, identified in the methods, can be used to block transcription  
 CC from the TR gene promoter through interaction of the 5' regulatory  
 CC sequences. These substances, e.g. antisense oligonucleotides  
 CC transcription factors, peptide nucleic acids and factors that disrupt  
 CC signal transduction, are useful for cancer therapy. In particular, gene  
 CC therapy (especially p62-codupp) comprising the promoter and a  
 CC viral thymidine kinase gene can be used to convert a prodrug, e.g.  
 CC ganciclovir, so that neoplasia can be controlled or treated. Direct  
 CC down-regulation of telomerase RNA gene through manipulation of  
 CC transcription factors may be effective anticancer therapy and the cloning  
 CC of the hTR gene promoter allows the analysis of therapeutic molecules  
 CC which modulate hTR promoter activity. Sequences AA207324-332 and  
 CC AA200332-340 represent constructs with hTR promoter sequence element  
 CC mutations.  
 CC  
 SQ Sequence 47 BP; 9 A; 7 C; 17 G; 14 T; 0 other;

Query Match 83.3%; Score 25; DB 20; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 0.00019;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GGGGAGGCGCATTTTGTCTAACC 27  
 |||||  
 Db 23 GGTGGTGGCATTTTGTCTAACC 47

RESULT 4  
 ID AAT89246 standard; DNA; 23 BP.  
 AAT89246;

DT 12-MAY-1998 (first entry)

DE DNA oligonucleotide 2, used in the measurement of Tm values.

KM Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;  
 KM inhibitor; human telomerase RNA; hTR; PCR; oligonucleotide; ss.

OS Synthetic.

PN WO978013-A1.

PD 16-OCT-1997.

PF 09-APR-1997; 97WO-US05931.

PR 09-APR-1996; 96US-0630019.

PA (GERO-) GERON CORP.

PI Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;

PS WPI; 1997-512647/47.

PT New peptide nucleic acids hybridising to mammalian telomerase RNA -  
 PT used to inhibit telomerase, for treating tumours and other  
 PT proliferative diseases, also for diagnosis

PS Example 2; Page 49; 76pp; English.

CC This is an oligonucleotide used in the measurement of Tm values and  
 CC their complementary peptide nucleic acids (PNAs). (e.g.  
 CC AAT89225-T89227). PNAs hybridise specifically to an RNA component of  
 CC mammalian telomerase, and include the sequence GGG for specific  
 CC hybridisation to the template region of this component. PNAs can be used  
 CC as probes to detect the RNA component of mammalian telomerase and as  
 CC inhibitors of telomerase activity, especially in the treatment of  
 CC cancer.

SQ Sequence 23 BP; 5 A; 7 C; 1 G; 10 T; 0 other;

Query Match 66.7%; Score 20; DB 18; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 CGATTTTGTCTAACCCTA 30  
 |||||  
 Db 1 CGATTTTGTCTAACCCTA 20

RESULT 5  
 ID AAA37568 standard; DNA; 23 BP.  
 AAA37568;

DT 15-AUG-2000 (first entry)

DE PNA sequence #26 used to inhibit telomerase activity.

KM Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;  
 KM inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 KM AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 KM paternity testing; ss.

OS Synthetic.

PN US6046307-A.

PD 04-APR-2000.

PF 09-APR-1997; 97US-0838545.

PR 09-APR-1996; 96US-0630019.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

PS WPI; 2000-292432/25.

PT New peptide nucleic acid (PNA) compounds that inhibit telomerase  
 PT activity in mammalian cells is useful as probes to detect the RNA  
 PT component of a mammalian telomerase

PS Example 2; Column 33; 45pp; English.

CC The present sequence represents a peptide nucleic acid molecule which  
 CC hybridises to the mRNA component of mammalian telomerase, and inhibits  
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 CC synthesizes one strand of the telomeric DNA, using as a template an 11  
 CC nucleotide sequence contained within the RNA component of the enzyme. The  
 CC invention relates to PNA molecules having a sequence of no more than 25  
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 CC backbone increases the melting temperature of associating strands, and  
 CC increases the rate of association with targeted nucleic acids, and  
 CC affords greater resistance to degradation by proteases or nucleases. The  
 CC therapeutic PNAs may be used for treating disease conditions such as  
 CC cancer, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 CC syndrome) and associated pathologies, fungal infections, and other  
 CC diseases characterized by abnormal telomere metabolism or telomerase  
 CC activity, in combination with antineoplastic and other cytotoxic or  
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be  
 CC used for molecular diagnostics, labelled PNAs are used as hybridization  
 CC probes to detect or quantitate polynucleotides having a human telomerase  
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification



XX Disclosure; Fig 19; 109pp; English.  
PS  
XX The invention relates to promoter regions from mouse and human  
CC telomerase RNA (TR) component genes. The TR gene promoter can be linked  
CC to a heterologous gene, especially a gene encoding a cytotoxin, for  
CC therapy of cancer, especially neoplasias. The telomerase is necessary for  
CC the unrestricted proliferative capacity of many human cancers. Mutation  
CC or dysregulation of the telomerase repression pathway may cause  
CC reactivation or upregulation of telomerase expression in cancer.  
CC Substances, identified in the methods, can be used to block transcription  
CC from the TR gene promoter through interaction of the 5' regulatory  
CC sequences. These substances, e.g., antisense oligonucleotides,  
CC transcription factors, peptide nucleic acids and factors that disrupt  
CC signal transduction, are useful for cancer therapy. In particular, gene  
CC therapy vectors (especially pGte2-codamp) comprising the promoter and a  
CC viral thymidine kinase gene can be used to convert a prodrug, e.g.,  
CC gancyclovir, so that neoplasia can be controlled or treated. Direct  
CC down-regulation of telomerase RNA gene through manipulation of  
CC transcription factors may be effective anticancer therapy and the cloning  
CC of the hTR gene promoter allows the analysis of therapeutic molecules  
CC which modulate hTR promoter activity. Sequences AA20332-332 and  
CC AA200332-340 represent constructs with hTR promoter sequence element  
CC mutations.  
XX  
SQ Sequence 47 BP; 8 A; 7 C; 19 G; 13 T; 0 other;  
Query Match 90.0%; Score 27; DB 20; Length 47;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGCGTGGTGGCCATTTTTGTCTAAC 27  
DB 21 GGCGTGGTGGCCATTTTTGTCTAAC 47  
RESULT 2  
AAZ00337  
ID AAZ00337 standard; DNA; 47 BP.  
XX  
AC AAZ00337;  
XX  
DT 22-OCT-1999 (first entry)  
XX  
DE Mutated hTR promoter fragment containing construct 112 (RCE).  
XX  
KM Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;  
KW gene therapy; thymidine kinase gene; anticancer therapy; human; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO938964-A2.  
XX  
PD 05-AUG-1999.  
XX  
PF 29-JAN-1999; 99WO-GB00308.  
XX  
PR 29-JAN-1998; 98GB-0001902.  
XX  
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
XX  
PI Keith MN;  
XX  
DR WPI; 1999-479183/40.  
XX  
PT Mouse and human telomerase RNA gene promoters, useful for tumor  
PT specific gene therapy  
XX  
PS Disclosure; Fig 19; 109pp; English.  
XX  
CC The invention relates to promoter regions from mouse and human  
CC telomerase RNA (TR) component genes. The TR gene promoter can be linked

CC to a heterologous gene, especially a gene encoding a cytotoxin, for  
CC therapy of cancer, especially neoplasias. The telomerase is necessary for  
CC the unrestricted proliferative capacity of many human cancers. Mutation  
CC or dysregulation of the telomerase repression pathway may cause  
CC reactivation or upregulation of telomerase expression in cancer.  
CC Substances, identified in the methods, can be used to block transcription  
CC from the TR gene promoter through interaction of the 5' regulatory  
CC sequences. These substances, e.g., antisense oligonucleotides,  
CC transcription factors, peptide nucleic acids and factors that disrupt  
CC signal transduction, are useful for cancer therapy. In particular, gene  
CC therapy vectors (especially pGte2-codamp) comprising the promoter and a  
CC viral thymidine kinase gene can be used to convert a prodrug, e.g.,  
CC gancyclovir, so that neoplasia can be controlled or treated. Direct  
CC down-regulation of telomerase RNA gene through manipulation of  
CC transcription factors may be effective anticancer therapy and the cloning  
CC of the hTR gene promoter allows the analysis of therapeutic molecules  
CC which modulate hTR promoter activity. Sequences AA20332-332 and  
CC AA200332-340 represent constructs with hTR promoter sequence element  
CC mutations.  
XX  
SQ Sequence 47 BP; 6 A; 7 C; 20 G; 14 T; 0 other;  
Query Match 83.3%; Score 25; DB 20; Length 47;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGCGTGGTGGCCATTTTTGTCTAAC 27  
DB 23 GGCGTGGTGGCCATTTTTGTCTAAC 47  
RESULT 3  
AAZ00338  
ID AAZ00338 standard; DNA; 47 BP.  
XX  
AC AAZ00338;  
XX  
DT 22-OCT-1999 (first entry)  
XX  
DE Mutated hTR promoter fragment containing construct 113 (mspl+mRCE).  
XX  
KM Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;  
KW gene therapy; thymidine kinase gene; anticancer therapy; human; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO938964-A2.  
XX  
PD 05-AUG-1999.  
XX  
PF 29-JAN-1999; 99WO-GB00308.  
XX  
PR 29-JAN-1998; 98GB-0001902.  
XX  
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
XX  
PI Keith MN;  
XX  
DR WPI; 1999-479183/40.  
XX  
PT Mouse and human telomerase RNA gene promoters, useful for tumor  
PT specific gene therapy  
XX  
PS Disclosure; Fig 19; 109pp; English.  
XX  
CC The invention relates to promoter regions from mouse and human  
CC telomerase RNA (TR) component genes. The TR gene promoter can be linked  
CC to a heterologous gene, especially a gene encoding a cytotoxin, for  
CC therapy of cancer, especially neoplasias. The telomerase is necessary for  
CC the unrestricted proliferative capacity of many human cancers. Mutation  
CC or dysregulation of the telomerase repression pathway may cause  
CC reactivation or upregulation of telomerase expression in cancer.

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OM nucleic - nucleic search, using bw model

Run on: June 23, 2003, 10:14:29 ; Search time 113.554 Seconds  
(without alignments)  
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Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 18: /SID52/gcgdata/geneseg/geneseqn-emb1/NA1997.DAT.\*
- 19: /SID52/gcgdata/geneseg/geneseqn-emb1/NA1998.DAT.\*
- 20: /SID52/gcgdata/geneseg/geneseqn-emb1/NA1999.DAT.\*
- 21: /SID52/gcgdata/geneseg/geneseqn-emb1/NA2000.DAT.\*
- 22: /SID52/gcgdata/geneseg/geneseqn-emb1/NA2001A.DAT.\*
- 23: /SID52/gcgdata/geneseg/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SID52/gcgdata/geneseg/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	90.0	47	20	AAZ00336
2	25	83.3	47	20	AAZ00337
3	25	83.3	47	20	AAZ00338
4	20	66.7	23	18	AA189246
5	20	66.7	23	21	AA189246
6	20	66.7	23	23	AA189246
7	20	66.7	23	23	AA189246
8	20	66.7	27	17	AA11045
9	20	66.7	28	20	AA190787
			47	20	AAZ00339

10	20	66.7	47	20	AAZ00340	Mutated htr promot
11	15	50.0	31	21	AA137591	Telomerase target
12	15	50.0	31	23	AA154564	Human telomerase R
13	14	46.7	20	17	AA110286	RNA component of m
14	14	46.7	20	17	AA110322	Antisense oligonuc
15	14	46.7	20	17	AA189245	DNA oligonucleotid
16	14	46.7	24	19	AA189245	Human telomerase R
17	14	46.7	24	19	AA137567	PNA sequence #25 u
18	14	46.7	24	23	AA154545	Oligonucleotide #1
19	14	46.7	25	21	AA137582	Telomerase RNA tar
20	14	46.7	25	21	AA154545	Human telomerase R
21	14	46.7	44	24	AA154545	Human telomerase R
22	13	43.3	13	18	AA189228	Peptide nucleic ac
23	13	43.3	13	20	AA137547	Human RRP-IC-A1 h
24	13	43.3	13	21	AA137547	PNA sequence #4 us
25	13	43.3	13	21	AA137588	Antisense sequence
26	13	43.3	13	21	AA137593	PNA sequence #51 u
27	13	43.3	13	21	AA137594	Phosphoramidate-11
28	13	43.3	13	22	AA181193	Phosphoramidate-11
29	13	43.3	13	22	AA126730	Phosphoramidate-11
30	13	43.3	13	22	AA126730	Phosphoramidate-11
31	13	43.3	13	23	AA154526	PNA 5'/3' inhibiti
32	13	43.3	13	23	AA154526	Phosphorothioate (
33	13	43.3	13	23	AA154564	PNA 3' inhibiting h
34	13	43.3	13	23	AA154564	PNA 2' inhibiting h
35	13	43.3	15	18	AA189229	Peptide nucleic ac
36	13	43.3	15	23	AA137548	PNA sequence #5 us
37	13	43.3	15	23	AA154527	PNA XII inhibiti
38	13	43.3	24	18	AA159091	Mycobacterium anti
39	13	43.3	31	19	AA159091	Antisense oligonuc
40	13	43.3	31	22	AA159091	Antisense oligonuc
41	13	43.3	33	18	AA159091	Mycobacterium anti
42	12	40.0	20	20	AA159091	Human beta catenin
43	12	40.0	20	21	AA159091	Human beta catenin
44	12	40.0	23	21	AA137291	Human POU5f4 forw
45	12	40.0	23	22	AA154446	Probe #48 used in

#### ALIGNMENTS

RESULT 1	
AAZ00336	standard; DNA; 47 BP.
AAZ00336;	
22-OCT-1999	(first entry)
Mutated htr promoter fragment containing construct 111 (mspl.4).	
Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; htr;	
gene therapy; thymidine kinase gene; anticancer therapy; human; ss.	
OS	Hom sapiens.
OS	Synthetic.
PN	WO9338964-A2.
PD	05-AUG-1999.
PF	29-JAN-1999; 99NO-GB00308.
PK	29-JAN-1998; 98GB-0001902.
PR	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
PI	Kelch W;
PI	WPI; 1999-479183/40.
DR	Mouse and human telomerase RNA gene promoters, useful for tumor
XX	specific gene therapy
PT	



FILED DATE: 25-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/330,123  
FILING DATE: Unknown  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William W  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000810  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-580-517-4

Query Match 46.7%; Score 14; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTA 30  
DB 20 TTGTCTAACCTA 7

RESULT 15  
US-08-838-545-25  
Sequence 25, Application US/08838545  
Patent No. 6046307  
GENERAL INFORMATION:  
APPLICANT: Shay, Jerry W.  
APPLICANT: Wright, Woodring E.  
APPLICANT: Piatydzek, Mieczyslaw A.  
APPLICANT: Corey, David R.  
APPLICANT: No. 60463070n, James C.  
TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,545  
FILING DATE: 09-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,019  
FILING DATE: 09-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "peptide nucleic acid (PNA)",  
DESCRIPTION: where (deoxy/ribose-phosphate linkages are replaced by  
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via  
DESCRIPTION: glycine amino N through a methylene carbonyl linker"  
US-08-838-545-25

Query Match 46.7%; Score 14; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTA 30  
DB 1 TTGTCTAACCTA 14

Search completed: June 24, 2003, 16:54:54  
Job time: 29.7603 secs

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; Sequence 6, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550A
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-520-550A-6

Query Match      46.7%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TTTGCTAACCTTA 30
      |||||
Db      20 TTTGCTAACCTTA 7

RESULT 13
US-08-998-443-26/c
; Sequence 26, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
```

```
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Scirella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-998-443-26

Query Match      46.7%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TTTGCTAACCTTA 30
      |||||
Db      20 TTTGCTAACCTTA 7

RESULT 14
US-09-580-517-4/c
; Sequence 4, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; FENG, Junli
; FUNK, Walter
; ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,517
```

NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000811US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-660-678A-26

Query Match 46.7%; Score 14; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30  
DB 20 TTGTCTAACCTTA 7

## RESULT 10

US-08-485-778-6/c  
Sequence 6, Application US/08485778  
Patent No. 5878979  
GENERAL INFORMATION:  
APPLICANT: Andrews, William H.  
APPLICANT: Avilion, Ariel Athena  
APPLICANT: Feng, Junli  
APPLICANT: Greider, Carol  
APPLICANT: Marhenda, Maria Antonia Blasco  
APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millita Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,778  
FILING DATE: 07-JE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/387,524  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-778-6

Query Match 46.7%; Score 14; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30  
DB 20 TTGTCTAACCTTA 7

## RESULT 11

US-08-472-802C-41/c  
Sequence 41, Application US/08472802C  
Patent No. 5958680  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,802C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000820  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-472-802C-41

Query Match 46.7%; Score 14; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30  
DB 20 TTGTCTAACCTTA 7

## RESULT 12

US-08-520-550A-6/c

Sequence 49, Application US/09349532  
Patent No. 6294650  
GENERAL INFORMATION:  
APPLICANT: Shay, Jerry W.  
APPLICANT: Wright, Woodring E.  
APPLICANT: Piatysek, Mieczyslaw A.  
APPLICANT: Corey, David R.  
APPLICANT: No. 6294650ton, James C.  
TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
TITLE OF INVENTION: Peptide Nucleic Acids  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/349,532  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/838,545  
FILING DATE: 09-APR-1997  
APPLICATION NUMBER: US 08/630,019  
FILING DATE: 09-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
US-09-349-532-49

Query Match 50.0%; Score 15; DB 4; Length 31;  
Best Local Similarity 53.3%; Pred. No. 13;  
Matches 8; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTGTCTAACCTTA 30  
DB 1 UUUUGCUAACCTTA 15

RESULT 8  
US-08-330-123A-4/c  
Sequence 4, Application US/08330123A  
Patent No. 5583016  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend Knourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California

COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/330,123A  
FILING DATE: 27-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000810  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-330-123A-4

Query Match 46.7%; Score 14; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTTGTCTAACCTTA 30  
DB 20 TTTGTCTAACCTTA 7

RESULT 9  
US-08-660-678A-26/c  
Sequence 26, Application US/08660678A  
Patent No. 5837857  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,678A  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:





US-08-838-545-26

Query Match 66.7%; Score 20; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCATTTTGTCTAACCTTA 30  
Db 1 CCATTTTGTCTAACCTTA 20

RESULT 2

US-09-349-532-26  
Sequence 26, Application US/09349532  
Patent No. 6294650

GENERAL INFORMATION:

APPLICANT: Shay, Jerry W.

APPLICANT: Wright, Woodring E.

APPLICANT: Piatysek, Mieczyslaw A.

APPLICANT: Corey, David R.

APPLICANT: No. 6294650ton, James C.

TITLE OF INVENTION: Modulation of Mammalian Telomerase by

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS: Peptide Nucleic Acids

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/349,532

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/838,545

FILING DATE: 09-APR-1997

APPLICATION NUMBER: US 08/630,019

FILING DATE: 09-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Stotella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-001610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0300

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "peptide nucleic acid (PNA),

DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by

DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via

DESCRIPTION: glycine amino N through a methylene carbonyl linker"

US-09-349-532-26

Query Match 66.7%; Score 20; DB 4; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCATTTTGTCTAACCTTA 30

Db 1 CCATTTTGTCTAACCTTA 20

RESULT 3

US-08-485-778-20  
Sequence 20, Application US/08485778  
Patent No. 5876979

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Avillion, Ariel Athena

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Greider, Carol

APPLICANT: Marhuenda, Maria Antonia Blasco

APPLICANT: Villeponteau, Bryant

TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith &amp; Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,778

FILING DATE: 07-JE-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/367,524

FILING DATE: 13-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL94-05A4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-485-778-20

Query Match 66.7%; Score 20; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGTGGCCATTTTGG 20

Db 8 GGGGTGTGGCCATTTTGG 27

RESULT 4

US-08-520-550A-20  
Sequence 20, Application US/08520550A  
Patent No. 6013468

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Avillion, Ariel A.

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using bw model

Run on: June 23, 2003, 19:12:24 ; Search time 28.7603 Seconds  
(without alignments)  
319,896 Million cell updates/sec

Title: US-08-770-564a-1\_COPY\_290\_319

Perfect score: 30

Sequence: 1 GGGGTGGTGGCCATTCTTCTACCCCTA 30

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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2: /cgn2\_6/ptodata/2/1na/5b\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/1na/6a\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/1na/6b\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/1na/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/1na/backfile01.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	66.7	23	3	US-08-838-545-26 Sequence 26, Appl
2	20	66.7	23	4	US-09-349-532-26 Sequence 26, Appl
3	20	66.7	27	2	US-08-485-778-20 Sequence 20, Appl
4	20	66.7	27	3	US-08-520-550A-20 Sequence 20, Appl
5	20	66.7	28	4	US-09-286-959B-3 Sequence 3, Appl
6	15	50.0	31	3	US-08-838-545-49 Sequence 49, Appl
7	15	50.0	31	4	US-09-349-532-49 Sequence 49, Appl
8	14	46.7	20	1	US-08-330-123A-4 Sequence 4, Appl
9	14	46.7	20	2	US-08-660-678A-26 Sequence 26, Appl
10	14	46.7	20	2	US-08-485-778-6 Sequence 6, Appl
11	14	46.7	20	2	US-08-472-802C-41 Sequence 41, Appl
12	14	46.7	20	3	US-08-530-550A-6 Sequence 6, Appl
13	14	46.7	20	3	US-08-988-443-26 Sequence 26, Appl
14	14	46.7	20	4	US-08-580-517-4 Sequence 4, Appl
15	14	46.7	24	3	US-08-838-545-25 Sequence 25, Appl
16	14	46.7	24	4	US-09-349-532-25 Sequence 25, Appl
17	14	46.7	24	4	US-09-018-125-4 Sequence 4, Appl
18	14	46.7	25	3	US-08-630-019A-26 Sequence 26, Appl
19	14	46.7	25	3	US-08-630-019A-36 Sequence 36, Appl
20	14	46.7	25	3	US-08-838-545-40 Sequence 40, Appl
21	14	46.7	25	4	US-09-349-532-40 Sequence 40, Appl
22	13	43.3	13	3	US-08-630-019A-17 Sequence 17, Appl
23	13	43.3	13	3	US-08-630-019A-41 Sequence 41, Appl
24	13	43.3	13	3	US-08-838-545-4 Sequence 4, Appl
25	13	43.3	13	3	US-08-838-545-46 Sequence 46, Appl
26	13	43.3	13	3	US-08-838-545-51 Sequence 51, Appl
27	13	43.3	13	3	US-08-838-545-52 Sequence 52, Appl

c 28	13	43.3	13	4	US-09-349-532-4 Sequence 4, Appl
c 29	13	43.3	13	4	US-09-349-532-46 Sequence 46, Appl
c 30	13	43.3	13	4	US-09-349-532-51 Sequence 51, Appl
c 31	13	43.3	13	4	US-09-349-532-52 Sequence 52, Appl
c 32	13	43.3	15	3	US-08-630-019A-18 Sequence 18, Appl
c 33	13	43.3	15	3	US-08-838-545-5 Sequence 5, Appl
c 34	13	43.3	15	3	US-09-349-532-5 Sequence 5, Appl
c 35	13	43.3	24	5	PCT-US96-09473-15 Sequence 15, Appl
c 36	13	43.3	33	5	PCT-US96-09473-13 Sequence 13, Appl
c 37	12	40.0	22	2	US-08-117-952-443 Sequence 443, Appl
c 38	12	40.0	29	2	US-08-944-604-22 Sequence 22, Appl
c 39	12	40.0	29	2	US-08-833-377-2 Sequence 2, Appl
c 40	12	40.0	30	2	US-08-399-696-11 Sequence 11, Appl
c 41	12	40.0	43	1	US-08-836-922-12 Sequence 12, Appl
c 42	11	36.7	11	3	US-08-630-019A-14 Sequence 14, Appl
c 43	11	36.7	11	3	US-08-630-019A-16 Sequence 16, Appl
c 44	11	36.7	11	3	US-08-838-545-3 Sequence 3, Appl
c 45	11	36.7	11	3	US-08-838-545-3 Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-08-838-545-26  
Sequence 26, Application US/08838545  
Patent No. 6046307  
GENERAL INFORMATION:  
APPLICANT: Shay, Jerry W.  
APPLICANT: Wright, Woodring E.  
APPLICANT: Piatydzek, Mieczyslaw A.  
APPLICANT: Corey, David R.  
APPLICANT: No. 6046307com, James C.  
TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,545  
FILING DATE: 09-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US 08/630,019  
FILING DATE: 09-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "peptide nucleic acid (PNA),  
DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by  
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via  
DESCRIPTION: glycine amino N through a methylencarbonyl linker"

OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-006-117A-348

Query Match 40.0%; Score 12; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTTGTGGCCAT 14  
|||||  
Db 6 GGTTGTGGCCAT 17

## RESULT 15

US-10-013-913A-348  
Sequence 348, Application US/10013913A  
Publication No. US20030083462A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2830P1C40  
CURRENT APPLICATION NUMBER: US/10/013,913A  
CURRENT FILING DATE: 2002-07-15  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 348  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-013-913A-348

Query Match 40.0%; Score 12; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTTGTGGCCAT 14  
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Db 6 GGTTGTGGCCAT 17

Search completed: June 24, 2003, 20:39:35  
Job time : 366.455 secs

;; PRIOR APPLICATION NUMBER: 60/101068  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101071  
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;; PRIOR APPLICATION NUMBER: 60/101279  
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;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103679  
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;; PRIOR APPLICATION NUMBER: 60/104257  
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;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
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;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
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;; PRIOR APPLICATION NUMBER: 60/105881  
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;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

Query Match 40.0%; Score 12; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GGTGGTGGCCAT 14  
Db 6 GGTGGTGGCCAT 17

RESULT 14  
US-10-006-117A-348  
Sequence 348, Application US/10006117A  
Publication No. US20030082627A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Guirey, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2830PC13  
CURRENT APPLICATION NUMBER: US/10/006,117A  
Prior Application removed - See File Wrapper or Palm  
Prior Filing Date: 2002-03-19  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 348  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

QY 3 GGTGGTGGCCAT 14  
|||||||  
Db 6 GGTGGTGGCCAT 17

## RESULT 12

US-10-015-869A-348  
; Sequence 348, Application US/10015869A  
; Publication No. US2003073130A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C45  
; CURRENT APPLICATION NUMBER: US/10/015,869A  
; CURRENT FILING DATE: 2002-06-25  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 348  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-015-869A-348

Query Match 40.0%; Score 12; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2,2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGGTGGCCAT 14  
|||||||  
Db 6 GGTGGTGGCCAT 17

## RESULT 13

US-10-006-116A-348  
; Sequence 348, Application US/10006116A  
; Publication No. US20030082626A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C45  
; CURRENT APPLICATION NUMBER: US/10/006,116A  
; CURRENT FILING DATE: 2001-12-16  
; Prior Application Number: 60/098716

; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
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;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101068  
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;; PRIOR FILING DATE: 1998-09-23  
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;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101477  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101479  
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;; PRIOR APPLICATION NUMBER: 60/101741  
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;; PRIOR APPLICATION NUMBER: 60/101743  
;; PRIOR FILING DATE: 1998-09-24  
;; PRIOR APPLICATION NUMBER: 60/101915  
;; PRIOR FILING DATE: 1998-09-24  
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;; PRIOR FILING DATE: 1998-09-24  
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;; PRIOR APPLICATION NUMBER: 60/102307  
;; PRIOR FILING DATE: 1998-09-29  
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;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102331  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102484  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102487  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102570  
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;; PRIOR APPLICATION NUMBER: 60/102687  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102965  
;; PRIOR FILING DATE: 1998-10-02  
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;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
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;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103328  
;; PRIOR FILING DATE: 1998-10-07  
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;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08

;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103679  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103711  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/104257  
;; PRIOR FILING DATE: 1998-10-14  
;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 40.0%; Score 12; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0;

QY 3 GGTGGTGGCCAT 14  
DB 6 GGTGGTGGCCAT 17

RESULT 11  
US-10-012-121A-348  
; Sequence 348, Application US/10012121A  
; Publication No. US2003073810A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC20  
; CURRENT APPLICATION NUMBER: US/10/012,121A  
; PRIOR FILING DATE: 2001-12-07  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-012-121A-348

Query Match 40.0%; Score 12; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0;

US-10-015-393A-348  
; Sequence 348, Application US/10015393A  
; Publication No. US20030069179A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C46  
; CURRENT APPLICATION NUMBER: US/10/015,393A  
; CURRENT FILING DATE: 2002-06-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 348  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-015-393A-348  
  
Query Match 40.0%; Score 12; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 GGGTGGGCGCAT 14  
Db 6 GGGTGGGCGCAT 17  
  
RESULT 10  
US-09-946-374-348  
; Sequence 348, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04

PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
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; PRIOR APPLICATION NUMBER: 60/098821  
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; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099754  
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; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099815  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099808  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099812  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099815  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099816  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/100385  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100388  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100584  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100627  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100661  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100662  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100664  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100683  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100684  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100710  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100711  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100849  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100919  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100930  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101014

```

; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide, linkages between positions 1
; OTHER INFORMATION: to 20 are phosphorothioates,
; OTHER INFORMATION: linkages between positions 22 to 34 are modified
; OTHER INFORMATION: by [N-(4-aminoethyl)glycine]methylene carbonyl
; OTHER INFORMATION: residues
; OTHER INFORMATION: position 21 n(L) = linker is
; OTHER INFORMATION: -O(PO2)-OCH2-CH-(CH2COOH)-(CH2)4-NH
US-09-817-387-21

```

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Query Match          43.3%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      18 TTGCTAACCTA 30
        |||||
        34 TTGCTAACCTA 22

```

## RESULT 6

```

US-09-817-387-7/c
; Sequence 7, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Deibrock-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: oligonucleotide, linkages between positions 1 to
; OTHER INFORMATION: 19 are phosphorothioates, linkages between
; OTHER INFORMATION: positions 19 to 35 are phosphodiester
; OTHER INFORMATION: positions 21 to 35 carry 2'-OCH3 modified ribosyl
; OTHER INFORMATION: residues
US-09-817-387-7

```

```

Query Match          43.3%; Score 13; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      18 TTGCTAACCTA 30
        |||||
        35 TTGCTAACCTA 23

```

## RESULT 7

```

US-10-006-856A-348
; Sequence 348, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

```

; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pan, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 348
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-348

```

```

Query Match          40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 GGTGGGGCCAT 14
        |||||
        6 GGTGGGGCCAT 17

```

## RESULT 8

```

US-10-006-818A-348
; Sequence 348, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pan, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 348
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-348

```

```

Query Match          40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 GGTGGGGCCAT 14
        |||||
        6 GGTGGGGCCAT 17

```

## RESULT 9



TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-09-057-351-40

Query Match 46.7%; Score 14; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30  
DB 20 TTGTCTAACCTTA 7

## RESULT 2

US-09-018-125-4  
; Sequence 4, Application US/09018125A  
; Patent No. US20010007902A1  
; GENERAL INFORMATION:  
; APPLICANT: Silverman, Robert H.  
; APPLICANT: Kondo, Seiji  
; APPLICANT: Cowell, John K.  
; APPLICANT: Li, Guyling  
; APPLICANT: Torrence, Paul F.  
; TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES  
; TITLE OF INVENTION: EFFECTIVE TO TREAT TELOMERASE-EXPRESSING MALIGNANCIES  
; FILE REFERENCE: 8656-022  
; CURRENT APPLICATION NUMBER: US/09/018, 125A  
; CURRENT FILING DATE: 1999-02-03  
; EARLIER APPLICATION NUMBER: 60/044,507  
; EARLIER FILING DATE: 1997-04-21  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-018-125-4

Query Match 46.7%; Score 14; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30  
DB 1 TTGTCTAACCTTA 14

## RESULT 3

US-09-817-387-8/C  
; Sequence 8, Application US/09817387  
; Patent No. US20010039263A1  
; GENERAL INFORMATION:  
; APPLICANT: Max-Debruck-Centrum fur Molekulare Medizin  
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof  
; FILE REFERENCE: 101195-24  
; CURRENT APPLICATION NUMBER: US/09/817,387  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: DE 197 20 151.2  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide, linkages between positions 1 to  
; OTHER INFORMATION: 15 are phosphorothioates, linkages between  
; OTHER INFORMATION: positions 15 to 17, 19 to 23 and 25 to 30 are  
; OTHER INFORMATION: phosphodiester,  
; OTHER INFORMATION: linkages between positions 17 to 19 and 23 to 25  
; OTHER INFORMATION: are N3' to N5' phosphoramidates  
US-09-817-387-8

Query Match 43.3%; Score 13; DB 10; Length 30;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTGTCTAACCTTA 30  
DB 30 TTGTCTAACCTTA 18

## RESULT 4

US-09-817-387-9/C  
; Sequence 9, Application US/09817387  
; Patent No. US20010039263A1  
; GENERAL INFORMATION:  
; APPLICANT: Max-Debruck-Centrum fur Molekulare Medizin  
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof  
; FILE REFERENCE: 101195-24  
; CURRENT APPLICATION NUMBER: US/09/817,387  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: DE 197 20 151.2  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 34  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:  
; OTHER INFORMATION: oligonucleotide, linkages between positions 1 to  
; OTHER INFORMATION: 15 are phosphorothioates, linkages between  
; OTHER INFORMATION: positions 15 to 20 are phosphodiester,  
; OTHER INFORMATION: position 21 n(l) = linker is  
; OTHER INFORMATION: 3'-O(P02)CH2CH(CH2COOH)-(CH2)4-NH-,  
; OTHER INFORMATION: linkages between positions 22 to 34 are  
; OTHER INFORMATION: [N-(2-aminoethyl)glycine] methylene carbonyl  
; OTHER INFORMATION: residues  
US-09-817-387-9

Query Match 43.3%; Score 13; DB 10; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTGTCTAACCTTA 30  
DB 34 TTGTCTAACCTTA 22

## RESULT 5

US-09-817-387-21/C  
; Sequence 21, Application US/09817387  
; Patent No. US20010039263A1  
; GENERAL INFORMATION:  
; APPLICANT: Max-Debruck-Centrum fur Molekulare Medizin  
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof  
; FILE REFERENCE: 101195-24  
; CURRENT APPLICATION NUMBER: US/09/817,387  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: DE 197 20 151.2  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21

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OM nucleic - nucleic search, using bw model

Run on: June 23, 2003, 20:29:49 ; Search time 365.455 Seconds

(without alignments)  
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Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 73373590 residues

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12: /cgn2\_6/ptodata/2/pubna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	46.7	20	10	US-09-057-351-40
2	14	46.7	24	10	US-09-018-125-4
3	13	43.3	30	10	US-09-817-387-8
4	13	43.3	34	10	US-09-817-387-9
5	13	43.3	34	10	US-09-817-387-21
6	13	43.3	35	10	US-09-817-387-7
7	12	40.0	23	9	US-10-006-856A-348
8	12	40.0	23	9	US-10-006-818A-348
9	12	40.0	23	9	US-10-015-93A-348
10	12	40.0	23	9	US-08-946-374-348
11	12	40.0	23	9	US-10-012-121A-348
12	12	40.0	23	9	US-10-015-869A-348
13	12	40.0	23	9	US-10-006-116A-348
14	12	40.0	23	9	US-10-006-117A-348
15	12	40.0	23	9	US-10-013-913A-348
16	12	40.0	23	9	US-10-017-527A-348
17	12	40.0	23	9	US-10-007-194A-348
18	12	40.0	23	9	US-10-013-430A-348
19	12	40.0	23	9	US-10-011-671A-348

20	12	40.0	23	9	US-10-012-755A-348	Sequence 348, App
21	12	40.0	23	9	US-10-015-386A-348	Sequence 348, App
22	12	40.0	23	9	US-10-011-692A-348	Sequence 348, App
23	12	40.0	25	9	US-10-098-263B-14446	Sequence 14446, A
24	12	40.0	25	9	US-10-098-263B-116941	Sequence 116941, A
25	12	40.0	25	9	US-09-976-674-50	Sequence 50, App
26	11	36.7	16	9	US-10-206-833-38	Sequence 38, App
27	11	36.7	20	9	US-09-966-451-83	Sequence 83, App
28	11	36.7	20	9	US-09-902-176A-39	Sequence 39, App
29	11	36.7	20	10	US-09-988-915-3	Sequence 3, App
30	11	36.7	24	9	US-10-091-135-57	Sequence 57, App
31	11	36.7	24	9	US-10-091-135-58	Sequence 711, App
32	11	36.7	24	9	US-09-940-185-711	Sequence 4677, App
33	11	36.7	25	9	US-09-940-185-4677	Sequence 12672, A
34	11	36.7	25	9	US-10-098-263B-12672	Sequence 14445, A
35	11	36.7	25	9	US-10-098-263B-14445	Sequence 68494, A
36	11	36.7	25	9	US-10-098-263B-68494	Sequence 75989, A
37	11	36.7	25	9	US-10-098-263B-75989	Sequence 79564, A
38	11	36.7	25	9	US-10-098-263B-79736	Sequence 79736, A
39	11	36.7	25	9	US-10-098-263B-82962	Sequence 82962, A
40	11	36.7	25	9	US-10-098-263B-86266	Sequence 86266, A
41	11	36.7	25	9	US-10-098-263B-90337	Sequence 90337, A
42	11	36.7	29	9	US-09-863-040-54	Sequence 54, App
43	11	36.7	29	9	US-10-098-263B-678-22	Sequence 22, App
44	11	36.7	30	10	US-09-946-678-22	Sequence 37, App
45	11	36.7	30	10	US-09-750-373-37	

#### ALIGNMENTS

RESULT 1  
US-09-057-351-40/c  
; Sequence 40, Application US/09057351  
; Patent No. US20010034439A1  
GENERAL INFORMATION:  
APPLICANT: Villetreuil, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000821US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200



APPLICANT: Feng, Junli  
 APPLICANT: Funk, Walter  
 APPLICANT: Greider, Carol  
 APPLICANT: Marhuenda, Maria A.B.  
 APPLICANT: Villeponteau, Bryant  
 TITLE OF INVENTION: RNA Component of Telomerase  
 FILE REFERENCE: CSHL94-05A7  
 CURRENT APPLICATION NUMBER: US/09/259,943  
 CURRENT FILING DATE: 1999-03-01  
 EARLIER APPLICATION NUMBER: 08/623,166  
 EARLIER FILING DATE: 1996-03-28  
 EARLIER APPLICATION NUMBER: 08/520,550  
 EARLIER FILING DATE: 1995-08-29  
 EARLIER APPLICATION NUMBER: 08/485,778  
 EARLIER FILING DATE: 1995-06-07  
 EARLIER APPLICATION NUMBER: 08/387,524  
 EARLIER FILING DATE: 1995-02-13  
 EARLIER APPLICATION NUMBER: 08/330,123  
 EARLIER FILING DATE: 1994-10-27  
 EARLIER APPLICATION NUMBER: 08/272,102  
 EARLIER FILING DATE: 1994-07-07  
 NUMBER OF SEQ ID NOS: 61  
 SOFTWARE: FASTSEQ for Windows Version 3.0  
 SEQ ID NO: 26  
 LENGTH: 20  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic oligonucleotides  
 US-09-259-943-26

Query Match 46.7%; Score 14; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTTGCTPACCCCTA 30  
 DB 20 TTTGCTPACCCCTA 7

RESULT 15  
 US-09-370-455-26  
 Sequence 26, Application US/09370455  
 GENERAL INFORMATION:  
 APPLICANT: Shay, Jerry W.  
 APPLICANT: Wright, Woodring E.  
 APPLICANT: Piatysek, Mieczyslaw A.  
 APPLICANT: Corey, David  
 APPLICANT: Norton, James C.  
 TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
 TITLE OF INVENTION: Peptide Nucleic Acids  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/370,455  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/630,019  
 FILING DATE: 09-JUN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Storella, John R.

REGISTRATION NUMBER: 32,944  
 REFERENCE/DOCKET NUMBER: 015389-001600US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "peptide nucleic acid (PNA),  
 DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by  
 DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via  
 DESCRIPTION: glycine amino nitrogen through a methylene-carbonyl linker"  
 US-09-370-455-26

Query Match 46.7%; Score 14; DB 17; Length 25;  
 Best Local Similarity 57.1%; Pred. No. 2.4e+03;  
 Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTTGCTPACCCCTA 30  
 DB 1 UUUUCUACCCCTA 14

Search completed: June 24, 2003, 18:22:28  
 Job time: 1298.44 secs

REFERENCE/DOCKET NUMBER: 15389-000850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
ANTI-SENSE: YES  
US-08-521-634-25

Query Match 46.7%; Score 14; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTTA 30  
Db 20 TTTGCTAACCTTA 7

RESULT 12  
US-08-660-678-4/c  
Sequence 4, Application US/08660678  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,678  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000811  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-660-678-4

Query Match 46.7%; Score 14; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTTA 30  
Db 20 TTTGCTAACCTTA 7

RESULT 13  
US-09-057-351-40/c  
Sequence 40, Application US/09057351  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000821US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-09-057-351-40

Query Match 46.7%; Score 14; DB 14; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTTA 30  
Db 20 TTTGCTAACCTTA 7

RESULT 14  
US-09-259-943-26/c  
Sequence 26, Application US/09259943  
GENERAL INFORMATION:  
APPLICANT: Andrews, William H.  
APPLICANT: Avilion, Ariel A.

STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,115A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000830  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-482-115A-4

Query Match 46.7%; Score 14; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTTA 30  
Db 20 TTTGCTAACCTTA 7

RESULT 10  
US-08-520-550-6/C  
Sequence 6, Application US/08520550  
GENERAL INFORMATION:  
APPLICANT: Andrews, William H.  
APPLICANT: Avilion, Ariel A.  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Greider, Carol  
APPLICANT: Marhuenda, Maria A. B.  
APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,550  
FILING DATE: 29-AUG-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/387,524  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A3B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-520-550-6

Query Match 46.7%; Score 14; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTTA 30  
Db 20 TTTGCTAACCTTA 7

RESULT 11  
US-08-521-634-25/C  
Sequence 25, Application US/08521634  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/521,634  
FILING DATE: 31-AUG-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,115  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 7-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy J.  
REGISTRATION NUMBER: 34,587

LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-272-102-7

Query Match 46.7%; Score 14; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTTGCTAACCTA 30  
DB 20 TTTGCTAACCTA 7

RESULT 7  
US-08-387-524-6/c  
Sequence 6, Application US/08387524  
GENERAL INFORMATION:  
APPLICANT: Andrews, William H.  
APPLICANT: Avilion, Ariel A.  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Greider, Carol  
APPLICANT: Marhuenda, Maria A. B.  
APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,524  
FILING DATE: 13-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
US-08-387-524-6

Query Match 46.7%; Score 14; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 17 TTTGCTAACCTA 30  
DB 20 TTTGCTAACCTA 7

DB 20 TTTGCTAACCTA 7

RESULT 8  
US-08-472-802B-41/c  
Sequence 41, Application US/08472802B  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,802B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000820  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-472-802B-41

Query Match 46.7%; Score 14; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTTGCTAACCTA 30  
DB 20 TTTGCTAACCTA 7

RESULT 9  
US-08-482-115A-4/c  
Sequence 4, Application US/08482115A  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco

Qy 1 GGGGTGTGGCCATTTTTG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 8 GGGGTGTGGCCATTTTTG 27

## RESULT 3

US-09-259-943-46  
; Sequence 46, Application US/09259943  
; GENERAL INFORMATION:  
; APPLICANT: Andrews, William H.  
; APPLICANT: Avilion, Ariel A.  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Greider, Carol  
; APPLICANT: Maruenda, Maria A.B.  
; APPLICANT: Villeponteau, Bryant  
; TITLE OF INVENTION: RNA Component of Telomerase  
; FILE REFERENCE: CSHL94-05A7  
; CURRENT APPLICATION NUMBER: US/09/259,943  
; CURRENT FILING DATE: 1999-03-01  
; EARLIER FILING DATE: 1996-03-28  
; EARLIER APPLICATION NUMBER: 08/520,550  
; EARLIER FILING DATE: 1995-08-29  
; EARLIER APPLICATION NUMBER: 08/485,778  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/387,524  
; EARLIER FILING DATE: 1995-02-13  
; EARLIER APPLICATION NUMBER: 08/330,123  
; EARLIER FILING DATE: 1994-10-27  
; EARLIER APPLICATION NUMBER: 08/272,102  
; EARLIER FILING DATE: 1994-07-07  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 46  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotides  
US-09-259-943-46

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Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 GGGGTGTGGCCATTTTTG 27

## RESULT 4

PCT-US99-07533-3  
; Sequence 3, Application PC/TUS9907533  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS  
; FILE REFERENCE: 07265/157MO  
; CURRENT APPLICATION NUMBER: PCT/US99/07533  
; CURRENT FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: 60/080,783  
; EARLIER FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
PCT-US99-07533-3

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Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 9 GGGGTGTGGCCATTTTTG 28

## RESULT 5

PCT-US99-07533-3  
; Sequence 3, Application PC/TUS9907533A  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS  
; FILE REFERENCE: 07265/157MO  
; CURRENT APPLICATION NUMBER: PCT/US99/07533A  
; CURRENT FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: 60/080,783  
; EARLIER FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
PCT-US99-07533-3

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 6

US-08-272-102-7/c  
; Sequence 7, Application US/08272102  
; GENERAL INFORMATION:  
; APPLICANT: VILLEPONTEAU, Bryant  
; APPLICANT: FENG, Junli  
; APPLICANT: FUNK, Walter  
; APPLICANT: ANDREWS, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; STREET: Townsend and Townsend Kourile and Crew  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; APPLICATION NUMBER: US/08/272,102  
; FILING DATE: 07-JUL-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15389-000800  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:



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C 25 13 43.3 13 42 US-10-255-535-3 Sequence 3, Appl
C 26 13 43.3 13 17 US-09-370-455-18 Sequence 18, Appl
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C 38 13 43.3 25 79 US-60-353-987-905467 Sequence 905467,
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C 40 13 43.3 31 9 US-08-510-736-1 Sequence 1, Appl
C 41 13 43.3 31 28 US-09-717-828A-1 Sequence 1, Appl
C 42 13 43.3 31 28 US-09-717-828B-1 Sequence 1, Appl
C 43 13 43.3 31 28 US-09-717-829A-1 Sequence 13, Appl
C 44 13 43.3 33 8 US-08-484-169-13 Sequence 9, Appl
C 45 13 43.3 34 31 US-09-817-387-9
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## ALIGNMENTS

RESULT 1  
US-08-524-20  
Sequence 20, Application US/08387524

GENERAL INFORMATION:

APPLICANT: Andrews, William H.  
APPLICANT: Avillion, Ariel A.

APPLICANT: Peng, Junli  
APPLICANT: Funk, Walter

APPLICANT: Greider, Carol  
APPLICANT: Marhuenda, Maria A. B.

APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive

CITY: Lexington  
STATE: MA

COUNTRY: US  
ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,524

FILING DATE: 13-FEB-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A3

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: DNA (genomic)  
US-08-524-20

Query Match 66.7%; Score 20; DB 7; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 GGGGTGTCGCCATTTTGG 27

RESULT 2  
US-08-520-550-20

Sequence 20, Application US/08520550

GENERAL INFORMATION:

APPLICANT: Andrews, William H.  
APPLICANT: Avillion, Ariel A.

APPLICANT: Peng, Junli  
APPLICANT: Funk, Walter

APPLICANT: Greider, Carol  
APPLICANT: Marhuenda, Maria A. B.

APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive

CITY: Lexington  
STATE: MA

COUNTRY: US  
ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,550

FILING DATE: 29-AUG-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/387,524

FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL94-05A3B  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-520-550-20

Query Match 66.7%; Score 20; DB 9; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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us-08-770-564a-1\_copy\_290\_319.oligo.rmp

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GenCore version 5.1.6  
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4	20	66.7	28	1	PCT-US99-07533-3	Sequence 3, Appl
5	20	66.7	28	1	PCT-US99-07533-3	Sequence 3, Appl
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7	14	46.7	20	7	US-08-387-524-6	Sequence 6, Appl
8	14	46.7	20	8	US-08-472-802B-1	Sequence 41, Appl
9	14	46.7	20	8	US-08-482-115A-4	Sequence 4, Appl
10	14	46.7	20	8	US-08-520-550-6	Sequence 6, Appl
11	14	46.7	20	9	US-08-521-634-25	Sequence 25, Appl
12	14	46.7	20	10	US-08-660-678-4	Sequence 25, Appl
13	14	46.7	20	14	US-09-057-351-40	Sequence 40, App
14	14	46.7	20	14	US-09-259-943-46	Sequence 26, App
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16	14	46.7	25	17	US-09-370-455-26	Sequence 36, App
17	14	46.7	25	67	US-60-233-638-46061	Sequence 46061, App
18	14	46.7	25	79	US-60-353-987-808955	Sequence 808955, App
19	14	46.7	25	79	US-60-353-987-808955	Sequence 865819, App
20	14	46.7	27	13	US-08-521-634-6	Sequence 6, Appl
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



Fri Jun 27 07:42:00 2003

us-08-770-564a-1\_copy\_290\_319.cligo.rnpn

Page 5

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; SOFTWARE: Patentin version 3.1  
; SEQ ID NO: 13  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
PCT-US02-33146-13

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Best Local Similarity 61.5%; Fred. No. 2.9e+03;  
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; Sequence 895384, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 895384  
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US-60-427-808-895384

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Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
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; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527  
; CURRENT APPLICATION NUMBER: US/60/427,836  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 639466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 475949  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-60-427-836-475949

Query Match 46.7%; Score 14; DB 12; Length 25;  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 13  
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; Sequence 490, Application PC/TUS0217674  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Sandberg, Jennifer  
; APPLICANT: Gordon, Gilad  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT  
; FILE REFERENCE: 400/047 (02-325)  
; CURRENT APPLICATION NUMBER: PCT/US02/17674

; CURRENT FILING DATE: 2003-03-25  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/708,690  
; PRIOR FILING DATE: 2000-11-07  
; PRIOR APPLICATION NUMBER: US 09/870,161  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 60/334,461  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 10/138,674  
; PRIOR FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 5989  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 490  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo Sapiens  
PCT-US02-17674-490

Query Match 43.3%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TGCCCATTTTGTG 20  
Db 15 TGCCCATTTTGTG 3

RESULT 14  
US-10-287-949A-7501/C  
; Sequence 7501, Application US/10287949A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7501  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-7501

Query Match 43.3%; Score 13; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TGCCCATTTTGTG 20  
Db 15 TGCCCATTTTGTG 3

RESULT 15  
PCT-US02-33146-13  
; Sequence 13, Application PC/TUS0233146  
; GENERAL INFORMATION:  
; APPLICANT: University of Rochester Medical Center  
; APPLICANT: Rowley, Peter  
; TITLE OF INVENTION: Telomerase Interference  
; FILE REFERENCE: FP-71506-2/RFT/SRN  
; CURRENT APPLICATION NUMBER: PCT/US02/33146

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STATE: California
COUNTRY: USA
ZIP: 94111-3814
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/359,935
FILING DATE: 07-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-359-935-40

Query Match          46.7%; Score 14; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTTGCTACCCCTA 30
DB 20 TTGTCTACCCCTA 7

RESULT 7
US-09-953-570-46061
Sequence 46061, Application US/09953570
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
FILE REFERENCE: 3110.1
CURRENT APPLICATION NUMBER: US/09/953,570
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 60/222,638
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 138410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46061
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces Cerevisiae
US-09-953-570-46061

Query Match          46.7%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTGGCAATTTTGG 20
DB 12 GTGGCAATTTTGG 25

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RESULT 8
US-10-355-577-808955
Sequence 808955, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/10/355,577
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 808955
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-355-577-808955

Query Match          46.7%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCATTTTGTGCTA 24
DB 2 CCATTTTGTGCTA 15

RESULT 9
US-10-355-577-865819
Sequence 865819, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/10/355,577
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 865819
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-355-577-865819

Query Match          46.7%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TTTTGTGCTACCC 27
DB 3 TTTTGTGCTACCC 16

RESULT 10
US-60-427-808-4727/c
Sequence 4727, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 4727
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-60-427-808-4727/c

Query Match          46.7%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 TGCCATTTTGTCTAAC 26  
:|||||:|||||  
Db 1 UGCGCAUUUUUGUCUAC 19

## RESULT 2

PCT-US03-04088-272/c  
; Sequence 272, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: MCSwigen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 272  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense  
; PCT-US03-04088-272

Query Match 63.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGCCATTTTGTCTAAC 26  
:|||||:|||||  
Db 19 TGCCATTTTGTCTAAC 1

## RESULT 3

PCT-US02-33146-9  
; Sequence 9, Application PC/TUS0233146  
; GENERAL INFORMATION:  
; APPLICANT: University of Rochester Medical Center  
; APPLICANT: Rowley, Peter  
; TITLE OF INVENTION: Telomerase Interference  
; FILE REFERENCE: FP-71506-2/RFT/SRN  
; CURRENT APPLICATION NUMBER: PCT/US02/33146  
; CURRENT FILING DATE: 2002-12-05  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PCT-US02-33146-9

Query Match 53.3%; Score 16; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 69;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGGGCCATTT 16  
:|||||:|||||  
Db 7 GGGGTGGGCCATTT 22

## RESULT 4

US-60-427-836-73/c  
; Sequence 73, Application US/60427836  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527  
; CURRENT APPLICATION NUMBER: US/60/427,836  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 73  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; US-60-427-836-73

Query Match 53.3%; Score 16; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTGGCCATTTTTT 19  
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Db 16 GTGCTGGCCATTTTTT 1

## RESULT 5

US-60-427-808-749867  
; Sequence 749867, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 749867  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; US-60-427-808-749867

Query Match 50.0%; Score 15; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTTTGTCTAACCT 29  
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Db 7 TTTTGTCTAACCT 21

## RESULT 6

US-10-359-935-40/c  
; Sequence 40, Application US/10359935  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Peng, Dunli  
; APPLICANT: Funk, Walter  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco

GenCore version 5.1.6  
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OW nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:09:29 ; Search time 1666.12 Seconds  
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125.426 Million cell updates/sec

Title: US-08-770-564a-1\_COPY\_290\_319

Perfect score: 1 GGGGTGGTGGCCATTGTTGCTAACCCCA 30

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Scoring table:

Gapop 60.0 , Gapext 60.0

Searched:

Word size: 0

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Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

Pending Patents NA New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	19	63.3	19	1	PCT-US03-04088-8
5	19	63.3	19	1	PCT-US03-04088-8
6	19	63.3	19	1	PCT-US03-04088-8
7	19	63.3	19	1	PCT-US03-04088-8
8	19	63.3	19	1	PCT-US03-04088-8
9	19	63.3	19	1	PCT-US03-04088-8
10	19	63.3	19	1	PCT-US03-04088-8
11	19	63.3	19	1	PCT-US03-04088-8
12	19	63.3	19	1	PCT-US03-04088-8
13	19	63.3	19	1	PCT-US03-04088-8
14	19	63.3	19	1	PCT-US03-04088-8
15	19	63.3	19	1	PCT-US03-04088-8
16	19	63.3	19	1	PCT-US03-04088-8
17	19	63.3	19	1	PCT-US03-04088-8
18	19	63.3	19	1	PCT-US03-04088-8
19	19	63.3	19	1	PCT-US03-04088-8
20	19	63.3	19	1	PCT-US03-04088-8

21	13	43.3	25	7	US-09-954-445A-123435	Sequence 123435
22	13	43.3	25	9	US-10-355-577-908561	Sequence 788561
23	13	43.3	25	9	US-10-355-577-908561	Sequence 908561
24	13	43.3	25	12	US-60-427-808-32047	Sequence 32047, A
25	13	43.3	25	12	US-60-427-808-31286	Sequence 31286, A
26	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
27	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
28	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
29	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
30	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
31	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
32	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
33	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
34	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
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44	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
45	13	43.3	25	12	US-60-427-808-122370	Sequence 122370

## ALIGNMENTS

RESULT 1

PCT-US03-04088-8

Sequence 8, Appl 1

GENERAL INFORMATION: PC/TUS0304088

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

APPLICANT: Beigelman, Leonard

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

FILE REFERENCE: 02-708-A (400/080)

CURRENT APPLICATION NUMBER: PCT/US03/04088

PRIOR FILING DATE: 2003-04-28

PRIOR APPLICATION NUMBER: US 60/396,600

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/409,293

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15

NUMBER OF SEQ ID NOS: 626

SOFTWARE: Patent version 3.2

SEQ ID NO: 8

LENGTH: 19

TYPE: RNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sRNA sense

OTHER INFORMATION: region

PCT-US03-04088-8

Query Match 63.3%; Score 19; DB 1; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.6;

Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;



Db           |||||||  
          29 TTTGCTTAC 19

Search completed: June 24, 2003, 16:52:45  
Job time : 789.207 secs

Trace considered overall poor quality  
Insert Length: 1314 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Quality

## FEATURES

Location/Qualifiers

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/clone="TWAGS:2264524"
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/classue_type="poorly differentiated endometrial
adenocarcinoma, 2 pooled tumours"
/lab_name="PH10b"
/note="Ntgi; uterus; Vector: PCMV-SPORT5; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.45 Kb. Life Technologies catalog #
11541-018"

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BASE COUNT	14 a	12 c	18 g	2 t
ORIGIN				

BASE COUNT  
ORIGIN

LaboratoryMouse DNA Resource (<http://www.jax.org/resources/documents/nhanes/>). The DNA was hydrodynamically sheared by repeated passages through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gll4721214[*gbl*Ap120721), a copy-number inducible derivative of p $\phi$ 120721. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      36.7%; Score 11; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels
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Qy	9	GGCCATTTT	19
Db	30	GGCCATTTT	20

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QY      1 GGGGTGGTGGC 11
          |||||
Db      24 GGGGTGGTGGC 34

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RESULT 14	LOCUS	DEFINITION
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	1M017215F	Mouse 10kb plasmid UUGC1M library M13
	clone UUGC1M017215 F,	DNA sequence.
		musculus genomic

RESULT 15					
AU105989/c					
AU105989	50 bp	mRNA	linear	EST 30-AUG-2001	
LOCUS					
DEFINITION	Sugano Homo sapiens cDNA library Homo sapiens cDNA clone				
	HS101865, mRNA sequence.				

ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus	
REFERENCE	1 (bases 1 to 46)
AUTHORS	Dunn, D., Acyga, A., Barber, M., Beacorn, T., Duvai, B., Hamil, C.,

ORGANISM	REFERENCE
<i>Homo sapiens</i>	1 (bases 1 to 50)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata	

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb

mapping of mRNA start sites

**JOURNAL**  
**COMMENT**  
Unpublished (2000)  
Contact: Robert B. Weiss

MEDLINE  
 21270072  
 Contact: Yutaka Suzuki  
 COMMENT

Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0172 row: 7 column: 15

Emura, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. *Gene* 200 (1-2), 149-156 (1997).

highly qualified sequence block: 46

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/clone_id="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-gold, T1-resistant, F-"
/notes="Vector: pMD29nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

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Query Match	36.7%	Score 11;	DB 9;	Length 50;
Best Local Similarity	100.0%	Pred. No. 1.6e+05;		
Matches	11;	Conservative	0;	Mismatches 0;
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				Gaps 0;
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; CURRENT APPLICATION NUMBER: US/10/330,872
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match      100.0%; Score 15; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATGAACG 15
Db      1 GCTCTAGATGAACG 15

RESULT 13
US-10-330-872A-5
; Sequence 5, Application US/10330872A
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-5

Query Match      100.0%; Score 15; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATGAACG 15
Db      1 GCTCTAGATGAACG 15

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; Sequence 36216, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36216
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-36216

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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      14 GCTCTAGATGAAC 1

RESULT 15
US-60-427-808-952738
; Sequence 952738, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 952738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-952738

Query Match      93.3%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATGAAC 14
Db      3 GCTCTAGATGAAC 16

Search completed: June 26, 2003, 04:15:19
Job time : 359.634 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1272.79 Seconds  
(without alignments)  
296.308 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15  
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Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 79: /cgn2\_6/ptodata/2/pna/US6035 COMB.seq.\*
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- 84: /cgn2\_6/ptodata/2/pna/US6040 COMB.seq.\*
- 85: /cgn2\_6/ptodata/2/pna/US6041 COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	15	100.0	15	11	US-08-770-564A-10
3	15	100.0	19	1	PCT-US97-23619-9
4	15	100.0	19	11	US-08-770-564A-9
5	15	100.0	25	16	US-09-250-336A-4
6	15	100.0	25	25	US-09-642-177-4
7	15	100.0	26	1	PCT-US96-14679-27
8	15	100.0	26	1	PCT-US96-14679A-27
9	15	100.0	26	1	PCT-US99-03302-4
10	15	100.0	26	1	PCT-US99-07533-4
11	15	100.0	26	1	PCT-US99-07533-4
12	15	100.0	26	7	US-08-272-102-23
13	15	100.0	26	7	US-08-387-524-19
14	15	100.0	26	8	US-08-472-802A-24
15	15	100.0	26	8	US-08-472-802B-24
16	15	100.0	26	8	US-08-482-115A-23
17	15	100.0	26	9	US-08-520-550-19
18	15	100.0	26	9	US-08-521-634-41
19	15	100.0	26	10	US-08-660-678-23
20	15	100.0	26	13	US-08-911-312-23
21	15	100.0	26	13	US-08-911-312A-23

22 Sequence 312, App  
23 Sequence 17, Appl  
24 Sequence 598, App  
25 Sequence 23, Appl  
26 Sequence 2, Appl  
27 Sequence 4, Appl  
28 Sequence 45, Appl  
29 Sequence 598, App  
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26 14 US-09-216-847-2  
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26 18 US-09-402-181A-598  
26 18 US-09-402-181B-598  
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30 9 US-08-510-736-5  
30 9 US-08-521-634-10  
30 11 US-08-770-564A-8  
30 21 US-09-540-119B-10  
30 28 US-09-717-828A-5

## ALIGNMENTS

RESULT 1  
PCT-US97-23619-10  
; Sequence 10, Application PC/TUS9723619  
; GENERAL INFORMATION:  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ron  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
; TITLE OF INVENTION: Against the RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,564A  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scorella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002200US  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-770-564A-10  
Query Match 100.0%; Score 15; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGANTGACG 15  
Db 1 GCTCTAGANTGACG 15  
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; Sequence 10, Application PC/TUS9723619  
; GENERAL INFORMATION:  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ron  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
; TITLE OF INVENTION: Against the RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,564A  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scorella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002200US  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-770-564A-10  
Query Match 100.0%; Score 15; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGANTGACG 15  
Db 1 GCTCTAGANTGACG 15

Sequence 9, Application PC/TUS9723619  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
NAME/KEY: -  
LOCATION: 1..19  
OTHER INFORMATION: /note= "oligo 21ab"  
PCT-US97-23619-9  
Query Match 100.0%; Score 15; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGAAATGAACG 15  
DB 1 GCTCTAGAAATGAACG 15  
RESULT 4  
US-08-770-564A-9  
Sequence 9, Application US/08770564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ron  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564A-9  
Query Match 100.0%; Score 15; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGAAATGAACG 15  
DB 1 GCTCTAGAAATGAACG 15  
RESULT 5  
US-09-250-336A-4  
Sequence 4, Application US/09250336A  
GENERAL INFORMATION:  
APPLICANT: STROVEL, Jeffrey W.  
APPLICANT: STAMBERG, Judith  
APPLICANT: ABRUZZO, Lynne V.  
APPLICANT: HIGHSMITH, Edward  
TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING  
TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS  
FILE REFERENCE: 10460-4 (210460.0004)  
CURRENT APPLICATION NUMBER: US/09/250,336A  
CURRENT FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: US 60/074,793  
PRIOR FILING DATE: 1998-02-16  
PRIOR APPLICATION NUMBER: PCT/US99/03302  
PRIOR FILING DATE: 1999-02-16  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 4  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer  
US-09-250-336A-4  
Query Match 100.0%; Score 15; DB 16; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGAAATGAACG 15  
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; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGHSWORTH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT APPLICATION NUMBER: US/09/642,177
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: R3c, Primer
US-09-642-177-4

Query Match      100.0%; Score 15; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAAATGAACG 15
        |||||
Db      4 GCTCTAGAAATGAACG 18

RESULT 7
PCT-US96-14679-27
; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679A-27

Query Match      100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAAATGAACG 15
        |||||
Db      5 GCTCTAGAAATGAACG 19

RESULT 8
PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679A-27

Query Match      100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAAATGAACG 15
        |||||
Db      5 GCTCTAGAAATGAACG 19

RESULT 9
PCT-US99-03302-4
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; Sequence 4, Application PC/TUS9903302
; GENERAL INFORMATION:
; APPLICANT: Strovel, Jeffrey W
; APPLICANT: Stamborg, Judith
; APPLICANT: Abruzzo, Lynne V
; APPLICANT: Highsmith, Edward
; TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening
; TITLE OF INVENTION: and Assessment of Disease Stage and Prognosis
; FILE REFERENCE: 1489JS 60/074,793
; CURRENT APPLICATION NUMBER: PCT/US99/03302
; CURRENT FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/074,793
; EARLIER FILING DATE: 1998-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn.Ver. 2.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: R3c,
; OTHER INFORMATION: synthesized, Gibco-BRL
PCT-US99-03302-4

Query Match          100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 10
PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match          100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 11
PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533A
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533A
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match          100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 12
US-08-272-102-23
; Sequence 23, Application US/08272102
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,102
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-272-102-23

Query Match          100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 13
US-08-387-524-19
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; Sequence 19, Application US/08387524
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,524
; FILING DATE: 13-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-387-524-19

Query Match 100.0%; Score 15; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 14
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

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; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-472-802A-24

Query Match 100.0%; Score 15; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 15
; Sequence 24, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994

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; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802B-24

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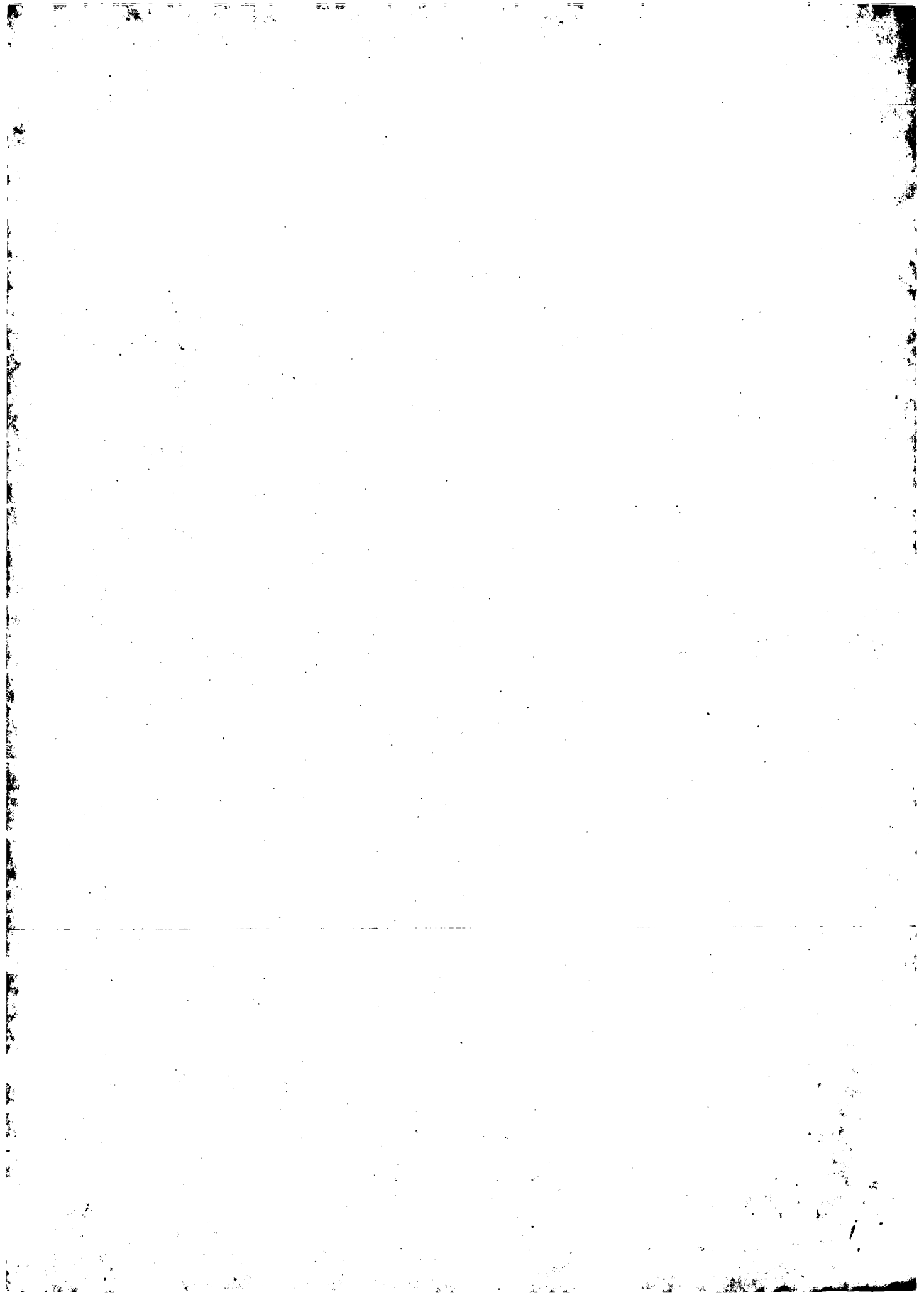
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Query Match      100.0%; Score 15; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATGAACG 15
        |||||
Db       5 GCTCTAGATGAACG 19

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Search completed: June 25, 2003, 06:20:26  
Job time : 1273.4 secs



GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 45.5976 Seconds  
(without alignments)  
482.732 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15

Sequence: 1 GCTCTAGATGAACG 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

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- 2: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	26	9	US-10-044-692-312
2	15	100.0	26	9	US-10-044-539-312
3	15	100.0	26	10	US-09-057-351-23
4	13	86.7	25	9	US-10-098-263B-118949
5	13	86.7	26	9	US-09-952-522B-19
6	13	86.7	26	10	US-09-844-006A-3
7	12.4	82.7	23	9	US-09-952-522B-31
8	12.4	82.7	26	9	US-10-011-366-16
9	12	80.0	23	9	US-09-952-522B-17
10	12	80.0	25	9	US-10-215-112-6862
11	12	80.0	25	9	US-10-098-263B-64498
12	11.8	78.7	25	9	US-10-215-112-12114
13	11.8	78.7	25	9	US-10-098-263B-74741
14	11.8	78.7	26	9	US-10-118-495-13
15	11.8	78.7	40	9	US-10-090-182A-255
16	11.8	78.7	41	9	US-10-090-182A-234
17	11.8	78.7	42	10	US-09-947-305-5
18	11.8	78.7	45	9	US-10-090-182A-235
19	11.8	78.7	45	9	US-10-090-182A-409

20	11.4	76.0	23	9	US-10-079-429-51	Sequence 51, Appl
21	11.4	76.0	24	9	US-10-245-813-2	Sequence 2, Appl
22	11.4	76.0	25	9	US-10-098-263B-4340	Sequence 4340, Ap
23	11.4	76.0	25	9	US-10-098-263B-30035	Sequence 30035, A
24	11.4	76.0	25	9	US-10-098-263B-33532	Sequence 33532, A
25	11.4	76.0	25	9	US-10-098-263B-34631	Sequence 34631, A
26	11.4	76.0	25	9	US-10-098-263B-118950	Sequence 118950,
27	11.4	76.0	29	10	US-09-905-992-5	Sequence 5, Appl
28	11.4	76.0	36	9	US-10-127-816-18	Sequence 18, Appl
29	11.4	76.0	46	9	US-09-876-082-58	Sequence 58, Appl
30	11.4	76.0	46	9	US-09-875-082-58	Sequence 58, Appl
31	11	73.3	21	9	US-09-997-868-13	Sequence 13, Appl
32	11	73.3	22	10	US-09-765-873A-5	Sequence 5, Appl
33	11	73.3	23	9	US-09-952-522B-9	Sequence 9, Appl
34	11	73.3	25	9	US-10-098-263B-10750	Sequence 10750, A
35	11	73.3	25	9	US-10-098-263B-44593	Sequence 44593, A
36	11	73.3	25	9	US-10-098-263B-44594	Sequence 44594, A
37	11	73.3	25	9	US-10-098-263B-104702	Sequence 104702,
38	11	73.3	26	9	US-10-118-495-11	Sequence 11, Appl
39	11	73.3	27	10	US-09-784-508-8	Sequence 8, Appl
40	11	73.3	29	9	US-10-162-223-2	Sequence 2, Appl
41	11	73.3	31	10	US-09-905-983-40	Sequence 40, Appl
42	11	73.3	33	9	US-09-848-616-12	Sequence 12, Appl
43	11	73.3	33	9	US-09-964-895-7	Sequence 7, Appl
44	11	73.3	33	9	US-09-964-895-15	Sequence 15, Appl
45	11	73.3	34	10	US-09-784-508-10	Sequence 10, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-044-692-312  
; Sequence 312, Application US/10044692  
; Publication No. US20030096344A1

GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.

Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 312:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Query Match 100.0%; Score 15; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15  
DB 5 GCTCTAGATGAACG 19

RESULT 2  
US-10-044-539-312  
Sequence 312, Application US/10044539  
Publication No. US20030100093A1  
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/044,539  
FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 312:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Query Match 100.0%; Score 15; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15  
DB 5 GCTCTAGATGAACG 19

RESULT 3

US-09-057-351-23  
Sequence 23, Application US/09057351  
Patent No. US20010034439A1  
GENERAL INFORMATION:

APPLICANT: Vilponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000821US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-057-351-23

Query Match 100.0%; Score 15; DB 10; Length 26;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 5 GCTCTAGAAATGAACG 19

RESULT 4

US-10-098-263B-118949/c  
; Sequence 118949, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 118949  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-118949

Query Match 86.7%; Score 13; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAAATGAACG 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 TCTAGAAATGAACG 8

RESULT 5

US-09-952-522B-19  
; Sequence 19, Application US/09952522B  
; Publication No. US20030082152A1  
; GENERAL INFORMATION:  
; APPLICANT: Katz, Adam J.  
; APPLICANT: Liull, Ramon  
; APPLICANT: Futrell, J. William  
; APPLICANT: Hedrick, Marc H.  
; APPLICANT: Benhaim, Prosper  
; APPLICANT: Lorenz, Hermann Peter  
; APPLICANT: Zhu, Min  
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
; FILE REFERENCE: 30448.77US11  
; CURRENT APPLICATION NUMBER: US/09/952,522B  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: PCT/US00/06232  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 60/123,711  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: 60/162,462  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Bone sialoprotein forward primer

US-09-952-522B-19

Query Match 86.7%; Score 13; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 13  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 GCTCTAGAAATGAACG 13

RESULT 6

US-09-844-006A-3  
; Sequence 3, Application US/09844006A  
; Patent No. US20020083496A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyatt, Sarah  
; APPLICANT: Tsou, Pei-Lan  
; APPLICANT: Robertson, Dominique  
; APPLICANT: Boss, Wendy  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES  
; FILE REFERENCE: 5051.503  
; CURRENT APPLICATION NUMBER: US/09/844,006A  
; PRIOR FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: 60/200,233  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(28)  
; OTHER INFORMATION: Synthetic Oligonucleotide.  
US-09-844-006A-3

Query Match 86.7%; Score 13; DB 10; Length 28;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 13  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 GCTCTAGAAATGAACG 13

RESULT 7

US-09-952-522B-31  
; Sequence 31, Application US/09952522B  
; Publication No. US20030082152A1  
; GENERAL INFORMATION:  
; APPLICANT: Katz, Adam J.  
; APPLICANT: Liull, Ramon  
; APPLICANT: Futrell, J. William  
; APPLICANT: Hedrick, Marc H.  
; APPLICANT: Benhaim, Prosper  
; APPLICANT: Lorenz, Hermann Peter  
; APPLICANT: Zhu, Min  
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
; FILE REFERENCE: 30448.77US11  
; CURRENT APPLICATION NUMBER: US/09/952,522B  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: PCT/US00/06232  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 60/123,711  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: 60/162,462  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 23





QY 1 GCTCTAGATGA 12  
|||||  
Db 15 GCTCTAGATGA 4

## RESULT 11

US-10-098-263B-64498/c  
; Sequence 64498, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 64498  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-64498

Query Match 80.0%; Score 12; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGATGAAC 14  
|||||  
Db 23 TCTAGATGAAC 12

## RESULT 12

US-10-215-112-12114/c  
; Sequence 12114, Application US/10215112  
; Publication No. US20030082596A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:  
; TITLE OF INVENTION: Test3  
; FILE REFERENCE: 3119  
; CURRENT APPLICATION NUMBER: US/10/215,112  
; CURRENT FILING DATE: 2002-08-08  
; NUMBER OF SEQ ID NOS: 14936  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12114  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-215-112-12114

Query Match 78.7%; Score 11.8; DB 9; Length 25;  
Best Local Similarity 86.7%; Pred. No. 2.1e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15  
|||||  
Db 21 GCTCTAGACGGACG 7

## RESULT 13

US-10-098-263B-74741/c  
; Sequence 74741, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 74741  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-74741

Query Match 78.7%; Score 11.8; DB 9; Length 25;  
Best Local Similarity 86.7%; Pred. No. 2.1e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15  
|||||  
Db 22 GCTCTAGATGAACG 8

## RESULT 14

US-10-118-495-13  
; Sequence 13, Application US/10118495  
; Publication No. US20030074688A1  
; GENERAL INFORMATION:  
; APPLICANT: Benning, Christoph  
; APPLICANT: Riekhof, Wayne  
; APPLICANT: Klug, Rouven  
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids  
; FILE REFERENCE: MSU-06897  
; CURRENT APPLICATION NUMBER: US/10/118,495  
; CURRENT FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: 60/283,812  
; PRIOR FILING DATE: 2001-04-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 13  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-118-495-13

Query Match 78.7%; Score 11.8; DB 9; Length 26;  
Best Local Similarity 86.7%; Pred. No. 2.1e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15  
|||||  
Db 1 GCTCTAGATGGCCG 15

## RESULT 15

US-10-090-182A-255  
; Sequence 255, Application US/10090182A  
; Publication No. US20030103936A1  
; GENERAL INFORMATION:  
; APPLICANT: Abrams, Mark A.

Bauer, S. C.  
Braford-Goldberg, Sarah R.  
Caparon, Mairé H.  
Easton, Alan M.  
Klein, Barbara K.  
McKearn, John P.  
Olins, Peter O.  
Paik, Kuman  
Thomas, John W.

TITLE OF INVENTION: Methods of Ex-vivo Expansion of  
Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple  
Mutation Polypeptides  
NUMBER OF SEQUENCES: 415

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: S. Christopher Bauer, Pharmacia Corp  
 STREET: 800 N. Lindbergh Blvd.  
 CITY: St. Louis  
 STATE: Missouri  
 COUNTRY: USA  
 ZIP: 63167  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/10/090,182A  
 FILING DATE: 03-Apr-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/764,114  
 FILING DATE: 09-DEC-1996  
 APPLICATION NUMBER: US 07/981,044  
 FILING DATE: 24-NOV-1992  
 APPLICATION NUMBER: PCT/US93/11197  
 FILING DATE: 22-NOV-1993  
 APPLICATION NUMBER: 08/411,795  
 FILING DATE: 04-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: S. Christopher Bauer  
 REGISTRATION NUMBER: 42,305  
 REFERENCE/DOCKET NUMBER: C2713/12  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (636)737-6257  
 TELEFAX: (736)737-6257  
 INFORMATION FOR SEQ ID NO: 255:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 40 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (synthetic)  
 SEQUENCE DESCRIPTION: SEQ ID NO: 255:  
 US-10-090-182A-255

Query Match 78.7%; Score 11.8; DB 9; Length 40;  
 Best Local Similarity 86.7%; Pred. No. 2.1e+03;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GCTCTAGATGACG 15  
 Db 12 GCTCTATATGATCG 26

Search completed: June 25, 2003, 22:25:07  
 Job time : 45.5976 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 46.9721 Seconds  
(without alignments)  
195.867 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30  
Sequence: 1 GCTTAGAATGAACGGTGGAGGCGGCAGG 30

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents\_NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	US-08-770-565-8	Sequence 8, Appli
2	29	96.7	30	US-08-833-377-6	Sequence 6, Appli
3	23	76.7	27	US-08-770-565-26	Sequence 26, Appli
4	22	73.3	26	US-08-330-123A-23	Sequence 23, Appli
5	22	73.3	26	US-08-482-115B-23	Sequence 23, Appli
6	22	73.3	26	US-08-660-678A-23	Sequence 23, Appli
7	22	73.3	26	US-08-710-249-26	Sequence 26, Appli
8	22	73.3	26	US-08-485-778-19	Sequence 19, Appli
9	22	73.3	26	US-08-472-802C-24	Sequence 24, Appli
10	22	73.3	26	US-08-520-550A-19	Sequence 19, Appli
11	22	73.3	26	US-08-998-443-23	Sequence 23, Appli
12	22	73.3	26	US-08-974-549A-598	Sequence 598, Appli
13	22	73.3	26	US-09-060-523-23	Sequence 23, Appli
14	22	73.3	26	US-09-220-157A-26	Sequence 26, Appli
15	22	73.3	26	US-09-286-959B-4	Sequence 4, Appli
16	22	73.3	26	US-09-580-517-23	Sequence 23, Appli
17	19	63.3	19	US-08-770-565-9	Sequence 9, Appli
18	15	50.0	15	US-08-770-565-10	Sequence 10, Appli
19	14	46.7	27	US-08-630-172-24	Sequence 24, Appli
20	14	46.7	27	US-09-375-419-24	Sequence 24, Appli
21	13	43.3	18	US-08-974-549A-543	Sequence 543, Appli
22	12	40.0	26	US-08-480-604A-16	Sequence 16, Appli
23	12	40.0	26	US-08-405-496A-16	Sequence 16, Appli
24	12	40.0	26	US-08-915-136-16	Sequence 16, Appli
25	12	40.0	26	US-08-957-310-16	Sequence 16, Appli
26	12	40.0	30	US-08-349-006-3	Sequence 3, Appli
27	12	40.0	30	US-08-495-743-50	Sequence 50, Appli

28	12	40.0	30	1	US-08-495-739-50	Sequence 50, Appli
29	12	40.0	30	1	US-08-495-741-50	Sequence 50, Appli
30	12	40.0	30	4	US-08-062-023-50	Sequence 50, Appli
31	12	40.0	30	5	PCT-US94-02107-3	Sequence 3, Appli
32	12	40.0	33	3	US-08-630-172-22	Sequence 22, Appli
33	12	40.0	33	4	US-03-375-419-22	Sequence 22, Appli
34	11	36.7	11	2	US-08-770-565-11	Sequence 11, Appli
35	11	36.7	15	1	US-08-363-240A-659	Sequence 659, Appli
36	11	36.7	15	1	US-08-363-240A-660	Sequence 660, Appli
37	11	36.7	18	1	US-08-363-240A-1203	Sequence 1203, Appli
38	11	36.7	20	3	US-08-974-180-4	Sequence 4, Appli
39	11	36.7	21	5	US-08-026-143B-13	Sequence 13, Appli
40	11	36.7	21	5	PCT-US92-10621-13	Sequence 13, Appli
41	11	36.7	21	5	PCT-US94-02233-13	Sequence 13, Appli
42	11	36.7	22	4	US-09-627-216A-5	Sequence 5, Appli
43	11	36.7	23	3	US-08-973-068-46	Sequence 46, Appli
44	11	36.7	24	4	US-08-697-610-11	Sequence 11, Appli
45	11	36.7	24	4	US-08-349-357-11	Sequence 11, Appli

## ALIGNMENTS

RESULT 1  
US-08-770-565-8  
; Sequence 8, Application US/08770565  
; Patent No. 5846723  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; TITLE OF INVENTION: Telomerase  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-00230005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-565-8

Query Match 100.0%; Score 30; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTTAGAATGAACGGTGGAGGCGGCAGG 30

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Db      1  GCTCTAGATGAACGGTGGGAAGCGCGCAGG 30
|||||
RESULT 2
US-08-833-377-6
; Sequence 6, Application US/08833377
; Patent No. 5968506
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; APPLICANT: Kealey, James T.
; TITLE OF INVENTION: Purified Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/833,377
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/510,736
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = 5' biotinylated guanosine"
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..30
; OTHER INFORMATION: /note= "Oligo 14"
US-08-833-377-6
Query Match      96.7%; Score 29; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  CTCTAGATGAACGGTGGGAAGCGCGCAGG 30
|||||
Db      2  CTCTAGATGAACGGTGGGAAGCGCGCAGG 30
|||||
RESULT 3
US-08-770-565-26
; Sequence 26, Application US/08770565
; Patent No. 5946723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-26
Query Match      76.7%; Score 23; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCTAGATGAACGGTGGGAAGG 23
|||||
Db      5  GCTCTAGATGAACGGTGGGAAGG 27
|||||
RESULT 4
US-08-330-123A-23
; Sequence 23, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match      73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAATGAACGGTGGAG 22
      |||||
DB      5 GCTCTAGAATGAACGGTGGAG 26

RESULT 5
US-08-482-115B-23
; Sequence 23, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115B
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match      73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAATGAACGGTGGAG 22
      |||||
DB      5 GCTCTAGAATGAACGGTGGAG 26
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; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match      73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAATGAACGGTGGAG 22
      |||||
DB      5 GCTCTAGAATGAACGGTGGAG 26

RESULT 6
US-08-660-678A-23
; Sequence 23, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,678A
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match      73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAATGAACGGTGGAG 22
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Db 5 GCTCTAGATGAACGGTGGGAAG 26

RESULT 7  
US-08-710-249-26  
; Sequence 26, Application US/08710249  
; Patent No. 5858777  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Methods and Reagents for Regulating  
; TITLE OF INVENTION: Telomere Length and Telomerase Activity  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,249  
FILING DATE: 13-SEP-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: US 08/583,808  
FILING DATE: 05-JAN-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/003,492  
FILING DATE: 08-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001220US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-710-249-26

Query Match 73.3%; Score 22; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAAG 22  
Db 5 GCTCTAGATGAACGGTGGGAAG 26

RESULT 8  
US-08-485-778-19  
; Sequence 19, Application US/08485778  
; Patent No. 5876979  
; GENERAL INFORMATION:  
; APPLICANT: Andrews, William H.  
; APPLICANT: Avilion, Ariel Athena  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Greider, Carol

APPLICANT: Marhuenda, Maria Antonia Blasco  
APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,778  
FILING DATE: 07-JE-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/387,524  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A4  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-778-19

Query Match 73.3%; Score 22; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAAG 22  
Db 5 GCTCTAGATGAACGGTGGGAAG 26

RESULT 9  
US-08-472-802C-24  
; Sequence 24, Application US/08472802C  
; Patent No. 5958680  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,802C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
FILING DATE: 27-OCT-1994  
APPLICATION NUMBER: US 08/330,123  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000820  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-472-802C-24

Query Match 73.3%; Score 22; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22  
|||||  
DB 5 GCTCTAGATGAACGGTGAAG 26

RESULT 10  
US-08-520-550A-19  
Sequence 19, Application US/08520550A  
Patent No. 6013468  
GENERAL INFORMATION:  
APPLICANT: Andrews, William H.  
APPLICANT: Avillion, Ariel A.  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Greider, Carol  
APPLICANT: Marhuenda, Maria A. B.  
APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,550A  
FILING DATE: 29-AUG-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/387,524  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A3B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-520-550A-19

Query Match 73.3%; Score 22; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00051;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22  
|||||  
DB 5 GCTCTAGATGAACGGTGAAG 26

RESULT 11  
US-08-998-443-23  
Sequence 23, Application US/08998443  
Patent No. 6054575  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,443  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,678  
FILING DATE: 05-JUN-1996  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000811US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-998-443-23

Query Match 73.3%; Score 22; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGGGAAG 22
DB 5 GCTCTAGAAATGAACGGTGGGAAG 26

RESULT 12
US-08-974-549A-598
; Sequence 598, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885

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; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..26
; OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598

Query Match 73.3%; Score 22; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGGGAAG 22
DB 5 GCTCTAGAAATGAACGGTGGGAAG 26

RESULT 13
US-09-060-523-23
; Sequence 23, Application US/09060523
; Patent No. 6258535
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,523
; FILING DATE: 14-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,678
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000813US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

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INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-09-060-523-23

Query Match 73.3%; Score 22; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.00051;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22

DB 5 GCTCTAGATGAACGGTGAAG 26

RESULT 14

US-09-220-157A-26

Sequence 26, Application US/09220157A

Patent No. 6300110

GENERAL INFORMATION:

APPLICANT: Villegonteau, Bryant

APPLICANT: Feng, Junli

APPLICANT: Adams, William H.

APPLICANT: Adams, Robert R.

TITLE OF INVENTION: Methods and Reagents for Regulating

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/220,157A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/710,249

FILING DATE: 13-SEP-1996

APPLICATION NUMBER: US 08/583,808

FILING DATE: 05-JAN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/003,492

FILING DATE: 08-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-001220US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-09-220-157A-26

Query Match 73.3%; Score 22; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.00051;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22

DB 5 GCTCTAGATGAACGGTGAAG 26

RESULT 15

US-09-286-959B-4

Sequence 4, Application US/09286959B

Patent No. 6300131

GENERAL INFORMATION:

APPLICANT: Johns Hopkins University

APPLICANT: Greider, Carol W.

APPLICANT: Le, Siyuan

TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS

FILE REFERENCE: 07265/157001

CURRENT APPLICATION NUMBER: US/09/286,959B

PRIOR FILING DATE: 1999-04-06

PRIOR APPLICATION NUMBER: 60/080,783

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 26

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer

US-09-286-959B-4

Query Match 73.3%; Score 22; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.00051;

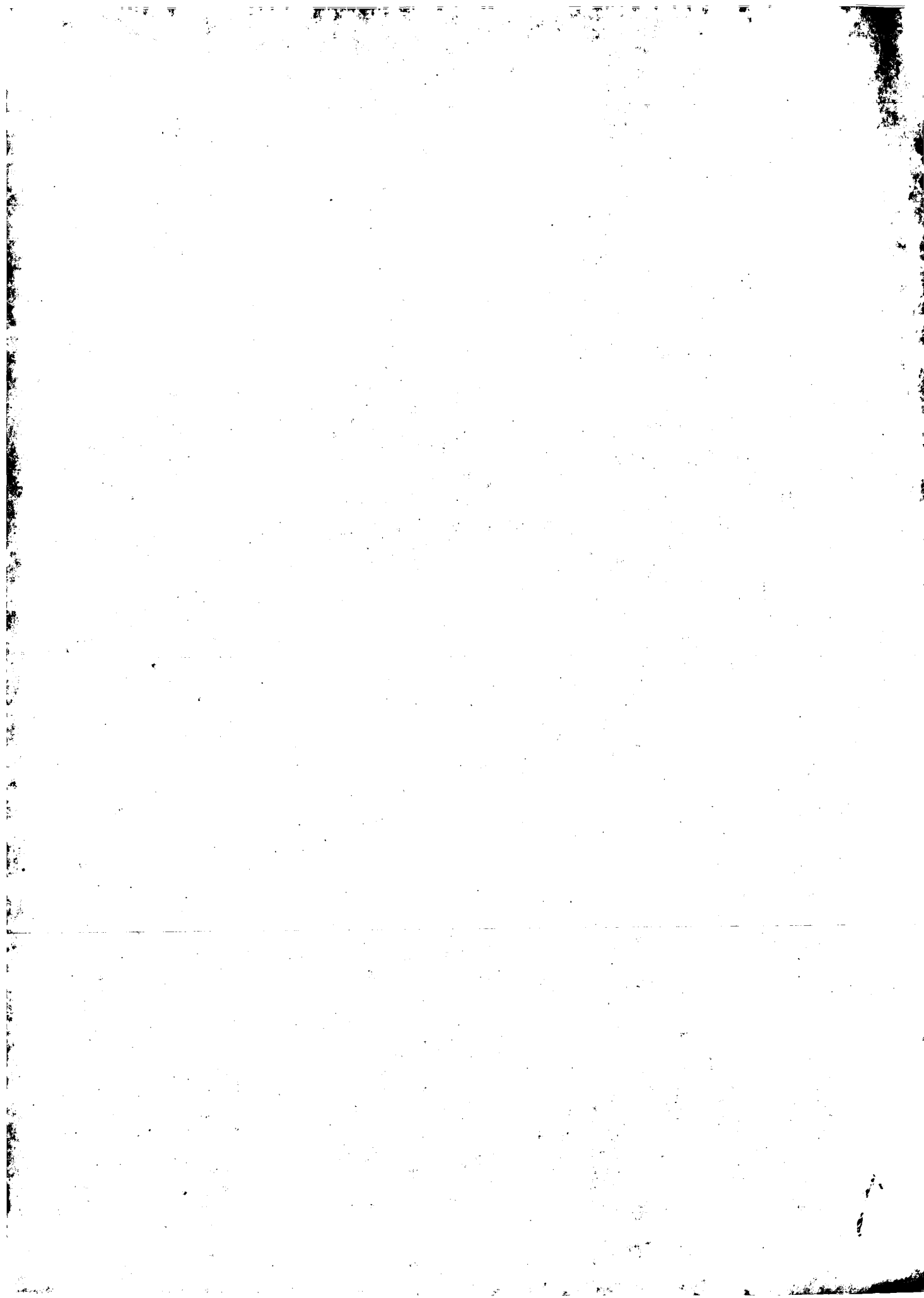
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22

DB 5 GCTCTAGATGAACGGTGAAG 26

Search completed: June 23, 2003, 10:17:06

Job time : 46.9721 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 199.363 Seconds  
(without alignments)  
338.880 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30  
Sequence: 1 GCTCTAGTAATGAACGGTGGAGCGCGCAGG 30

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_101002.\*

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- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*
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- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*
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- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	19 AAV63649	Antisense oligonuc
2	30	100.0	30	19 AAV41175	RNA component of h
3	30	100.0	30	20 AAZ23631	Human clone 28-1 t
4	30	100.0	30	22 AAS09476	Antisense oligonuc
5	30	100.0	30	23 AAS15928	Human telomerase p
6	30	100.0	30	24 ABA91517	Oligonucleotide us
7	23	76.7	27	19 AAV41193	RNA component of h
8	23	76.7	27	24 ABA95497	Human telomerase R
9	22	73.3	25	20 AAZ08704	Human telomerase R

10	22	73.3	26	17	AAT10304	RNA component of h	
11	22	73.3	26	17	AAT10299	RNA component of h	
12	22	73.3	26	17	AAT11044	Primer for product	
13	22	73.3	26	18	AAT58811	Human telomerase p	
14	22	73.3	26	19	AAV19489	Human hTR gene RT-	
15	22	73.3	26	19	AAV17033	Telomerase PCR pri	
16	22	73.3	26	20	AAX90788	Human telomerase R	
17	22	73.3	26	20	AAX77402	Human telomerase R	
18	22	73.3	26	20	AAX01542	PCR primer for Hum	
19	22	73.3	26	21	AAA88250	Human telomerase R	
20	22	73.3	26	24	ABK48024	Human telomerase-a	
21	22	73.3	26	24	ABD24246	Human telomerase (	
22	19	63.3	19	19	AAV41176	RNA component of h	
23	15	50.0	15	19	AAV41177	RNA component of h	
24	15	50.0	15	23	AAS15927	Human telomerase p	
25	15	50.0	15	23	AAS15931	Human telomerase p	
26	15	50.0	15	23	AAS15932	Human telomerase p	
27	14	46.7	27	18	AAT97049	Sense primer for h	
28	13	43.3	13	23	AAS15921	Human telomerase p	
29	13	43.3	13	23	AAS15922	Human telomerase p	
30	13	43.3	13	23	AAS15923	Human telomerase p	
31	13	43.3	13	23	AAS15924	Human telomerase p	
32	13	43.3	13	23	AAS15925	Human telomerase p	
33	13	43.3	13	23	AAS15926	Human telomerase p	
34	13	43.3	13	23	AAS15930	Human telomerase p	
35	13	43.3	28	24	ABA04366	CRT C-domain-green	
36	13	43.3	32	21	AAA46113	Human GPCR TDAG8(I	
C	37	13	43.3	46	22	AAS11788	PCR primer #1 used
	38	12	40.0	17	22	AAF57369	Murine Cdc25A intr
	39	12	40.0	24	22	AAI62045	Soybean 318013 reg
C	40	12	40.0	24	24	ABQ03136	Oligonucleotide ad
C	41	12	40.0	24	24	ABQ10149	Oligonucleotide ad
KW	42	12	40.0	24	24	ABQ10190	Oligonucleotide ad
XX	43	12	40.0	26	17	AAT29258	C. difficile toxin
OS	44	12	40.0	26	19	AAV30567	Clostridium diffic
XX	45	12	40.0	26	21	ABK09963	Novel recombinant
ALIGNMENTS							
RESULT 1							
AAV63649							
ID	AAV63649 standard; DNA; 30 BP.						
AC	AAV63649;						
XX							
DT	15-FEB-1999 (first entry)						
XX	Antisense oligonucleotide 14 for human telomerase RNA component.						
DE	Human; telomerase RNA component; anticancer therapy; purification;						
KW	assay; vaccine; cancer; antisense oligonucleotide; ss.						
XX	Synthetic.						
OS	Homo sapiens.						
XX							
Key	Location/Qualifiers						
modified_base	1						
FT	/*tag= a						
FT	/note= "biotinylated"						
XX							
PN	WO9845450-A1.						
XX							
PD	15-OCT-1998.						
XX							
XX	04-APR-1997; 97WO-US06012.						
XX							
PR	04-APR-1997; 97WO-US06012.						
XX							
PA	(GERO-) GERON CORP.						
XX							
PI	Atkinson EM, Kealey JT, Lichtsteiner SP, Pruзан RA:						

## ALIGNMENTS

RESULT 1	
AAV63649	
ID	AAV63649 standard; DNA; 30 BP.
XX	
AC	AAV63649;
XX	
DT	15-FEB-1999 (first entry)
XX	
DE	Antisense oligonucleotide 14 for human telomerase RNA component.
XX	
KW	Human; telomerase RNA component; anticancer therapy; purification;
KW	assay; vaccine; cancer; antisense oligonucleotide; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	modified_base 1
FT	/*tag= a
FT	/note= "biotinylated"
XX	
PN	WO9845450-A1.
XX	
PD	15-OCT-1998.
XX	
PF	04-APR-1997; 97WO-US06012.
XX	
PR	04-APR-1997; 97WO-US06012.
XX	
PA	(GERO-) GERON CORP.
XX	
PI	Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA;

PI Vasserot AP, Weinrich SL;

XX WPI; 1998-594485/50.

XX Purification of telomerase on affinity material - useful for, e.g.

PT diagnosis and treatment of cancer

XX Disclosure; Page 24; 76pp; English.

XX The present sequence represents an antisense oligonucleotide  
CC directed against the human telomerase RNA component gene sequences.  
CC The oligonucleotide can be used as an affinity agent in the methods of  
CC the invention, which are used to purify human telomerase. The methods  
CC involve the use of several sequential steps, including the use of two  
CC matrices that bind molecules bearing negative charges, a matrix that  
CC binds molecules bearing positive charges, an affinity purification step  
CC and a size separation. Telomerase is a particular target of anticancer  
CC therapies, and is useful in assays for characterizing (pre)cancerous  
CC cells. Telomerase can also be used to screen for specific modulators,  
CC for biochemical analysis of its activity, and in preparation of  
CC antibodies. Fragments of telomerase, or nucleic acid encoding them,  
CC are used in vaccines, and for treating over expression of telomerase,  
CC particularly in cancer.

SQ Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 19; Length 30;  
Best Local Similarity 100.0%; Fred. No. 7.6e-08;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATGACGGTGGAGCGGCAGG 30

Db 1 GCTCTAGATGACGGTGGAGCGGCAGG 30

RESULT 2

AAV41175  
ID AAV41175 standard; DNA; 30 BP.

XX AAV41175;

DT 08-OCT-1998 (first entry)

XX RNA component of human telomerase (hTR) antisense oligo 21.

XX RNA component; human telomerase; antisense oligonucleotide; infection;  
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;  
KW contraception; sterilization; immunosuppression; therapeutic; hTR;  
KW immune system down-regulation; anti-inflammatory therapy; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9828442-A1.

PN 02-JUL-1998.

XX 19-DEC-1997; 97WO-US23619.

XX 20-DEC-1996; 96US-0770565.

PR 20-DEC-1996; 96US-0770564.

XX (GERO-) GERON CORP.

XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;

XX WPI; 1998-377670/32.

XX New polynucleotide(s) anti-sense to human telomerase - used for  
PT detecting or inhibiting human telomerase, e.g. for treating cancers,  
PT contraception, immuno-suppression or treating infection

XX Claim 11; Page 65; 80pp; English.

XX Sequences shown in AAV41169 to AAV41181 represent antisense  
CC oligonucleotides to the RNA component of human telomerase (hTR). These  
CC antisense oligonucleotides specifically hybridize to a nucleotide  
CC sequence within an accessible region of the hTR, but that does not  
CC hybridize to a sequence within the template region of hTR. These  
CC oligonucleotides may specifically be used for detection of an RNA  
CC component of human telomerase in a sample. This is useful for diagnosing  
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),  
CC and providing prognosis for a cancer patient. The inhibitory  
CC oligonucleotides can inhibit the telomerase activity level in a cell by  
CC interfering with transcription of the RNA component, decreasing the  
CC half-life of the telomerase RNA component transcript, inhibiting assembly  
CC of the RNA component into the telomerase holoenzyme, or inhibiting the  
CC polymerase activity of telomerase. These antisense oligonucleotides can  
CC be used for inhibiting telomerase activity in both cultured cells and in  
CC cells in vivo. They can be used in therapeutics for treating or  
CC preventing cancer, for contraception or sterilization, for  
CC immunosuppression, and for selectively down-regulating specific branches  
CC of the immune system, e.g. a specific subset of T-cells, in  
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,  
CC parasites or fungi.

SQ Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 19; Length 30;

Best Local Similarity 100.0%; Fred. No. 7.6e-08; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATGACGGTGGAGCGGCAGG 30

Db 1 GCTCTAGATGACGGTGGAGCGGCAGG 30

RESULT 3

AAZ23631  
ID AAZ23631 standard; DNA; 30 BP.

XX AAZ23631;

DT 07-JAN-2000 (first entry)

XX Human clone 28-1 telomerase oligonucleotide oligo-14.

XX Telomerase; human; immune response; cancer; vaccine; treatment;  
KW disease; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT modified\_base 1  
FT /tag= a  
FT /note= "5'-biotinylated guanosine"

XX US9568506-A.

XX 19-OCT-1999.

XX 04-APR-1997; 97US-0833377.

XX 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

XX Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;

PI Vasserot AP;

XX WPI; 1999-590379/50.

XX Compositions comprising human telomerase, useful for treating diseases  
PT associated with overexpression of telomerase e.g. cancer -

PS Disclosure; Column 45-46; 34pp; English.

CC This invention describes a novel composition comprising human telomerase having at least 2000-fold (preferably at least 6000-fold) increased relative purity compared with crude extract of cells from adenovirus-transformed kidney cell line. The composition is useful for eliciting an immune response in animals and may therefore be used as a vaccine for treating diseases associated with the overexpression of telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used in the isolation of human clone 28-1 which contains a fragment of the human telomerase described in the method of the invention.

XX

SQ Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 20; Length 30;  
Best Local Similarity 100.0%; Pred. No. 7.6e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCGGAGG 30  
|||||  
Db 1 GCTCTAGATGAACGGTGGAGCGGCGGAGG 30

RESULT 4

AAS09476

ID AAS09476 standard; DNA; 30 BP.

XX

AC AAS09476;

XX

DT 24-OCT-2001 (first entry)

XX

DE Antisense oligonucleotide for human telomerase, Oligo 14.

XX

KW Human; Telomerase; vaccine; antibody; cancer; BP2H;  
KW nucleolin; antisense oligonucleotide; Oligo 14; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT modified\_base 1

FT /\*tag= a

FT /\*mod\_base= G

FT /\*note= "G is biotinylated"

XX

PN US6261556-B1.

XX

PD 17-JUL-2001.

XX

PF 18-OCT-1999; 99US-0420056.

XX

PR 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

XX

PA (GERO-) GERON CORP.

XX

PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA;  
PI Kealey JT;

PI WPI; 2001-450477/48.

DR

XX

PT Purified human telomerase, useful for inducing immune response in animals, comprises several thousand folds increased purity compared with cytoplasmic crude cell preparations -

PT

PS Disclosure; Column 18; 29pp; English.

XX

CC The sequence represents a biotinylated antisense oligonucleotide used in the purification of human telomerase. The invention relates to a purified human telomerase core enzyme protein comprising 2000-fold increased purity compared with a crude extract of cells from adenovirus-transformed kidney cell line (293 cells) and when associated with telomerase RNA component has DNA polymerase activity and a molecular weight of 200-2000 kilo Daltons (kDa). The purified telomerase is useful

CC

CC for inducing a humoral or cell-mediated immune response in an animal.

CC Purified telomerase or immunogenic fragments are useful as vaccines for treating diseases associated with over-expression of telomerase, such as cancer and for producing antibodies that recognize telomerase, which are useful as affinity agents in isolating the proteins and for detecting the presence of proteins in a sample, such as cell or tissue. Identification of telomerase aids in diagnosis of cancer or pre-cancerous states.

CC Telomerase and/or telomerase associated proteins are also useful for screening compounds to identify agents that alter the association of telomerase-associated proteins, such as nucleolin or BP2H with telomerase.

XX

SQ Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 30;  
Best Local Similarity 100.0%; Pred. No. 7.6e-08;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCGGAGG 30  
|||||  
Db 1 GCTCTAGATGAACGGTGGAGCGGCGGAGG 30

RESULT 5

AAS15928

ID AAS15928 standard; DNA; 30 BP.

XX

AC AAS15928;

XX

DT 27-FEB-2002 (first entry)

XX

DE Human telomerase polynucleotide inhibitor #9.

XX

KW Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;  
KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;  
KW fertility; inflammatory condition; tumour; cancer; veterinary;  
KW immunosuppression; telomerase inhibitor; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1.30

FT /\*tag= a

FT /\*mod\_base= OTHER

FT /\*note= "N3'-PS' phosphoramidate linkages"

XX

PN WO200174136-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US10476.

XX

PR 31-MAR-2000; 2000US-0540119.

XX

PA (GERO-) GERON CORP.

XX

PI Gryaznov SM, Pruzan R, Weinrich SL;  
PI WPI; 2001-656955/75.

DR

XX

PT New polynucleotide useful for inhibiting telomerase activity in cells, or for treating telomerase-mediated condition or disease, such as cancers, tumours, Hodgkin's disease, or inflammatory conditions -

PT

PS Example 3; Page 32; 48pp; English.

XX

CC The invention relates to polynucleotide inhibitors (I) and methods for inhibiting telomerase activity. (I) are useful in inhibiting telomerase activity and proliferation of a telomerase positive cell, and in manufacturing a medicament for inhibiting telomerase activity in a cell and in treating telomerase-mediated condition or disease, such as adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,

CC Hodgkin's disease, fertility and inflammatory conditions. (1) are also  
 CC useful in treating a tumour or in manufacturing a medicament for the  
 CC treatment of tumour. The polynucleotide inhibitors may also be used in  
 CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase  
 CC activity in cells in vivo is useful in prophylactic and therapeutic  
 CC methods of treating cancer and other disorders involving inappropriate  
 CC expression of telomerase, and in treating veterinary proliferative  
 CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful  
 CC for immunosuppression and for selectively down-regulating specific  
 CC branches of the immune system. The present sequence represents  
 CC human telomerase polynucleotide inhibitor #9, as described in the  
 CC method of the invention.

CC Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 23; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-08;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30  
 DB 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30

# RESULT 6

ID ABA91517 standard; DNA; 30 BP.

AC ABA91517;

DT 18-APR-2002 (first entry)

DE Oligonucleotide used in gold nanoparticle complex.

KW Silver staining; signal detection; nanoparticle; diagnosis;  
 KW screening; ss.

OS Synthetic.

Key Location/Qualifiers  
 modified\_base 1..30  
 /\*tag= a  
 /note= "phosphoramidate linkage"

FT WO200204681-A2.  
 PN (NANO-) NANOSPHERE INC.

PD 17-JAN-2002.

PF 11-JUL-2001; 2001WO-US21846.

PR 11-JUL-2000; 2000US-217782P.

PA (NANO-) NANOSPHERE INC.

PI Letsinger RL, Garimella V;

DR WPI; 2002-164654/21.

PT Amplifying signal by contacting nanoparticles (N) having bound  
 PT oligonucleotides to silver deposited on substrate to form N-silver  
 PT sandwich that is contacted with silver, reducing agent to form  
 PT silver-N-silver sandwich

PS Example 1; Page 12; 24pp; English.

CC The present sequence is that of an oligonucleotide prepared using  
 CC phosphoramidite chemistry. A nanoparticle conjugate was prepared  
 CC by joining the 5'-mercaptoalkyl oligonucleotide to gold  
 CC nanoparticles. The nanoparticle conjugate was used to enhance  
 CC the sandwich amplification of a silver signal on glass slides  
 CC containing silver spots from oligonucleotide assays performed  
 CC using silver staining. This illustrated the method of the  
 CC invention, which is based on the discoveries that: (1) gold

CC nanoparticles coated with oligonucleotides bind to silver that has  
 CC previously been deposited on gold nanoparticle-oligonucleotide  
 CC conjugates immobilised by hybridisation on a glass substrate or  
 CC plate; and (2) that the gold-nanoparticle-oligonucleotide-silver-gold  
 CC oligonucleotide structures function as a catalyst for the further  
 CC deposition of silver ions. The discoveries were applied to a method  
 CC for amplifying signal by enhancing silver deposition in detecting  
 CC systems where the formation of a silver spot serves as a reporter  
 CC for the presence of a molecule, including proteins, nucleic acids  
 CC and small molecules. The detecting systems include detection of  
 CC molecules in situ (e.g. on cells or in a tissue sample) and assays  
 CC where the target molecule is bound to a substrate or is captured by  
 CC a capture molecule. The method has special utility in increasing  
 CC the signal strength in diagnostic and screening applications  
 CC involving detection of target molecules arrayed at discrete  
 CC positions on a solid surface. It provides a means for greatly  
 CC enhancing the sensitivity of tests carried out on microarrays or  
 CC microchips. The method is simple, economical, and provides a large  
 CC enhancement in signal and sensitivity.

CC Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 24; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-08;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30

DB 1 GCTCTAGATGAACGGTGGAGCGCGCAGG 30

# RESULT 7

AAV41193 standard; DNA; 27 BP.

AC AAV41193;

DT 08-OCT-1998 (first entry)

DE RNA component of human telomerase (hTR) amplifying reverse primer.

KW RNA component; human telomerase; antisense oligonucleotide; infection;  
 KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;  
 KW contraception; sterilisation; immunosuppression; therapeutic; hTR;  
 KW immune system down-regulation; anti-inflammatory therapy; RT-PCR;  
 KW primer; ss.

OS Synthetic.

OS Homo sapiens.

PN WO9828442-A1.

PD 02-JUL-1998.

PF 19-DEC-1997; 97WO-US23619.

PR 20-DEC-1996; 96US-0770565.

PR 20-DEC-1996; 96US-0770564.

PA (GERO-) GERON CORP.

PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;

DR WPI; 1998-377670/32.

PT New polynucleotide(s) anti-sense to human telomerase - used for  
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,  
 PT contraception, immuno-suppression or treating infection

PS Claim 65; Page 75; 80pp; English.

CC This primer is used for the RT-PCR amplification of an RNA component of  
 CC human telomerase (hTR). This is used in the method of invention of

CC determining the amount of hTR in a sample. The method comprises  
 CC amplifying a sequence of hTR and a control polynucleotide from a sample  
 CC and determining an amount of amplified hTR and an amount of amplified  
 CC control polynucleotide. The amount of amplified hTR is normalised with  
 CC respect to the amount of amplified control polynucleotide to provide a  
 CC normalised amount of hTR which provides a determination of the amount of  
 CC hTR in the sample. The invention provides a determination of an RNA component  
 CC of human telomerase in a sample. This is useful for diagnosing cancer  
 CC (especially neuroblastoma, bladder, colon and prostate cancer), and  
 CC providing prognosis for a cancer patient. The antisense oligonucleotides  
 CC can be used for inhibiting telomerase activity in both cultured cells and  
 CC in cells in vivo. They can be used in therapeutics for treating or  
 CC preventing cancer, for contraception or sterilisation, for  
 CC immunosuppression, and for selectively down-regulating specific branches  
 CC of the immune system, e.g. a specific subset of T-cells, in anti-  
 CC inflammatory therapies or for treating infections by, e.g. yeast,  
 CC parasites or fungi.

XX Sequence 27 BP; 7 A; 3 C; 10 G; 7 T; 0 other;

Query Match 76.7%; Score 23; DB 19; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.00079;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGTAATGAACGGTGAAGG 23  
 |||||  
 Db 5 GCTCTAGTAATGAACGGTGAAGG 27

# RESULT 8

ABA95497  
 ID ABA95497 standard; DNA; 27 BP.

XX ABA95497;

DT 12-MAR-2002 (first entry)

DE Human telomerase RNA, hTR, antisense PCR primer.

XX Human; telomerase RNA; PCR primer; cancer; breast; ovarian; stomach;  
 KW colon; hTR; ss.

XX Homo sapiens.

PN EP1158055-A1.

XX 28-NOV-2001.

XX 26-MAY-2000; 2000EP-0111370.

XX 26-MAY-2000; 2000EP-0111370.

PA (CHEN/) CHEN X Q.

PA (STRO/) STROUN M.

XX (ANKP/) ANKER P.

PI Chen XQ, Stroun M, Anker P;

DR WPI; 2002-099090/14.

XX Accurate, reliable diagnosis and/or prognosis of cancer, e.g. breast

PS cancer, by analyzing the RNA components of telomerase in plasma or

XX serum -

XX Example; Column 3; 6pp; French.

CC The present invention relates to a method for diagnosing and/or  
 CC monitoring the evolution of cancers. The method comprises analysing  
 CC enzyme telomerase RNA in blood plasma or serum. The method is typically  
 CC used for diagnosing breast, ovarian, stomach or colon cancer and/or  
 CC monitoring the evolution of the cancers after treatment by chemotherapy  
 CC or operations. The present sequence is a PCR primer for human telomerase

CC RNA (hTR), which was used in the example from the present invention.  
 XX Sequence 27 BP; 7 A; 3 C; 10 G; 7 T; 0 other;

Query Match 76.7%; Score 23; DB 24; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.00079;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGTAATGAACGGTGAAGG 23  
 |||||  
 Db 5 GCTCTAGTAATGAACGGTGAAGG 27

# RESULT 9

AAZ08704  
 ID AAZ08704 standard; DNA; 25 BP.

XX AAZ08704;

DT 20-OCT-1999 (first entry)

DE Human telomerase RNA template PCR primer R3C.

XX Telomerase; body fluid; cancer; tumour; screening; TRAP; diagnosis;  
 KW telomeric repeat amplification protocol; detection; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

PN WO9941406-A1.

XX 19-AUG-1999.

XX 16-FEB-1999; 99WO-US03302.

XX 16-FEB-1999; 98US-0074793.

XX (UYMA-) UNIV MARYLAND BALTIMORE.

XX Abruzzo LV, Highsmith B, Stamberg J, Strovel JW;

DR WPI; 1999-508655/42.

XX Detecting telomerase activity in non-cellular body fluid using a

XX modified telomeric repeat amplification protocol

XX Disclosure; Page 16; 32pp; English.

CC A method has been developed for detecting telomerase activity in a  
 CC non-cellular portion of body fluid from a cancer patient using a  
 CC modified telomeric repeat amplification protocol (TRAP). A method for  
 CC detecting cancer comprises: (a) removing the cellular portion of a body  
 CC fluid specimen from the patient; (b) preparing a protein extract from  
 CC the body fluid remainder; (c) assaying the extract for the presence and  
 CC quantity of telomerase RNA or telomerase activity; and (d) comparing the  
 CC results with normal levels, to determine the presence of cancer. The  
 CC methods are used in cancer diagnosis and prognosis, and also to monitor  
 CC cancer therapy effectiveness. Unlike prior art telomerase activity  
 CC assays in cancer patients, the method allows noninvasive sample  
 CC collection. The methods are also more reliable and less tumour specific  
 CC than other methods which detect circulating tumour markers. The present  
 CC sequence represents a human telomerase RNA template PCR primer used in  
 CC the exemplification of the present invention.

XX Sequence 25 BP; 7 A; 3 C; 9 G; 6 T; 0 other;

Query Match 73.3%; Score 22; DB 20; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGTAATGAACGGTGAAG 22  
 |||||  
 Db 4 GCTCTAGTAATGAACGGTGAAG 25

```

XX RNA component of human telomerase antisenese plasmid PCR primer R3c.
DE
XX
XX RNA component; human; telomerase; lung fibroblast; cell line WI-38;
KW recombinant production; synthesis; mutant; detection; mammalian;
KW identification; modulating agent; neoplastic condition;
KW transcriptional regulatory sequence; gene therapy; disease;
XX polymerase chain reaction; antisense plasmid; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO9601835-A1.
XX
XX 25-JAN-1996.
XX
XX 06-JUL-1995; 95WO-US08530.
XX
XX 07-JUN-1995; 95US-0482115.
XX 07-JUL-1994; 94US-0272102.
XX 27-OCT-1994; 94US-0330123.
XX 07-JUN-1995; 95US-0472802.
XX
XX (GERO-) GERON CORP.
XX
XX Andrews WH, Feng J, Funk W, Villeponteau B;
XX
XX WPI; 1996-097581/10.
XX
XX RNA component of mammalian telomerase, esp. human - useful in
XX identifying e.g. candidate telomerase-modulating agents
XX
XX Example 8; Page 80; 114pp; English.
XX
XX The present sequence is a PCR primer for a RNA component of human
XX telomerase (RCHT), antisense plasmid. RCHT was derived from a
XX genomic DNA library obtained from the human lung fibroblast cell line
XX WI-38. The RCHT can be used in the recombinant production of an active
XX telomerase molecule, capable of adding sequences to chromosomal DNA
XX telomeres, and in the synthesis of mutant sequences for the
XX detection of mutant mammalian telomerase RNA component
XX polynucleotides. The RCHT may also be used in the identification
XX of telomerase modulating agents, and in the detection of
XX telomerase related, or neoplastic conditions in a patient.
XX Polynucleotides of at least 25 consecutive nucleotides identical,
XX or complementary to the RCHT sequence linked to heterologous
XX transcriptional regulatory sequences, can be used for the gene
XX therapy of human diseases.
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
SQ
Query Match 73.3%; Score 22; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGACGGTGGAG 22
DB 5 GCTCTAGAATGACGGTGGAG 26

RESULT 12
AAT11044
ID AAT11044 standard; DNA; 26 BP.
XX
XX AAT11044;
XX
XX 02-JUL-1996 (first entry)
XX
XX Primer for production of telomerase antisense oligonucleotide.
XX
XX Telomerase; mammal; antisense; triplex forming oligonucleotide;
XX plasmid; probe; primer; ribozyme; ss.
XX
XX Synthetic.

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XX RNA component of human telomerase nested PCR primer R3c.
DE
XX
XX RNA component; human; telomerase; polymerase chain reaction;
KW recombinant production; synthesis; mutant; detection; mammalian;
KW identification; modulating agent; neoplastic condition;
KW transcriptional regulatory sequence; gene therapy; disease;
XX PCR primer; ss.
XX
OS Synthetic.
XX
XX WO9601835-A1.
XX
XX 25-JAN-1996.
XX
XX 06-JUL-1995; 95WO-US08530.
XX
XX 07-JUN-1995; 95US-0482115.
XX 07-JUL-1994; 94US-0272102.
XX 27-OCT-1994; 94US-0330123.
XX 07-JUN-1995; 95US-0472802.
XX
XX (GERO-) GERON CORP.
XX
XX Andrews WH, Feng J, Funk W, Villeponteau B;
XX
XX WPI; 1996-097581/10.
XX
XX RNA component of mammalian telomerase, esp. human - useful in
XX identifying e.g. candidate telomerase-modulating agents
XX
XX Example 10; Page 82; 114pp; English.
XX
XX The present sequence, a nested PCR primer for the RNA component
XX of human telomerase (RCHT), was used in a 5' RACE procedure. The
XX RCHT can be used in the recombinant production of an active telomerase
XX molecule, capable of adding sequences to chromosomal DNA telomeres, and
XX in the synthesis of mutant sequences for the detection of mutant
XX mammalian telomerase RNA component polynucleotides. The RCHT may
XX also be used in the identification of telomerase modulating agents,
XX and in the detection of telomerase related, or neoplastic
XX conditions in a patient. Polynucleotides of at least 25
XX consecutive nucleotides identical, or complementary to the RCHT
XX sequence linked to heterologous transcriptional regulatory
XX sequences, can be used for the gene therapy of human diseases.
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
SQ
Query Match 73.3%; Score 22; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGACGGTGGAG 22
DB 5 GCTCTAGAATGACGGTGGAG 26

RESULT 11
AAT10299
ID AAT10299 standard; DNA; 26 BP.
XX
XX AAT10299;
XX
XX 09-SEP-1996 (first entry)

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XX PN WO9601614-A2.
XX XX
XX PD
XX XX
XX XX
XX PF 25-JAN-1996.
XX XX
XX PP 07-JUL-1995; 95WO-US08620.
XX XX
XX PR 07-JUN-1995; 95US-0485778.
XX PR 07-JUL-1994; 94US-0272102.
XX PR 27-OCT-1994; 94US-0330123.
XX PR 13-FEB-1995; 95US-0387524.
XX XX
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX PA (GERO-) GERON CORP.
XX XX
XX PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
XX PI Marhuenda MA, Villeponteau B;
XX XX
XX DR WPI; 1996-097428/10.
XX XX
XX PT RNA components of (non)human mammalian telomerase(s) - useful in
XX PT studying cell senescence and immortalisation
XX XX
XX PS Example 8; Page 53; 85pp; English.
XX XX
XX CC The RNA components of (non) human mammalian telomerase(s) especially
XX CC from mouse, rat and chinese hamster are all claimed. Antisense
XX CC oligonucleotides can be used to block the activity of the
XX CC telomerase; probes and primers can be used in detection; vectors and
XX CC host cells transformed with the isolated telomerase genes can be
XX CC used for production of telomerases; RNA and DNA ribozymes and triplex
XX CC forming oligonucleotides directed against the telomerase genes can
XX CC be used therapeutically as can plasmids. A mouse which lacks the
XX CC telomerase gene (also claimed) can be used for study of telomere
XX CC regulation in vivo, and the role it plays in immortalisation.
XX CC Three primers (AAT11040, AAT11043, AAT11044) were used to produce
XX CC antisense oligonucleotides which were then used to produce antisense
XX CC expression plasmids. AAT11040 was used alongside both AAT11043 and
XX CC AAT11044 to produce two different antisense molecules.
XX XX
XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
XX XX
XX Query Match 73.3%; Score 22; DB 17; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 0.003;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
DB 5 GCTCTAGATGAACGGTGAAG 26

RESULT 13
AAT58811
XX ID AAT58811 standard; DNA; 26 BP.
XX AC
XX AC AAT58811;
XX XX
XX DT 20-NOV-1997 (first entry)
XX XX
XX DE Human telomerase PCR 3'-primer R3C.
XX XX
XX KW Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;
XX KW protozoa; tumour; antibody; polymerase chain reaction; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO9640868-A1.
XX XX
XX PD 19-DEC-1996.
XX XX
XX PF 06-JUN-1996; 96WO-US09517.
XX XX
XX PR 07-JUN-1995; 95US-0478352.

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XX XX
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX XX
XX PI Autexier C, Greider C;
XX XX
XX DR WPI; 1997-099928/09.
XX XX
XX PT DNA encoding essential RNA components of human telomerase - also
XX PT truncated or recombinant telomerase, useful for diagnosis and
XX PT treatment of cancer and infection by eukaryotic parasites
XX XX
XX PS Example 5; Page 32; 48pp; English.
XX XX
XX CC The present sequence represents PCR 3'-primer R3C used for
XX CC amplifying the human telomerase (hTR). The RNA and DNA can be used in
XX CC hybridisation assays to detect or quantify telomerase activity in cells,
XX CC tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites
XX CC (yeast and protozoa) or tumours. It is also useful as primers for
XX CC amplification assays. The truncated or recombinant vertebrate telomerase
XX CC is used therapeutically to increase telomerase activity (also as
XX CC as antisense molecules, are used to reduce such activity. Typical
XX CC applications are initiation/restoration of activity to cause senescence
XX CC or to prevent immortalisation of cells in tumours or parasites. The DNA
XX CC is also used to produce recombinant telomerase, which can then be used
XX CC conventionally to raise antibodies for diagnostic detection of
XX CC telomerase. Detecting telomerase allows early diagnosis of tumour or
XX CC infection, before clinical signs manifest. Telomerase inhibitors
XX CC directed against e.g. Trypanosoma should cause fewer side effects than
XX CC drugs currently used to treat such infections. The DNA encodes those
XX CC parts of hTR RNA essential for activity but are significantly shorter
XX CC than the endogenous RNA component.
XX XX
XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
XX XX
XX Query Match 73.3%; Score 22; DB 18; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 0.003;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
DB 5 GCTCTAGATGAACGGTGAAG 26

RESULT 14
AAV19489
XX ID AAV19489 standard; DNA; 26 BP.
XX AC
XX AC AAV19489;
XX XX
XX DT 28-AUG-1998 (first entry)
XX XX
XX DE Human hTR gene RT-PCR primer R3c.
XX XX
XX KW hTR gene; TPC2; TPC3; telomere length; telomerase; human; cancer;
XX KW gene therapy; diagnosis; PCR; primer; ss.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9811204-A1.
XX XX
XX PD 19-MAR-1998.
XX XX
XX PF 13-SEP-1996; 96WO-US14679.
XX XX
XX PR 13-SEP-1996; 96WO-US14679.
XX XX
XX PA (GERO-) GERON CORP.
XX XX
XX PI Adams RR, Andrews WH, Feng J, Villeponteau B;
XX XX
XX DR WPI; 1998-207373/18.

```

XX Human TPC3 and TR genes - regulate telomere length or modulate  
 PT telomerase activity  
 XX  
 PS Disclosure; Page 49; 86pp; English.  
 XX  
 CC Primers R3c and F3b (see AAV19488) were designed for the PCR  
 CC amplification of the human telomerase hTR gene (see AAV19481). hTR  
 CC mRNA levels were shown to correlate with telomerase activity  
 CC levels in a variety of mortal and immortal cell lines. Methods of  
 CC the invention allow detection and quantitation of TPC2 (see  
 CC AAV19479), TPC3 (see AAV19480) and/or TPC2 gene products and can be  
 CC used to detect immortal cells, especially telomerase positive  
 CC cancer cells.  
 XX  
 SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;  
 Query Match 73.3%; Score 22; DB 19; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTCTAGAATGACGGTGGGAAG 22  
 Db 5 GCTCTAGAATGACGGTGGGAAG 26  
 RESULT 15  
 AAV17033  
 ID AAV17033 standard; DNA; 26 BP.  
 AC AAV17033;  
 XX  
 DT 13-AUG-1998 (first entry)  
 XX  
 DE Telomerase PCR primer R3c.  
 KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;  
 KW Prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;  
 KW PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN GB2317891-A.  
 XX  
 PD 08-APR-1998.  
 XX  
 PF 01-OCT-1997; 97GB-0020890.  
 XX  
 PR 14-AUG-1997; 97US-0915503.  
 PR 01-OCT-1996; 96US-0724643.  
 PR 18-APR-1997; 97US-0844419.  
 PR 25-APR-1997; 97US-0846017.  
 PR 06-MAY-1997; 97US-0851843.  
 PR 09-MAY-1997; 97US-0854050.  
 PR 14-AUG-1997; 97US-0911312.  
 PR 14-AUG-1997; 97US-0912951.  
 XX  
 PA (GERO-) GERON CORP.  
 PA (UYTE-) UNIV TECHNOLOGY CORP.  
 XX  
 PI Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;  
 PI Morin GB, Nakamura T, Harley CB;  
 XX  
 DR WPI; 1998-171633/16.  
 XX  
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its  
 PT variants - are useful in the diagnosis, prognosis and treatment of  
 PT cell proliferation conditions especially cancer and ageing  
 XX  
 PS Example 2; Page 218; 387pp; English.  
 XX  
 CC \*\*\* The present sequence represents a PCR primer from the present invention

CC which describes human telomerase reverse transcriptase (hTERT). The  
 CC present invention also describes the following methods: (A) determining  
 CC whether a test compound is a modulator of hTERT, by detecting the change  
 CC in hTERT recombinant protein or polynucleotide, on administration of the  
 CC compound; (B) preparation of recombinant telomerase by contacting a  
 CC protein preparation of hTERT with a telomerase RNA component; (C)  
 CC detection of the hTERT RNA or protein in a sample by binding a relevant  
 CC probe to the sample and detecting the complex formed or, in the case of  
 CC RNA detection, amplifying the product and correlating the presence of  
 CC complex or amplification product with presence of hTERT in the sample;  
 CC and (D) increasing the proliferation of a vertebrate cell by increasing  
 CC hTERT expression; and (E) the use of an agent that causes an increase in  
 CC cell vertebrate cell proliferation to create a medicament that inhibits  
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding  
 CC hTERT can be used in the manufacture of medicaments for inhibiting the  
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be  
 CC used to treat conditions that are associated with high telomerase  
 CC activity. A protein preparation of hTERT can also be used in the new  
 CC methods.  
 XX  
 SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;  
 Query Match 73.3%; Score 22; DB 19; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTCTAGAATGACGGTGGGAAG 22  
 Db 5 GCTCTAGAATGACGGTGGGAAG 26  
 Search completed: June 23, 2003, 05:43:38  
 Job time : 200.67 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 197.701 Seconds  
(without alignments)  
2502.502 Million cell updates/sec

Title: US-08-770-564A-14  
Perfect score: 17  
Sequence: 1 CGGGCCAGCAGTGACA 17

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_scs.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_scs.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_hgt\_hum.\*
- 31: em\_hgt\_inv.\*
- 32: em\_hgt\_other.\*
- 33: em\_hgt\_mus.\*
- 34: em\_hgt\_pln.\*
- 35: em\_hgt\_rod.\*
- 36: em\_hgt\_man.\*
- 37: em\_hgt\_vrt.\*
- 38: em\_sy.\*
- 39: em\_hgt\_hum.\*
- 40: em\_hgt\_mus.\*
- 41: em\_hgt\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17	100.0	17	6	AR063838	Sequence
2	17	100.0	25	6	AX019566	Sequence
3	17	100.0	30	6	A84595	Sequence
4	17	100.0	30	6	AR079892	Sequence
5	15	88.2	25	6	AR016058	Sequence
6	15	88.2	25	6	AR075530	Sequence
7	14	82.4	24	6	AX255631	Sequence
8	12	70.6	17	6	AX009124	Sequence
9	12	70.6	18	6	AR192804	Sequence
10	12	70.6	18	6	AR192805	Sequence
11	12	70.6	22	6	AX092789	Sequence
12	12	70.6	47	6	AX146611	Sequence
13	12	70.6	50	6	AR079681	Sequence
14	12	70.6	50	6	AR079685	Sequence
15	12	70.6	50	6	AR081211	Sequence
16	12	70.6	50	6	AR081215	Sequence
17	12	70.6	50	6	AR141990	Sequence
18	12	70.6	50	6	AR141994	Sequence
19	12	70.6	50	6	AR170571	Sequence
20	12	70.6	50	6	AR170575	Sequence
21	12	70.6	50	6	AX146616	Sequence
22	11	64.7	12	6	A01745	DNA fragment
23	11	64.7	17	6	AR021242	Sequence
24	11	64.7	17	6	AR034106	Sequence
25	11	64.7	17	6	AR093907	Sequence
26	11	64.7	17	6	AR191738	Sequence
27	11	64.7	18	6	AX118331	Sequence
28	11	64.7	19	6	AX369321	Sequence
29	11	64.7	19	6	AX395172	Sequence
30	11	64.7	20	6	AR086198	Sequence
31	11	64.7	20	6	AR126692	Sequence
32	11	64.7	20	6	AR176764	Sequence
33	11	64.7	20	6	AX139028	Sequence
34	11	64.7	20	6	BD011428	Determina
35	11	64.7	21	6	AX477227	Sequence
36	11	64.7	22	6	AR016064	Sequence
37	11	64.7	22	6	AR075540	Sequence
38	11	64.7	22	6	AX105072	Sequence
39	11	64.7	27	6	AR069390	Sequence
40	11	64.7	27	6	AR189756	Sequence
41	11	64.7	30	6	AX233628	Sequence
42	11	64.7	31	6	AR195952	Sequence
43	11	64.7	31	6	BD002481	Gene comp
44	11	64.7	33	6	AR111921	Sequence
45	11	64.7	33	6	AR119977	Sequence

## ALIGNMENTS

RESULT 1	AR063838	Sequence 14 from patent US 5846723.	17 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR063838	Sequence 14 from patent US 5846723.				
DEFINITION	AR063838					
ACCESSION	AR063838					
VERSION	AR063838.1	GI:5993146				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 17)					
AUTHORS	Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.					
TITLE	Methods for detecting the RNA component of telomerase					
JOURNAL	Patent: US 5846723-A 14 08-DEC-1998;					
FEATURES	Location/Qualifiers					

```

source
1. 17
4 a 6 c 6 g 1 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 17; DB 6; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 1 CGGGCCAGCAGCTGACA 17

RESULT 2
AX019566
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Keith W.N.
TITLES
Promoter regions of the mouse and human telomerase rna component
JOURNAL
Patent: WO 938964-A 20 05-AUG-1999;
KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES
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/organism="synthetic construct"
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Query Match
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 7 CGGGCCAGCAGCTGACA 23

RESULT 3
A84595
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Atkinson,E.M. and Kealey,J.T.
TITLES
PURIFIED TELOMERASE
JOURNAL
Patent: WO 9845450-A 5 15-OCT-1998;
GERON CORP (US)
FEATURES
source
1. 30
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 4
AR079892
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vasserot,A.P.,
Przan,R.A. and Kealey,J.T.
TITLES
Purified telomerase
JOURNAL
Patent: US 5968506-A 5 19-OCT-1999;
FEATURES
source
1. 30
Location/Qualifiers
/organism="unknown"
6 a 6 c 7 g 10 t 1 others
BASE COUNT
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Best Local Similarity 100.0%; Score 17; DB 6; Length 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 5
AR016058
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLES
Assays for the DNA component of human telomerase
JOURNAL
Patent: US 5776679-A 26 07-JUL-1998;
FEATURES
source
1. 25
Location/Qualifiers
/organism="unknown"
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BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCCAGCAGCTGACA 17
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RESULT 6
AR075530
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Sanger,W., Coulson,A.R., Hopper,B., Mayhew,M.W., Smith,A.J.H.,
Staden,R. and Young,R.A.
TITLES
Sequencing with chain-terminating dideoxynucleotides
JOURNAL
Patent: US 4,375,119 1980-04-02;
FEATURES
source
1. 27
Location/Qualifiers
/organism="unknown"
25 bp DNA linear PAT 30-AUG-2000

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE       Mammalian telomerase
JOURNAL     Patent: US 5958680-A 27 28-SEP-1999;
FEATURES    Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  9  GGCCAGCAGCTGACA 23

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ACCESSION  AX255631
VERSION     AX255631.1 GI:16074687
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            artificial sequences.
            Beger,C., Barber,J. and Wong-Staal,P.
            Brca-1 regulators and methods of use
            Patent: WO 0170982-A 52 27-SEP-2001;
            Immunol incorporated (US); Beger, Carmela (DE)
            Location/Qualifiers
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            /notes="Primer"
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  23 CGGGCCAGCAGCTG 10

RESULT 8
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LOCUS      AX009124
DEFINITION Sequence 157 from Patent WO9963975.
ACCESSION  AX009124
VERSION     AX009124.1 GI:9996498
KEYWORDS   human.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 17)
REFERENCE  1 Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     Patent: WO 9963975-A 157 16-DEC-1999;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
            HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
            Location/Qualifiers

KEYWORDS   source
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Db  1  CCAGCAGCTGAC 12

RESULT 9
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DEFINITION Sequence 8292 from patent US 6346398.
ACCESSION  AR192804
VERSION     AR192804.1 GI:20238769
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 8292 12-FEB-2002;
            Location/Qualifiers
            1..18
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Qy  5  CCAGCAGCTGAC 16
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RESULT 10
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LOCUS      AR192805
DEFINITION Sequence 8293 from patent US 6346398.
ACCESSION  AR192805
VERSION     AR192805.1 GI:20238770
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 8293 12-FEB-2002;
            Location/Qualifiers
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Qy  5  CCAGCAGCTGAC 16
Db  12 CCAGCAGCTGAC 1

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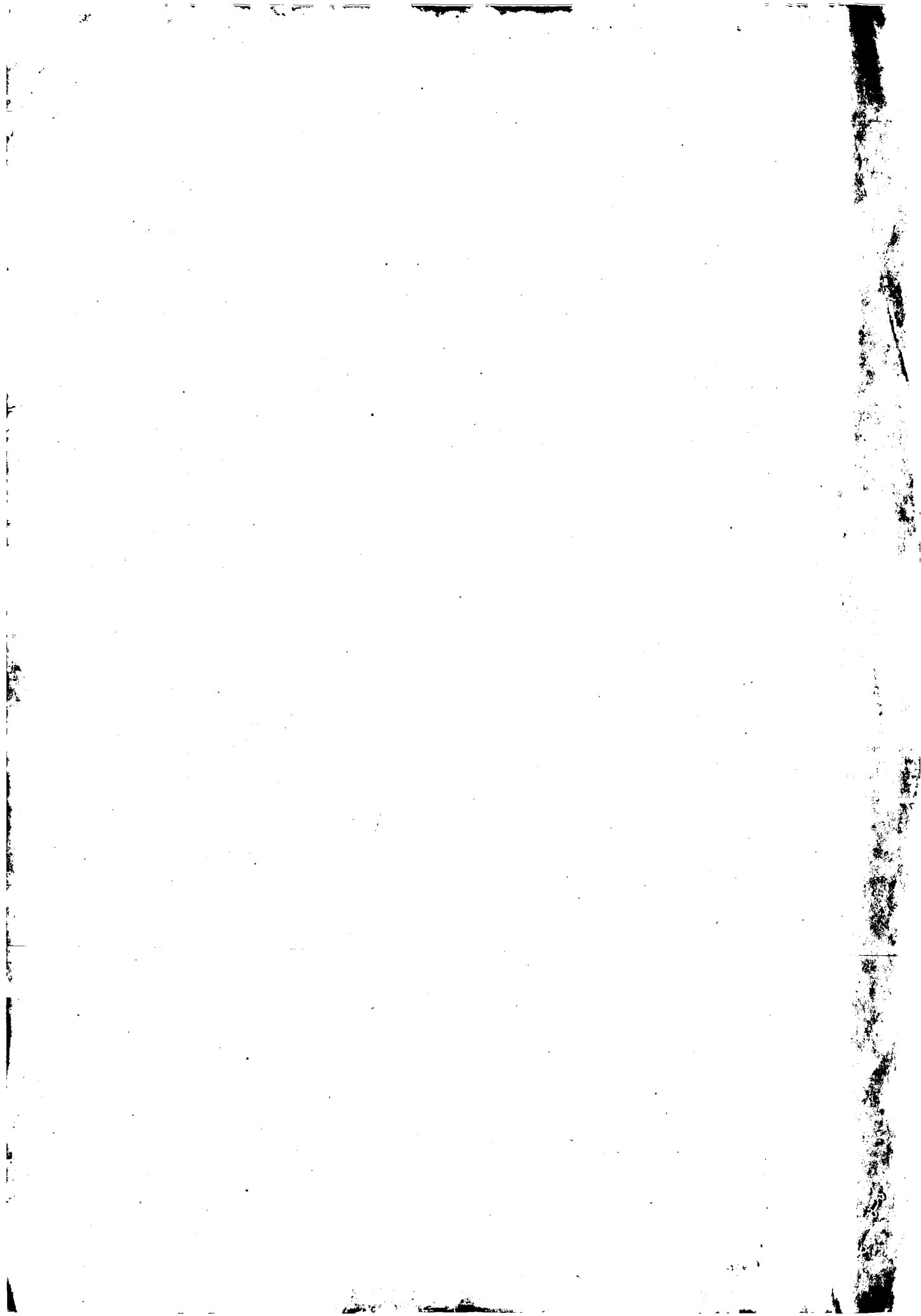
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LOCUS AX092789 22 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 201 from Patent WO0115676.  
ACCESSION AX092789  
VERSION AX092789.1 GI:13444846  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.  
TITLE Compositions and methods for modulating Hdl cholesterol and  
triglyceride levels  
JOURNAL Patent: WO 0115676-A 201 08-MAR-2001; Xenon Genetics Inc. (CA)  
UNIVERSITY of British Columbia (CA);  
FEATURES  
Location/Qualifiers  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 12 CAGCAGCTGACA 1  
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LOCUS AX146611 47 bp DNA linear PAT 31-MAY-2001  
DEFINITION Sequence 73 from Patent WO0134654.  
ACCESSION AX146611  
VERSION AX146611.1 GI:14285004  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 47)  
AUTHORS Strauch, K.  
TITLE Hedgehog fusion proteins and uses  
JOURNAL Patent: WO 0134654-A 73 17-MAY-2001;  
BIOGEN, INC. (US)  
FEATURES  
Location/Qualifiers  
1..47  
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/db\_xref="taxon:9606"  
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Best Local Similarity 100.0%; Pred. No. 8.6e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 35 CCAGCAGCTGAC 46  
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LOCUS AR079681 50 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 5 from patent US 5965726.  
ACCESSION AR079681  
VERSION AR079681.1 GI:10006422

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Pavlakis, G.N. and Felber, B.K.  
TITLE Method of eliminating inhibitory/ instability regions of mRNA  
JOURNAL Patent: US 5965726-A 5 12-OCT-1999;  
FEATURES  
Location/Qualifiers  
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BASE COUNT 26 a 10 c 12 g 2 t  
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Best Local Similarity 100.0%; Pred. No. 8.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CAGCAGCTGACA 17  
Db 35 CAGCAGCTGACA 46  
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AR079685  
LOCUS AR079685 50 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 9 from patent US 5965726.  
ACCESSION AR079685  
VERSION AR079685.1 GI:10006426  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Pavlakis, G.N. and Felber, B.K.  
TITLE Method of eliminating inhibitory/ instability regions of mRNA  
JOURNAL Patent: US 5965726-A 9 12-OCT-1999;  
FEATURES  
Location/Qualifiers  
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/organism="unknown"  
BASE COUNT 20 a 13 c 15 g 2 t  
ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 8.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CAGCAGCTGACA 17  
Db 35 CAGCAGCTGACA 46  
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AR081211  
LOCUS AR081211 50 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 5 from patent US 5972596.  
ACCESSION AR081211  
VERSION AR081211.1 GI:10007937  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Pavlakis, G.N. and Felber, B.K.  
TITLE Nucleic acid constructs containing HIV genes with mutated  
inhibitory/instability regions and methods of using same  
JOURNAL Patent: US 5972596-A 5 26-OCT-1999;  
FEATURES  
Location/Qualifiers  
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Query Match 70.6%; Score 12; DB 6; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17  
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 Db 35 CAGCAGCTGACA 46

Search completed: June 23, 2003, 06:34:27  
 Job time : 200.163 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 10.6255 Seconds  
(without alignments)  
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Title: US-08-770-564A-12

Perfect score: 7

Sequence: 1 GCTTCAG 7

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Maximum Match 100%

Listing first 45 summaries

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# SUMMARIES

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1	7	100.0	8	3	US-08-859-954-86
2	7	100.0	10	1	US-08-235-503B-28
3	7	100.0	10	1	US-07-951-715A-49
4	7	100.0	10	2	US-08-459-448A-49
5	7	100.0	10	3	US-08-899-786-10
6	7	100.0	10	3	US-08-459-595A-49
7	7	100.0	10	3	US-08-459-504B-49
8	7	100.0	10	3	US-08-459-444-49
9	7	100.0	10	4	US-09-424-518-1
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12	7	100.0	11	1	US-08-093-383-16
13	7	100.0	11	2	US-08-811-949-9
14	7	100.0	12	4	US-09-281-418-93
15	7	100.0	12	4	US-09-404-430-3
16	7	100.0	13	1	US-08-254-811D-10
17	7	100.0	13	4	US-08-981-988A-39
18	7	100.0	13	6	5182195-35
19	7	100.0	14	1	US-08-332-747-4
20	7	100.0	14	1	US-08-332-747-12
21	7	100.0	14	3	US-08-904-871-14
22	7	100.0	14	4	US-08-535-249-41
23	7	100.0	15	1	US-08-365-189-10
24	7	100.0	15	1	US-08-311-760A-72
25	7	100.0	15	1	US-08-311-760A-233
26	7	100.0	15	1	US-08-363-240A-610
27	7	100.0	15	1	US-08-471-033-34

28	7	100.0	15	2	US-08-471-044-34	Sequence 34, Appl
29	7	100.0	15	2	US-08-463-483A-34	Sequence 34, Appl
30	7	100.0	15	2	US-08-471-046A-34	Sequence 34, Appl
31	7	100.0	15	2	US-08-470-566B-34	Sequence 34, Appl
32	7	100.0	15	2	US-08-585-684B-73	Sequence 73, Appl
33	7	100.0	15	2	US-08-585-684B-681	Sequence 681, Appl
34	7	100.0	15	2	US-08-585-684B-682	Sequence 682, Appl
35	7	100.0	15	2	US-08-585-684B-683	Sequence 683, Appl
36	7	100.0	15	2	US-08-585-684B-1815	Sequence 1815, Appl
37	7	100.0	15	2	US-08-774-310-72	Sequence 72, Appl
38	7	100.0	15	2	US-08-774-310-233	Sequence 233, Appl
39	7	100.0	15	2	US-08-469-334-34	Sequence 34, Appl
40	7	100.0	15	3	US-09-289-750-8	Sequence 8, Appl
41	7	100.0	15	3	US-09-300-529-34	Sequence 34, Appl
42	7	100.0	15	4	US-09-038-073-73	Sequence 73, Appl
43	7	100.0	15	4	US-09-038-073-681	Sequence 681, Appl
44	7	100.0	15	4	US-09-038-073-682	Sequence 682, Appl
45	7	100.0	15	4	US-09-038-073-683	Sequence 683, Appl

## ALIGNMENTS

RESULT 1  
US-08-859-954-86  
; Sequence 86, Application US/08859954  
; Patent No. 6083695  
; GENERAL INFORMATION:  
; APPLICANT: Hardin, Susan H.  
; APPLICANT: Homayouni, Ramin  
; APPLICANT: Hardin, Paul E.  
; TITLE OF INVENTION: Design and Optimized Primer Library for  
; TITLE OF INVENTION: Gene Sequencing and Method Thereof  
; NUMBER OF SEQUENCES: 566  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,954  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/632,782  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5900  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/651-5325  
; TELEFAX: 713/651-5246  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "oligonucleotide"  
; HYPOTHETICAL: YES  
; ANTI-SENSE: YES  
US-08-859-954-86

Query Match 100.0%; Score 7; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 3.6e+07;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
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DB 1 GCTTCAG 7

## RESULT 2

US-08-235-503B-28  
; Sequence 28, Application US/08235503B  
; Patent No. 563036  
; GENERAL INFORMATION:  
; APPLICANT: Peterson, Michael G  
; APPLICANT: Baichwal, Vijay R  
; APPLICANT: Strulovici, Berta  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,503B  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: A-59332/RAO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 7811989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-235-503B-28

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
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DB 1 GCTTCAG 7

## RESULT 3

US-07-951-715A-49  
; Sequence 49, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lytle D.  
; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8615  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: Desc = "Primer C1 - second half"  
; HYPOTHETICAL: NO  
US-07-951-715A-49

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
|||||  
DB 2 GCTTCAG 8

## RESULT 4

US-08-459-448A-49  
; Sequence 49, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lytle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 589336artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,448A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION/DOCKET NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer C1 - second half"  
HYPOTHETICAL: NO  
US-08-459-448A-49

Query Match 100.0%; Score 7; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 2 GCTTCAG 8

RESULT 5  
US-08-899-786-10/c  
Sequence 10, Application US/08899786  
Patent No. 6001572  
GENERAL INFORMATION:  
APPLICANT: Toothman, Penelope  
TITLE OF INVENTION: Method of Identifying Aloe Using  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM pc compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,786  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/022,611  
FILING DATE: 26-JULY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION/DOCKET NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: UNI. 07  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-899-786-10

Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 7 GCTTCAG 1

RESULT 6  
US-08-459-595A-49  
Sequence 49, Application US/08459595A  
Patent No. 6018104  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6018104artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHEICAL: NO
US-08-459-595A-49

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Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

```

```

RESULT 7
US-08-459-504B-49
; Sequence 49, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995

```

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,504B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHEICAL: NO
US-08-459-504B-49

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Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

```

```

RESULT 8
US-08-459-444-49
; Sequence 49, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; TITLE OF INVENTION: NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995

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CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer C1 - second half"  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
US-08-459-444-49

Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 2 GCTTCAG 8

RESULT 9  
US-09-424-518-1/C  
Sequence 1, Application US/09424518  
Patent No. 6260034  
GENERAL INFORMATION:  
APPLICANT: Bjorksten, Lennart  
TITLE OF INVENTION: A Method and a System for Nucleic Acid Sequence Analysis  
Patent No. 6260034  
FILE REFERENCE: 45687-00004  
CURRENT APPLICATION NUMBER: US/09/424,518  
CURRENT FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: PCT/SE98/01005  
PRIOR FILING DATE: 1998-05-27  
PRIOR APPLICATION NUMBER: 9702008-5  
PRIOR FILING DATE: 1997-05-28  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-424-518-1

Query Match 100.0%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 8 GCTTCAG 2

RESULT 10  
US-09-547-422-49  
Sequence 49, Application US/09547422  
Patent No. 6320100  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
Desai, Nalini M.

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauris, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 632010artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-Apr-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer C1 - second half"  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
US-09-547-422-49

Query Match 100.0%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 2 GCTTCAG 8

RESULT 11  
PCT-US95-05265-28  
Sequence 28, Application PC/TUS9505265  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05265  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,503  
FILING DATE: 29-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: FP-592332-PC/RAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-1249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US95-05265-28

Query Match 100.0%; Score 7; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 1 GCTTCAG 7

RESULT 12  
US-08-093-383-16  
Sequence 16, Application US/08093383  
Patent No. 5489529  
GENERAL INFORMATION:  
APPLICANT: DeBoer, Herman A.  
APPLICANT: Heyneker, Herbert L.  
APPLICANT: Seeburg, Peter H.  
TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch; 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,383  
FILING DATE: 14-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/619827  
FILING DATE: 28-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/198824  
FILING DATE: 05-APR-1988

PRIOR APPLICATION DATA: 06/632361  
APPLICATION NUMBER:  
FILING DATE: 19-JUL-1984  
PRIOR APPLICATION DATA: 06/303687  
APPLICATION NUMBER:  
FILING DATE: 18-SEP-1981  
ATTORNEY/AGENT INFORMATION:  
NAME: Johnston, Sean A.  
REGISTRATION NUMBER: P35,910  
REFERENCE/DOCKET NUMBER: 46C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-3562  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-093-383-16

Query Match 100.0%; Score 7; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 2 GCTTCAG 8

RESULT 13  
US-08-811-949-9  
Sequence 9, Application US/08811949  
Patent No. 5840533  
GENERAL INFORMATION:  
APPLICANT: NIWA, MINEO  
APPLICANT: SAITO, YOSHIMASA  
APPLICANT: SASAKI, HITOSHI  
APPLICANT: HAYASHI, MASAKO  
APPLICANT: NOTANI, JOUJI  
APPLICANT: KOBAYASHI, MASAKAZU  
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/811,949  
FILING DATE: 05-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 18-966-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"  
US-08-811-949-9

Query Match 100.0%; Score 7; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
Db 2 GCTTCAG 8

## RESULT 14

US-09-281-418-93  
; Sequence 93, Application US/09281418  
; Patent No. 6287769  
; GENERAL INFORMATION:  
; APPLICANT: Inoue, Takakazu  
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F  
; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi  
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant  
; FILE REFERENCE: 9982-7  
; CURRENT APPLICATION NUMBER: US/09/281,418  
; CURRENT FILING DATE: 1999-03-30  
; EARLIER APPLICATION NUMBER: JP/1998/87651  
; EARLIER FILING DATE: 1998-03-31  
; EARLIER APPLICATION NUMBER: JP/1999/69694  
; EARLIER FILING DATE: 1999-03-16  
; NUMBER OF SEQ ID NOS: 216  
; SEQ ID NO 93  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-281-418-93

Query Match 100.0%; Score 7; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
Db 4 GCTTCAG 10

## RESULT 15

US-09-404-430-3  
; Sequence 3, Application US/09404430  
; Patent No. 6350853  
; GENERAL INFORMATION:  
; APPLICANT: Neilsen, Peter  
; APPLICANT: Knudsen, Helle  
; TITLE OF INVENTION: Conjugated Peptide Nucleic Acids Having Enhanced  
; TITLE OF INVENTION: Cellular Uptake  
; FILE REFERENCE: ISIS4181  
; CURRENT APPLICATION NUMBER: US/09/404,430  
; CURRENT FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US08/564,765  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6350853el Sequence  
US-09-404-430-3

Query Match 100.0%; Score 7; DB 4; Length 12;





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 360.904 Seconds  
(without alignments)  
314.123 Million cell updates/sec

Title: US-08-770-564A-12  
Perfect score: 7  
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO\_NUC  
Gapex\_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_nam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	19	AZ621656	AZ621656 1M0455C01
2	7	100.0	19	AZ858978	AZ858978 2M0164E24
3	7	100.0	25	AU257776	AU257776 AU257776
4	7	100.0	25	BM399457	BM399457 5009-0-57
5	7	100.0	25	AZ310966	AZ310966 1M0026K08
6	7	100.0	27	H84968	H84968 ya89c08.r1

7	7	100.0	27	AZ320101	AZ320101 1M0040B04
8	7	100.0	27	TA80D02P	TA80D02P
9	7	100.0	28	AI429345	AI429345 mn95c09.x
10	7	100.0	28	AZ592130	AZ592130 1M0402J17
11	7	100.0	28	AZ603080	AZ603080 1M0422J09
12	7	100.0	30	T99092	T99092 ye67f08.s1
13	7	100.0	30	AZ656638	AZ656638 1M0532N15
14	7	100.0	30	BH864835	BH864835 SALK 0969
15	7	100.0	30	AL764630	AL764630 Arabidops
16	7	100.0	31	AI004094	AI004094 ot50e03.s
17	7	100.0	31	AI126669	AI126669 QC52c04.x
18	7	100.0	31	AI346598	AI346598 qp51h06.x
19	7	100.0	31	AU259365	AU259365
20	7	100.0	31	BM007283	BM007283 603615061
21	7	100.0	31	AZ628881	AZ628881 1M0481A19
22	7	100.0	32	BE547551	BE547551 601075188
23	7	100.0	32	BM051667	BM051667 603638A19
24	7	100.0	32	AZ826678	AZ826678 2M0102F06
25	7	100.0	33	AV834163	AV834163
26	7	100.0	33	BJ076555	BJ076555
27	7	100.0	33	AZ781782	AZ781782 2M0021E23
28	7	100.0	33	AZ785987	AZ785987 2M0030G18
29	7	100.0	34	AI337457	AI337457 tb99h06.x
30	7	100.0	34	AV852639	AV852639
31	7	100.0	34	AW698792	AW698792 r378 non-
32	7	100.0	34	BF973182	BF973182 602241A32
33	7	100.0	34	BG536263	BG536263 603565A86
34	7	100.0	34	W47928	W47928 mc87b02.r1
35	7	100.0	34	AZ807688	AZ807688 2M0070N07
36	7	100.0	34	BH864764	BH864764 SALK_0968
37	7	100.0	34	TA163C01P	TA163C01P
38	7	100.0	34	TA9H02P	TA9H02P
39	7	100.0	35	AZ471193	AZ471193 1M0285J12
40	7	100.0	36	BI766883	BI766883 603053118
41	7	100.0	36	AZ788319	AZ788319 2M0035N17
42	7	100.0	36	TA146G01Q	TA146G01Q
43	7	100.0	37	AI024153	AI024153 ov73b09.s
44	7	100.0	37	AI079739	AI079739 oy55f02.s
45	7	100.0	37	AA228354	AA228354 nc39c12.r

## ALIGNMENTS

RESULT 1	AZ621656	19 bp	DNA	linear	GSS 13-DEC-2000
LOCUS	1M0455C01F	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0455C01 F, DNA sequence.				
ACCESSION	AZ621656				
VERSION	AZ621656.1	GI:11743846			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00				

Plate: 0455 row: C column: 01  
 Seq primer: CGTTGTAACAGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

# FEATURES

Location/Qualifiers  
 1..19  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0455C01"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"

/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 3 c 7 g 7 t  
 ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
 |||||  
 Db 9 GCTTCAG 15

# RESULT 2

AZ858978/c  
 LOCUS 2M0164F24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0164F24 F, DNA sequence.  
 ACCESSION AZ858978  
 VERSION GSS.  
 KEYWORDS GSS.  
 SOURCE house mouse.

ORGANISM  
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00

Plate: 0164 row: F column: 24  
 Seq primer: CGTTGTAACAGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

# FEATURES

Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0164F24"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"

/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 3 c 7 g 5 t  
 ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
 |||||  
 Db 15 GCTTCAG 9

# RESULT 3

AU257776/c  
 LOCUS AU257776 3'-directed mouse cDNA library Mus musculus cDNA clone  
 DEFINITION BED0011369 3', mRNA sequence.

ACCESSION AU257776  
 VERSION AU257776.1 GI:20322727  
 KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)  
 Kato, K. and Matoba, R.  
 Generation of expressed sequence tags from mouse brain  
 TITLE Unpublished (2002)  
 JOURNAL Contact: Kikuya Kato

COMMENT Graduate School of Biological Sciences  
 Nara Institute of Science and Technology  
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
 Tel: 81-743-72-5581  
 Fax: 81-743-72-5589  
 Email: kkatob@nara.ac.jp  
 URL: http://love2.aist-nara.ac.jp/BED/index.html.

# FEATURES

Location/Qualifiers  
 1..25  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="BED0011369"

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/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/notes="Vector: pGEM-T-easy"
BASE COUNT      12 a      5 c      3 g      5 t
ORIGIN

Query Match      100.0%; Score 7; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
      |||||
Db      22 GCTTCAG 16

RESULT 4
BM399457/c
LOCUS
DEFINITION
5009-0-57-H06.t.2 Chilcoat/turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM399457
VERSION
BM399457.1 GI:18199510
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
J. and Klobutcher,L.
Esr from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
CONTACT: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
Location/Qualifiers
1..25
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK-; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      6 a      6 c      9 g      4 t
ORIGIN

Query Match      100.0%; Score 7; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
      |||||
Db      10 GCTTCAG 4

RESULT 5
AZ310966
LOCUS
DEFINITION
1M0026K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0026K08 F, DNA sequence.
ACCESSION
AZ310966
VERSION
AZ310966.1 GI:10353460
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 Row: K Column: 08
Seq primer: CTTGTAAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
FEATURES
Location/Qualifiers
1..25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0026K08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN

Query Match      100.0%; Score 7; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
      |||||
Db      4 GCTTCAG 10

RESULT 6
H84968/c
LOCUS
DEFINITION
Y89C08.r1 Soares retina N2b5HR Homo sapiens cDNA clone
IMAGE:221966 5', similar to gb|U73048|HUMU3AAA Human U3 small
nuclear RNA (rRNA);, mRNA sequence.
ACCESSION
H84968
VERSION
H84968.1 GI:1064601
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE  
AUTHORS  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 27)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilton RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

JOURNAL  
COMMENT  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 308 Std Error: 0.00  
Seq primer: M13RPI  
High quality sequence stop: 1.

Location/Qualifiers  
1. 27

FEATURES  
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/organism="Homo sapiens"  
/db\_xref="GDB:385072"  
/db\_xref="taxon:9606"  
/clone="IMAGE:221966"  
/clone\_lib="Soares retina N2BSHR"  
/sex="male"  
/tissue="retina"  
/dev\_stage="55 year old"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: eye; Vector: pT73D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCATCTCAAGTGGGCGCGCGCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector into  
(Pharmacia). The retinas were obtained from a 55 year old  
Caucasian and total cellular poly(A)<sup>+</sup> RNA was extracted 6  
hrs after their removal. The retina RNA was kindly  
provided by Rodrick R. McInnes M.D. Ph.D. from the  
University of Toronto. Library constructed by Bento  
Soares and M.Fatima Bonaldo."

BASE COUNT 6 a 8 c 8 g 4 t 1 others

ORIGIN

Query Match 100.0%; Score 7; DB 14; Length 27;

Best Local Similarity 100.0%; Pred. NO. 3.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7

Db 27 GCTTCAG 21

RESULT 7

AZ320101

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 27)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauser, A.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0040 row: B column: 04

Seq primer: CGTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 27.

Location/Qualifiers

1. 27

FEATURES

source

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUCCLM0040504"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (GI4732114|cb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 4 a 7 c 4 g 12 t

ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 27;

Best Local Similarity 100.0%; Pred. NO. 3.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7

Db 9 GCTTCAG 15

RESULT 8

AZ320101

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 27)

REFERENCE

AUTHORS

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 Direct Submission  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and rhlesanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
 Email: nleasay@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

# FEATURES

source

1. .27  
 /organism="Trypanosoma brucei"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="80d02" 7 g 9 t

## BASE COUNT

ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7

Db 23 GCTTCAG 17

## RESULT 9

AI429345/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI429345 28 bp mRNA linear EST 09-MAR-1999  
 mn95c09.x1 Stragatene mouse lung 937302 Mus musculus cDNA clone  
 IMAGE:551824 3' similar to TR:015157 O15157 DOLICHOLO MONOPHOSPHATE  
 MANNOSE SYNTHASE ;, mRNA sequence.  
 AI429345  
 AI429345.1 GI:4275271  
 EST.  
 house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 28)  
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person  
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter  
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterston, R., and Wilson, R.  
 The WashU-NCI Mouse EST Project 1999  
 Unpublished (1999)  
 Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 This clone was previously sequenced on the 5' end only, this new  
 data is from the 3' end  
 Trace considered overall poor quality  
 Possible reversed clone; similarity on wrong strand  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. .28

## FEATURES

source

1. .28

/organism="Mus musculus"  
 /strain="C57BL/6 x CBA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:551824"  
 /clone.lib="Stratagene mouse lung 937302"  
 /sex="female"  
 /tissue\_type="lung"  
 /dev\_stage="6-8 month old"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI  
 ; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo  
 dt. 6-8 month old female lung and 1.5 year old male lung  
 were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP  
 XR Vector; -5' adaptor sequence: 5' GAATTCGACGACG 3' -3'  
 adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"  
 7 a 5 c 5 g 11 t  
 BASE COUNT  
 ORIGIN  
 Query Match 100.0%; Score 7; DB 9; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 Db 18 GCTTCAG 12

## RESULT 10

AZ592130/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .28

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUCG1M0402J17"

/clone.lib="Mouse 10kb plasmid UUCG1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA

AZ592130 28 bp DNA linear GSS 13-DEC-2000  
 IM0402J17R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 clone UUCG1M0402J17 R, DNA sequence.  
 AZ592130  
 AZ592130.1 GI:11714320  
 GSS.  
 house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 28)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112 USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Place: 0402 row: J column: 17  
 Seq primer: CACACAGGAACAGGTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
 1. .28

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUCG1M0402J17"

/clone.lib="Mouse 10kb plasmid UUCG1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 6 c 4 g 9 t  
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 28;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
| | | | |  
Db 13 GCTTCAG 7

RESULT 11  
AZ603080/c  
LOCUS  
DEFINITION  
1M0422J09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0422J09 F, DNA sequence.

ACCESSION  
AZ603080  
VERSION  
GSS.  
GI:11725270

SOURCE  
house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 28)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg.; 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0422 row: J column: 09

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

FEATURES

source

1..28  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0422J09"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 9 c 6 g 8 t  
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 28;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
| | | | |  
Db 16 GCTTCAG 10

RESULT 12

T99092

LOCUS

DEFINITION

ye67f08.sl Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
IMAGS:122823 3' similar to gb:L27670 Human Landsteiner-Wiener blood  
group glycoprotein (HUMAN); mRNA sequence.

ACCESSION

T99092

VERSION

EST.

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 30)

REFERENCE

AUTHORS

Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,

M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston,

R., Williamson, A., Wohlmann, F., and Wilson, R.

The WashU-Merck EST Project

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1341

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL This clone is available royalty-free

through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)

for further information. Trace considered overall poor quality

Insert Length: 1341

Seq primer: -21m13

High quality sequence stop: 1.

Location/Qualifiers

1..30

/organism="Homo sapiens"

/db\_xref="GDB:475368"

/db\_xref="taxon:9606"

/clone="IMAGE:122823"

/clone\_lib="Soares fetal liver spleen INFLS"

/sex="male"

/dev\_stage="20 week-post conception fetus"

/lab\_host="DH10B (ampicillin resistant)"

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer  
[5' ACTGCGAATAAATAAGATCTTTTCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pVT3 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 7 a 8 c 8 g 7 t  
ORIGIN

Query Match 100.0%; Score 7; DB 14; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
|||||  
DB 23 GCTTCAG 29

RESULT 13  
AZ656638/c  
LOCUS 30 bp DNA linear GSS 14-DEC-2000  
DEFINITION 1M0532N15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0532N15 F, DNA sequence.

ACCESSION AZ656638.1 GI:11793784  
VERSION  
KEYWORDS GSS.

SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0532 row: N column: 15  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 30.

FEATURES  
source

1..30  
Location/Qualifiers  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0532N15"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 10 a 6 c 4 g 10 t  
ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
|||||  
DB 25 GCTTCAG 19

RESULT 14  
BH864835/c  
LOCUS 30 bp DNA linear GSS 05-AUG-2002  
DEFINITION SALK\_096946 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
thaliana genomic clone SALK\_096946, DNA sequence.

ACCESSION BH864835  
VERSION BH864835.1 GI:22100733  
KEYWORDS GSS.

SOURCE thale cress.  
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadtrina  
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.  
; Zimmerman,J., and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome

JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within 300 bases of the 3' end of  
At4g37400.  
Class: TDNA tagged.  
Location/Qualifiers  
1..30  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_096946"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

FEATURES  
source

1..30  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_096946"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 10 a 7 c 5 g 8 t

Query Match 100.0%; Score 7; DB 17; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
|||||  
DB 29 GCTTCAG 23

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RESULT 15
AL764630/c
LOCUS          30 bp      DNA      linear      GSS 19-JUN-2002
DEFINITION    Arabidopsis thaliana T-DNA flanking sequence GK-128H09-012669,
               genomic survey sequence.
ACCESSION     AL764630
VERSION       AL764630.1  GI:21517673
KEYWORDS      GSS.
SOURCE        thale cress.
ORGANISM      Arabidopsis thaliana
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE     1 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
               and Weisshaar,B.
               A pipeline for automated high-throughput generation of FSTs
               (flanking sequence tags) from Arabidopsis thaliana T-DNA
               transformed lines
               unpublished
               2
               Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
               A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
               for flanking sequence tag based reverse genetics
               unpublished
               3 (bases 1 to 30)
               Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.
               Direct Submission
               Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
               Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
               This sequence is recovered from the left border of the T-DNA. It
               indicates an insertion close to or within gene At3g62580. The
               sequences are generated at the MPI for plant Breeding Research in
               the context of the GABI-Kat project. GABI-Kat is part of the German
               plant Genomics program designated 'GABI'. Information on line
               availability can be found at:
               http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source            1..30
                       /organism="Arabidopsis thaliana"
                       /strain="Columbia 0"
                       /db_xref="taxon:3702"
                       /clone="GK-128H09-012669"
                       /clone_11b="Arabidopsis thaliana T-DNA insertion lines"
                       /notes="PCR was performed on DNA from Arabidopsis thaliana
                       plants (T1) which were transformed with the T-DNA from
                       vector pAC161. The lines contain one or more T-DNA
                       insertions. The DNA fragment(s) resulting from the PCR
                       were directly sequenced to determine the genomic sequence
                       flanking the insertion. Sequences displaying significant
                       similarity to the A. thaliana nuclear genome sequence were
                       processed for submission. T-DNA derived sequences were
                       removed"
BASE COUNT          8 a      6 c      7 g      9 t
ORIGIN
Query Match          100.0%; Score 7; DS 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTTCAG 7
        |||||
Db      28 GCTTCAG 22

Search completed: June 23, 2003, 10:10:32
Job time : 364.058 secs

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 307.275 Seconds  
(without alignments)  
158.668 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7

Sequence: 1 GCTTCAG 7

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents\_NA\_New.\*

- 1: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	7	100.0	10	9 US-10-329-465-53	Sequence 53, Appl
C 2	7	100.0	10	10 US-10-293-222-131	Sequence 131, Appl
C 3	7	100.0	11	9 US-10-314-322-34	Sequence 34, Appl
C 4	7	100.0	12	9 US-10-240-580-38	Sequence 38, Appl
C 5	7	100.0	13	9 US-10-106-799-13	Sequence 13, Appl
C 6	7	100.0	13	9 US-10-106-799-14	Sequence 14, Appl
C 7	7	100.0	13	9 US-10-146-505-84	Sequence 84, Appl
C 8	7	100.0	14	9 US-10-303-778-13859	Sequence 13859, A
C 9	7	100.0	15	9 US-10-294-035-747	Sequence 747, Appl
C 10	7	100.0	15	9 US-10-294-035-748	Sequence 748, Appl
C 11	7	100.0	15	9 US-10-294-035-940	Sequence 940, Appl
C 12	7	100.0	15	9 US-10-294-038-1008	Sequence 1008, Appl
C 13	7	100.0	15	9 US-10-294-038-2682	Sequence 2682, Appl
C 14	7	100.0	15	9 US-10-294-038-4251	Sequence 4251, Appl
C 15	7	100.0	15	9 US-10-287-822-1580	Sequence 1580, Appl
C 16	7	100.0	15	9 US-10-310-188-33324	Sequence 33324, A
C 17	7	100.0	15	9 US-10-310-188-72013	Sequence 72013, A
C 18	7	100.0	15	9 US-10-305-273-169	Sequence 169, Appl
C 19	7	100.0	15	9 US-10-305-273-1191	Sequence 1191, Appl
C 20	7	100.0	15	9 US-10-305-275-550	Sequence 550, Appl

C 21	7	100.0	15	9 US-10-316-956-1230	Sequence 1230, Appl
C 22	7	100.0	15	9 US-10-316-956-1239	Sequence 1239, Appl
C 23	7	100.0	15	9 US-10-316-956-1250	Sequence 1250, Appl
C 24	7	100.0	15	9 US-10-316-956-1251	Sequence 1251, Appl
C 25	7	100.0	15	9 US-10-316-956-1252	Sequence 1252, Appl
C 26	7	100.0	15	9 US-10-316-954-413	Sequence 413, Appl
C 27	7	100.0	15	9 US-10-316-954-1307	Sequence 1307, Appl
C 28	7	100.0	15	9 US-10-316-954-2852	Sequence 2852, Appl
C 29	7	100.0	15	9 US-10-316-954-2853	Sequence 2853, Appl
C 30	7	100.0	15	9 US-10-316-954-3393	Sequence 3393, Appl
C 31	7	100.0	15	9 US-10-316-954-4902	Sequence 4902, Appl
C 32	7	100.0	15	9 US-10-316-954-4903	Sequence 4903, Appl
C 33	7	100.0	15	9 US-10-321-854-1864	Sequence 1864, Appl
C 34	7	100.0	15	9 US-10-321-854-3261	Sequence 3261, Appl
C 35	7	100.0	15	9 US-10-310-157-1213	Sequence 1213, Appl
C 36	7	100.0	15	9 US-10-310-157-1214	Sequence 1214, Appl
C 37	7	100.0	15	9 US-10-310-157-3299	Sequence 3299, Appl
C 38	7	100.0	15	9 US-10-310-157-4486	Sequence 4486, Appl
C 39	7	100.0	15	9 US-10-310-157-5923	Sequence 5923, Appl
C 40	7	100.0	15	9 US-10-310-157-5935	Sequence 5935, Appl
C 41	7	100.0	15	9 US-10-310-157-6009	Sequence 6009, Appl
C 42	7	100.0	15	9 US-10-305-273A-169	Sequence 169, Appl
C 43	7	100.0	15	9 US-10-305-273A-1191	Sequence 1191, Appl
C 44	7	100.0	15	9 US-10-305-275A-550	Sequence 550, Appl
C 45	7	100.0	15	10 US-10-367-892-657	Sequence 657, Appl

#### ALIGNMENTS

RESULT 1  
US-10-329-465-53/c  
; Sequence 53, Application US/10329465  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN ML-  
; FILE REFERENCE: 27373/37928A  
; CURRENT APPLICATION NUMBER: US/10/329,465  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: US 60/343,826  
; PRIOR FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-329-465-53

Query Match 100.0%; Score 7; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
|||||||  
Db 7 GCTTCAG 1

RESULT 2  
US-10-293-222-131/c  
; Sequence 131, Application US/10293222  
; GENERAL INFORMATION:  
; APPLICANT: Versteeg, Rogier  
; APPLICANT: Caron, Hubertus N.  
; TITLE OF INVENTION: MYC targets  
; FILE REFERENCE: 2183-5580US  
; CURRENT APPLICATION NUMBER: US/10/293,222  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: PCT/NL01/00361  
; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: EP 00201698.8  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: EP 00202284.6  
; PRIOR FILING DATE: 2000-06-29  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 131  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-293-222-131

Query Match 100.0%; Score 7; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 10 GCTTCAG 4

## RESULT 3

US-10-314-322-34/C  
; Sequence 13, Application US/10314322

; GENERAL INFORMATION:  
; APPLICANT: Heber-Katz, Ellen  
; TITLE OF INVENTION: Compositions and Methods for Wound  
; FILE REFERENCE: 000486.00016  
; CURRENT APPLICATION NUMBER: US/10/314,322  
; PRIOR FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/074,737  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/097,937  
; PRIOR FILING DATE: 1998-08-26  
; PRIOR APPLICATION NUMBER: US 60/102,051  
; PRIOR FILING DATE: 1998-09-28  
; PRIOR APPLICATION NUMBER: US 09/249,155  
; PRIOR FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-314-322-34

Query Match 100.0%; Score 7; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 10 GCTTCAG 4

## RESULT 4

US-10-240-580-38  
; Sequence 38, Application US/10240580

; GENERAL INFORMATION:  
; APPLICANT: INOUE, Takakazu  
; TITLE OF INVENTION: METHOD AND APPARATUS FOR MICROORGANISM DISCRIMINATION, METHOD OF  
; TITLE OF INVENTION: DATABASE FOR MICROORGANISM DISCRIMINATION, AND MICROORGANISM DIS  
; TITLE OF INVENTION: PROGRAM AND RECORDING MEDIUM ON WHICH SUCH PROGRAM IS RECORDED  
; FILE REFERENCE: 9982-24  
; CURRENT APPLICATION NUMBER: US/10/240,580  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/JF01/02516  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: JP 2000-99482  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 38  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-240-580-38

Query Match 100.0%; Score 7; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 4 GCTTCAG 10

## RESULT 5

US-10-106-799-13  
; Sequence 13, Application US/10106799

; GENERAL INFORMATION:  
; APPLICANT: Council of Scientific and Industrial Research  
; TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran  
; TITLE OF INVENTION: method thereof  
; FILE REFERENCE: US 673  
; CURRENT APPLICATION NUMBER: US/10/106,799  
; CURRENT FILING DATE: 2002-10-31  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: AP34 arbitrary primer for differential display  
US-10-106-799-13

Query Match 100.0%; Score 7; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 3 GCTTCAG 9

## RESULT 6

US-10-106-799-14  
; Sequence 14, Application US/10106799

; GENERAL INFORMATION:  
; APPLICANT: Council of Scientific and Industrial Research  
; TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran  
; TITLE OF INVENTION: method thereof  
; FILE REFERENCE: US 673  
; CURRENT APPLICATION NUMBER: US/10/106,799  
; CURRENT FILING DATE: 2002-10-31  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: AP35 arbitrary primer for differential display  
US-10-106-799-14

Query Match 100.0%; Score 7; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 3 GCTTCAG 9

RESULT 7  
US-10-146-505-84/c  
; Sequence 84, Application US/10146505  
; GENERAL INFORMATION:  
; APPLICANT: Sale, Julian E.  
; APPLICANT: Neuberger, Michael S.  
; APPLICANT: Cumbers, Sarah J.  
; TITLE OF INVENTION: Method of Generating Diversity  
; FILE REFERENCE: 18396/2005B  
; CURRENT APPLICATION NUMBER: US/10/146,505  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/828,717  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 09/879,813  
; PRIOR FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: PCT/GB99/03358  
; PRIOR FILING DATE: 1999-10-08  
; PRIOR APPLICATION NUMBER: GB 9822104.7  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: GB 9901141.3  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: GB 9913435.5  
; PRIOR FILING DATE: 1999-06-09  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 84  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (8)-(8)  
; OTHER INFORMATION: F220  
; OTHER INFORMATION: The sequence TGACCTCTGTG is deleted  
US-10-146-505-84

Query Match 100.0%; Score 7; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
|||  
Db 7 GCTTCAG 1

RESULT 8  
US-10-303-778-13859/c  
; Sequence 13859; Application US/10303778  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL  
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF  
; FILE REFERENCE: 47416  
; CURRENT APPLICATION NUMBER: US/10/303,778  
; CURRENT FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 17608  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13859  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-303-778-13859

Query Match 100.0%; Score 7; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
|||  
Db 8 GCTTCAG 2

RESULT 9  
US-10-294-035-747/c  
; Sequence 747, Application US/10294035  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/294,035  
; CURRENT FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1377  
; SOFTWARE: Proprietary  
; SEQ ID NO 747  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Mycobacterium leprae strain TN complete genome.  
; FEATURE:  
; LOCATION: (1626549)...(1626563)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1041  
US-10-294-035-747

Query Match 100.0%; Score 7; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
|||  
Db 12 GCTTCAG 6

RESULT 10  
US-10-294-035-748/c  
; Sequence 748, Application US/10294035  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/294,035  
; CURRENT FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1377  
; SOFTWARE: Proprietary  
; SEQ ID NO 748  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Mycobacterium leprae strain TN complete genome.  
; FEATURE:  
; LOCATION: (1626549)...(1626563)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1040  
US-10-294-035-748

Query Match 100.0%; Score 7; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
|||  
Db 12 GCTTCAG 6

RESULT 11  
US-10-294-035-940/c  
; Sequence 940, Application US/10294035  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/294,035  
; CURRENT FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1377  
; SOFTWARE: Proprietary  
; SEQ ID NO 940  
; LENGTH: 15  
; TYPE: DNA

```

; ORGANISM: Mycobacterium leprae strain TN complete genome.
; FEATURE:
; LOCATION: (2080233)...(2080248)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1297
US-10-294-035-940

```

```

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

```

```

QY 1 GCTTCAG 7
    |||||
Db 7 GCTTCAG 1

```

```

RESULT 12
US-10-294-038-1008
; Sequence 1008, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 1008
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (371601)...(371615)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1249
US-10-294-038-1008

```

```

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

```

```

QY 1 GCTTCAG 7
    |||||
Db 8 GCTTCAG 14

```

```

RESULT 13
US-10-294-038-2682
; Sequence 2682, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 2682
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (1117875)...(1117888)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3354
US-10-294-038-2682

```

```

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

```

```

QY 1 GCTTCAG 7
    |||||
Db 1 GCTTCAG 7

```

```

RESULT 14
US-10-294-038-4251
; Sequence 4251, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 4251
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (1902455)...(1902469)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 5315
US-10-294-038-4251

```

```

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

```

```

QY 1 GCTTCAG 7
    |||||
Db 8 GCTTCAG 14

```

```

RESULT 15
US-10-287-822-1580/c
; Sequence 1580, Application US/10287822
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Synchocystis PCC6803 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,822
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 5726
; SOFTWARE: Proprietary
; SEQ ID NO 1580
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Synchocystis PCC6803 complete genome.
; FEATURE:
; LOCATION: (959678)...(959693)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2089
US-10-287-822-1580

```

```

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

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QY 1 GCTTCAG 7
    |||||
Db 11 GCTTCAG 5

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Job time : 307.275 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 587.108 Seconds  
(without alignments)  
299.770 Million cell updates/sec

Title: US-08-770-564A-12  
Perfect score: 7  
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents\_NA\_Main:\*

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- 4: /cgn2\_6/ptodata/2/pna/US08 COMB.seq:\*
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- 23: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
- 24: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
- 25: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
- 26: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
- 27: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
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- 36: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
- 37: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
- 38: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
- 39: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
- 40: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*
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- 43: /cgn2\_6/ptodata/2/pna/US09 COMB.seq:\*

- 44: /cgn2\_6/ptodata/2/pna/US6000 COMB.seq:\*
- 45: /cgn2\_6/ptodata/2/pna/US6001 COMB.seq:\*
- 46: /cgn2\_6/ptodata/2/pna/US6002 COMB.seq:\*
- 47: /cgn2\_6/ptodata/2/pna/US6003 COMB.seq:\*
- 48: /cgn2\_6/ptodata/2/pna/US6004 COMB.seq:\*
- 49: /cgn2\_6/ptodata/2/pna/US6005 COMB.seq:\*
- 50: /cgn2\_6/ptodata/2/pna/US6006 COMB.seq:\*
- 51: /cgn2\_6/ptodata/2/pna/US6007 COMB.seq:\*
- 52: /cgn2\_6/ptodata/2/pna/US6008 COMB.seq:\*
- 53: /cgn2\_6/ptodata/2/pna/US6009 COMB.seq:\*
- 54: /cgn2\_6/ptodata/2/pna/US6010 COMB.seq:\*
- 55: /cgn2\_6/ptodata/2/pna/US6011 COMB.seq:\*
- 56: /cgn2\_6/ptodata/2/pna/US6012 COMB.seq:\*
- 57: /cgn2\_6/ptodata/2/pna/US6013 COMB.seq:\*
- 58: /cgn2\_6/ptodata/2/pna/US6014 COMB.seq:\*
- 59: /cgn2\_6/ptodata/2/pna/US6015 COMB.seq:\*
- 60: /cgn2\_6/ptodata/2/pna/US6016 COMB.seq:\*
- 61: /cgn2\_6/ptodata/2/pna/US6017 COMB.seq:\*
- 62: /cgn2\_6/ptodata/2/pna/US6018 COMB.seq:\*
- 63: /cgn2\_6/ptodata/2/pna/US6019 COMB.seq:\*
- 64: /cgn2\_6/ptodata/2/pna/US6020 COMB.seq:\*
- 65: /cgn2\_6/ptodata/2/pna/US6021 COMB.seq:\*
- 66: /cgn2\_6/ptodata/2/pna/US6022 COMB.seq:\*
- 67: /cgn2\_6/ptodata/2/pna/US6023 COMB.seq:\*
- 68: /cgn2\_6/ptodata/2/pna/US6024 COMB.seq:\*
- 69: /cgn2\_6/ptodata/2/pna/US6025 COMB.seq:\*
- 70: /cgn2\_6/ptodata/2/pna/US6026 COMB.seq:\*
- 71: /cgn2\_6/ptodata/2/pna/US6027 COMB.seq:\*
- 72: /cgn2\_6/ptodata/2/pna/US6028 COMB.seq:\*
- 73: /cgn2\_6/ptodata/2/pna/US6029 COMB.seq:\*
- 74: /cgn2\_6/ptodata/2/pna/US6030 COMB.seq:\*
- 75: /cgn2\_6/ptodata/2/pna/US6031 COMB.seq:\*
- 76: /cgn2\_6/ptodata/2/pna/US6032 COMB.seq:\*
- 77: /cgn2\_6/ptodata/2/pna/US6033 COMB.seq:\*
- 78: /cgn2\_6/ptodata/2/pna/US6034 COMB.seq:\*
- 79: /cgn2\_6/ptodata/2/pna/US6035 COMB.seq:\*
- 80: /cgn2\_6/ptodata/2/pna/US6036 COMB.seq:\*
- 81: /cgn2\_6/ptodata/2/pna/US6037 COMB.seq:\*
- 82: /cgn2\_6/ptodata/2/pna/US6038 COMB.seq:\*
- 83: /cgn2\_6/ptodata/2/pna/US6039 COMB.seq:\*
- 84: /cgn2\_6/ptodata/2/pna/US6040 COMB.seq:\*
- 85: /cgn2\_6/ptodata/2/pna/US6041 COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	7	100.0	11	US-08-770-564A-12
2	7	100.0	8	US-08-632-782-86
3	7	100.0	10	PCT-US00-04606-65
4	7	100.0	10	PCT-US01-10743A-43
5	7	100.0	10	PCT-US01-10743A-44
6	7	100.0	10	PCT-US01-18814-44
7	7	100.0	10	PCT-US01-18814-49
8	7	100.0	10	PCT-US01-21306-130
9	7	100.0	10	PCT-US01-21306-118
10	7	100.0	10	PCT-US01-29207-36
11	7	100.0	10	PCT-US01-42727-58
12	7	100.0	10	PCT-US02-24250-52
13	7	100.0	10	PCT-US97-13001-10
14	7	100.0	10	PCT-US99-13800-226
15	7	100.0	10	PCT-US99-13800-149
16	7	100.0	8	US-08-458-785-49
17	7	100.0	10	US-08-459-444-49
18	7	100.0	10	US-08-459-448-49
19	7	100.0	10	US-08-459-504-49
20	7	100.0	10	US-08-459-504A-49
21	7	100.0	10	US-08-459-595-49
Sequence 12, Appl				
Sequence 65, Appl				
Sequence 43, Appl				
Sequence 44, Appl				
Sequence 44, Appl				
Sequence 49, Appl				
Sequence 118, App				
Sequence 36, Appl				
Sequence 58, Appl				
Sequence 52, Appl				
Sequence 10, Appl				
Sequence 226, App				
Sequence 1449, App				
Sequence 49, Appl				
Sequence 49, Appl				
Sequence 49, Appl				
Sequence 49, Appl				

Sequence 49, Appl  
Sequence 369, Appl  
Sequence 2641, AD  
Sequence 2931, AD  
Sequence 4373, AD  
Sequence 8177, AD  
Sequence 8178, AD  
Sequence 1613, AD  
Sequence 1701, AD  
Sequence 4067, AD  
Sequence 4990, AD  
Sequence 61, Appl  
Sequence 69, Appl  
Sequence 226, Appl  
Sequence 1449, AD  
Sequence 81, Appl  
Sequence 34, Appl  
Sequence 34, Appl  
Sequence 3, Appl  
Sequence 20, Appl  
Sequence 3, Appl  
Sequence 2823, AD  
Sequence 7616, AD  
Sequence 25, Appl

# ALIGNMENTS

RESULT 1  
US-08-770-564A-12  
; Sequence 12, Application US/08770564A  
; GENERAL INFORMATION:  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ron  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
; TITLE OF INVENTION: Against the RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002200US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA

US-08-770-564A-12  
; Sequence 12, Application US/08770564A  
; GENERAL INFORMATION:  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ron  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
; TITLE OF INVENTION: Against the RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002200US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA

US-08-770-564A-12  
; Sequence 12, Application US/08770564A  
; GENERAL INFORMATION:  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ron  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
; TITLE OF INVENTION: Against the RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002200US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA

Query Match 100.0%; Score 7; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.5e+09;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTTCAG 7  
Db 1 GCTTCAG 7  
RESULT 2  
US-08-632-782-86  
; Sequence 86, Application US/08632782  
; GENERAL INFORMATION:  
; APPLICANT: Hardin, Susan H.  
; APPLICANT: Homayouni, Ramin  
; APPLICANT: Hardin, Paul E.  
; TITLE OF INVENTION: Design and Optimized Primer Library for  
; TITLE OF INVENTION: Gene Sequencing and Method Thereof  
; NUMBER OF SEQUENCES: 566  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/632,782  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5900  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/651-5325  
; TELEFAX: 713/651-5246  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "oligonucleotide"  
; HYPOTHETICAL: YES  
; ANTI-SENSE: YES  
US-08-632-782-86  
Query Match 100.0%; Score 7; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.1e+09;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTTCAG 7  
Db 1 GCTTCAG 7  
RESULT 3  
PCT-US00-04606-65/c  
; Sequence 65, Application PC/TUS0004606  
; GENERAL INFORMATION:  
; APPLICANT: Genesense Pharmaceuticals, Inc.  
; APPLICANT: Nandabalan, Krishnan  
; APPLICANT: Schulz, Vincent P  
; APPLICANT: Stephens, J. Claiborne  
; APPLICANT: Chew, Anne  
; TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the Tumor  
; TITLE OF INVENTION: Necrosis Factor Receptor 1 Gene  
; FILE REFERENCE: MWH0030PCT

; CURRENT APPLICATION NUMBER: PCT/US00/04606  
; CURRENT FILING DATE: 2000-02-23  
; EARLIER APPLICATION NUMBER: 60/121,314  
; EARLIER FILING DATE: 1999-02-23  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 65  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
PCT-US00-04606-65

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
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Db 9 GCTTCAG 3

RESULT 4  
PCT-US01-10743A-43/c  
; Sequence 43, Application PC/TUS0110743A  
; GENERAL INFORMATION:  
; APPLICANT: Genassance Pharmaceuticals, Inc.  
; APPLICANT: Chew, Anne  
; APPLICANT: Choi, Julie Y.  
; APPLICANT: Koshy, Beena  
; TITLE OF INVENTION: Haplotypes of the SCN2B Gene  
; FILE REFERENCE: MWH-0481PCT SCN2B  
; CURRENT APPLICATION NUMBER: PCT/US01/10743A  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/196,597  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapien  
PCT-US01-10743A-43

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
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Db 7 GCTTCAG 1

RESULT 5  
PCT-US01-10743A-44  
; Sequence 44, Application PC/TUS0110743A  
; GENERAL INFORMATION:  
; APPLICANT: Genassance Pharmaceuticals, Inc.  
; APPLICANT: Chew, Anne  
; APPLICANT: Choi, Julie Y.  
; APPLICANT: Koshy, Beena  
; TITLE OF INVENTION: Haplotypes of the SCN2B Gene  
; FILE REFERENCE: MWH-0481PCT SCN2B  
; CURRENT APPLICATION NUMBER: PCT/US01/10743A  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/196,597  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapien  
PCT-US01-10743A-44

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
Db 3 GCTTCAG 9

RESULT 6  
PCT-US01-18814-44/c  
; Sequence 44, Application PC/TUS0118814  
; GENERAL INFORMATION:  
; APPLICANT: Genassance Pharmaceuticals, Inc.  
; APPLICANT: Choi, Julie Y.  
; APPLICANT: Koshy, Beena  
; APPLICANT: Sanchis, Angela  
; APPLICANT: Sausker, Elizabeth Ann  
; TITLE OF INVENTION: HAPLOTYPES OF THE PHKG2 GENE  
; FILE REFERENCE: MWH-0770PCT PHKG2  
; CURRENT APPLICATION NUMBER: PCT/US01/18814  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 60/210,568  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US01-18814-44

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
Db 10 GCTTCAG 4

RESULT 7  
PCT-US01-18814-49  
; Sequence 49, Application PC/TUS0118814  
; GENERAL INFORMATION:  
; APPLICANT: Genassance Pharmaceuticals, Inc.  
; APPLICANT: Choi, Julie Y.  
; APPLICANT: Koshy, Beena  
; APPLICANT: Sanchis, Angela  
; APPLICANT: Sausker, Elizabeth Ann  
; TITLE OF INVENTION: HAPLOTYPES OF THE PHKG2 GENE  
; FILE REFERENCE: MWH-0770PCT PHKG2  
; CURRENT APPLICATION NUMBER: PCT/US01/18814  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 60/210,568  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US01-18814-49

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
Db 4 GCTTCAG 10

RESULT 8  
 PCT-US01-23106-130  
 ; Sequence 130, Application PC/TUS0123106  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genaisance Pharmaceuticals, Inc.  
 ; APPLICANT: Bentivegna, Steven C  
 ; APPLICANT: Bieglecki, Karyn M.  
 ; APPLICANT: Kazemi, Amir  
 ; APPLICANT: Koshiy, Beena  
 ; TITLE OF INVENTION: Haplotypes of the ETFB Gene  
 ; FILE REFERENCE: MMH-0902PCT ETFB  
 ; CURRENT APPLICATION NUMBER: PCT/US01/23106  
 ; CURRENT FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: 60/215,984  
 ; PRIOR FILING DATE: 2000-07-05  
 ; NUMBER OF SEQ ID NOS: 141  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 130  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US01-23106-130

Query Match 100.0%; Score 7; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 Db 3 GCTTCAG 9

RESULT 9  
 PCT-US01-23100-118  
 ; Sequence 118, Application PC/TUS0123100  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genaisance Pharmaceuticals  
 ; APPLICANT: Duda, Amy  
 ; APPLICANT: Koshiy, Beena  
 ; APPLICANT: Sanchis, Angela  
 ; TITLE OF INVENTION: Haplotypes of the CHRNA1 Gene  
 ; FILE REFERENCE: MMH-071PCT CHRNA1  
 ; CURRENT APPLICATION NUMBER: PCT/US01/23100  
 ; CURRENT FILING DATE: 2001-07-20  
 ; PRIOR APPLICATION NUMBER: 60/219,538  
 ; PRIOR FILING DATE: 2000-07-20  
 ; NUMBER OF SEQ ID NOS: 189  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 118  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US01-23100-118

Query Match 100.0%; Score 7; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 Db 2 GCTTCAG 8

RESULT 10  
 PCT-US01-29207-36  
 ; Sequence 36, Application PC/TUS0129207  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genaisance Pharmaceuticals  
 ; APPLICANT: Koshiy, Beena  
 ; APPLICANT: Sanchis, Angela  
 ; APPLICANT: Tirrell, Charles  
 ; TITLE OF INVENTION: Haplotypes of the GPR7 Gene

FILE REFERENCE: MMH-1293PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US01/29207  
 ; CURRENT FILING DATE: 2001-09-17  
 ; PRIOR APPLICATION NUMBER: 60/232,900  
 ; PRIOR FILING DATE: 2000-09-15  
 ; NUMBER OF SEQ ID NOS: 46  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 36  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US01-29207-36

Query Match 100.0%; Score 7; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 Db 1 GCTTCAG 7

RESULT 11  
 PCT-US01-42727-58/c  
 ; Sequence 58, Application PC/TUS0142727  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genaisance Pharmaceuticals, Inc.  
 ; APPLICANT: Anastasio, Allison E.  
 ; APPLICANT: Chew, Anne  
 ; APPLICANT: Han, Jin-Hua  
 ; APPLICANT: Sanchis, Angela  
 ; TITLE OF INVENTION: HAPLOTYPES OF THE CYP27A1 GENE  
 ; FILE REFERENCE: CYP27A1 MMH-1279PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US01/42727  
 ; CURRENT FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 60/239,942  
 ; PRIOR FILING DATE: 2000-10-13  
 ; NUMBER OF SEQ ID NOS: 74  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 58  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US01-42727-58

Query Match 100.0%; Score 7; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 Db 7 GCTTCAG 1

RESULT 12  
 PCT-US02-24250-52/c  
 ; Sequence 52, Application PC/TUS0224250  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genaisance Pharmaceuticals, Inc.  
 ; APPLICANT: Drysdale, Connie M.  
 ; APPLICANT: Hoffman, Michael  
 ; APPLICANT: Judson, Richard S.  
 ; APPLICANT: Maerz, Winfried  
 ; APPLICANT: Nandabalan, Krishnan  
 ; APPLICANT: Stack, Catherine B.  
 ; APPLICANT: Stephens, J. Claiborne  
 ; APPLICANT: Vanden Eng, Jodi  
 ; APPLICANT: Winkelmann, Bernhard R.  
 ; TITLE OF INVENTION: Association of Low Density Lipoprotein Receptor (LDLR) Gene Haplot;  
 ; TITLE OF INVENTION: Therapeutic  
 ; TITLE OF INVENTION: Response To Statins  
 ; FILE REFERENCE: MMH-2889PCT LDLR



; CURRENT APPLICATION NUMBER: PCT/US02/24250  
 ; CURRENT FILING DATE: 2002-07-30  
 ; PRIOR APPLICATION NUMBER: US 60/308,688  
 ; PRIOR FILING DATE: 2001-07-30  
 ; NUMBER OF SEQ ID NOS: 103  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 52  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US02-24250-52

Query Match 100.0%; Score 7; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
 Db 10 GCTTCAG 4

# RESULT 13

PCT-US97-13001-10/c  
 ; Sequence 10, Application PC/TUS9713001  
 ; GENERAL INFORMATION:

; APPLICANT: Toothman, Penelope  
 ; TITLE OF INVENTION: Method of Identifying Aloe Using  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.  
 ; STREET: 8400 E. Prentice Avenue, Suite 200  
 ; CITY: Englewood  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80111

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
 ; COMPUTER: IBM pc compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Wordperfect 8.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US97/13001  
 ; FILING DATE:

; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/022,611  
 ; FILING DATE: 26-JULY-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Barry J. Swanson  
 ; REGISTRATION NUMBER: 33,215  
 ; REFERENCE/DOCKET NUMBER: UNI.07/PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 793-3333  
 ; TELEFAX: (303) 793-3433  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE:  
 PCT-US97-13001-10

Query Match 100.0%; Score 7; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
 Db 7 GCTTCAG 1

# RESULT 14

PCT-US99-13800-226/c  
 ; Sequence 226, Application PC/TUS9913800  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genzyme Corporation  
 ; APPLICANT: Roberts, Bruce L.  
 ; APPLICANT: Shankara, Srinivas  
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
 ; FILE REFERENCE: 68126881206940  
 ; CURRENT APPLICATION NUMBER: PCT/US99/13800  
 ; CURRENT FILING DATE: 1999-06-18  
 ; EARLIER APPLICATION NUMBER: 60/090,039  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,040  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,041  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,853  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,997  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,079  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,035  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,993  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,992  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,072  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,878  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,991  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,000  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,048  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,999  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,043  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,042  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,036  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,044  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,844  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,080  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,833  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/089,994  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,077  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,078  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,047  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,076  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/090,045  
 ; EARLIER FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: 60/111,715  
 ; EARLIER FILING DATE: 1998-12-08  
 ; NUMBER OF SEQ ID NOS: 2138  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 226  
 ; LENGTH: 10  
 ; TYPE: DNA

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; ORGANISM: Homo sapiens
PCT-US99-13800-226

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 9 GCTTCAG 3

RESULT 15
PCT-US99-13800-1449/c
; Sequence 1449, Application PC/TUS9913800
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce L.
; APPLICANT: Shankara, Srinivas
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: 68126881206940
; CURRENT APPLICATION NUMBER: PCT/US99/13800
; CURRENT FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/090,039
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,040
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,041
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,853
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,997
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,079
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,035
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,993
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,992
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,072
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,878
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,991
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,000
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,048
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,999
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,043
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,042
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,036
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,044
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,844
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,080
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,833
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; EARLIER APPLICATION NUMBER: 60/089,994
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,077
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,078
; EARLIER FILING DATE: 1998-06-19

; EARLIER APPLICATION NUMBER: 60/090,047
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,076
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,045
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/111,715
; EARLIER FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 2138
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1449
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-13800-1449

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 10 GCTTCAG 4

Search completed: June 23, 2003, 16:08:23
Job time : 588.185 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 56.251 Seconds  
(without alignments)  
182.610 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7  
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US05\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	10	9	US-09-988-462-49
2	7	100.0	10	10	US-09-816-763-61
3	7	100.0	10	12	US-10-033-145-226
4	7	100.0	10	12	US-10-033-145-1449
5	7	100.0	11	9	US-09-249-155-34
6	7	100.0	13	9	US-09-879-813-84
7	7	100.0	13	9	US-10-146-505-84
8	7	100.0	13	10	US-09-770-601-4
9	7	100.0	13	10	US-09-770-601-6
10	7	100.0	14	9	US-10-146-058-41
11	7	100.0	15	9	US-10-146-575-21
12	7	100.0	15	9	US-10-145-289-2
13	7	100.0	15	10	US-09-922-261-10
14	7	100.0	16	9	US-10-146-058-39
15	7	100.0	17	9	US-09-879-813-51
16	7	100.0	17	9	US-10-041-856-79
17	7	100.0	17	9	US-09-780-164-249
18	7	100.0	17	9	US-09-780-164-250
19	7	100.0	17	9	US-09-780-164-612

## ALIGNMENTS

### RESULT 1

US-09-988-462-49  
; Sequence 49, Application US/09988462  
; Publication No. US20030046726A1  
; GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027

Sequence 613, App  
Sequence 738, App  
Sequence 825, App  
Sequence 928, App  
Sequence 1066, App  
Sequence 6, Appl  
Sequence 7, Appl  
Sequence 248, App  
Sequence 249, App  
Sequence 250, App  
Sequence 251, App  
Sequence 252, App  
Sequence 253, App  
Sequence 254, App  
Sequence 255, App  
Sequence 256, App  
Sequence 257, App  
Sequence 258, App  
Sequence 1537, App  
Sequence 1538, App  
Sequence 1539, App  
Sequence 1540, App  
Sequence 1541, App  
Sequence 1542, App  
Sequence 1543, App  
Sequence 1544, App

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; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigle, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-988-462-49

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

RESULT 2
US-09-816-763-61
; Sequence 61, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Remacle, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
US-09-816-763-61

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 1 GCTTCAG 7

RESULT 3
US-10-033-145-226/c
; Sequence 226, Application US/10033145
; Patent No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
```

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; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 226
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-226

Query Match 100.0%; Score 7; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 9 GCTTCAG 3

RESULT 4
US-10-033-145-1449/c
; Sequence 1449, Application US/10033145
; Patent No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1449
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1449

Query Match 100.0%; Score 7; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 10 GCTTCAG 4

RESULT 5
US-09-249-155-34/c
; Sequence 34, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 34
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-34

Query Match      100.0%; Score 7; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
        |||||
Db      10 GCTTCAG 4

RESULT 6
US-09-879-813-84/c
; Sequence 84, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: F220
; OTHER INFORMATION: The sequence TGAGCTCTGTG is deleted
US-09-879-813-84

Query Match      100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
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Db      7 GCTTCAG 1

RESULT 7
US-10-146-505-84/c
; Sequence 84, Application US/10146505
; Publication No. US2003010889A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
US-10-146-505-84/c

Query Match      100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
        |||||
Db      7 GCTTCAG 1

RESULT 8
US-09-770-601-4
; Sequence 4, Application US/09770601
; Patent No. US20020104110A1
; GENERAL INFORMATION:
; APPLICANT: Lipes, Myra A.
; APPLICANT: Chen, Qian
; TITLE OF INVENTION: IMMUNOLOGICALLY PRIVILEGED CELLS AND
; FILE REFERENCE: 10276-015002
; CURRENT APPLICATION NUMBER: US/09/770,601
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/127,276
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/054,730
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-770-601-4

Query Match      100.0%; Score 7; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
        |||||
Db      7 GCTTCAG 13

RESULT 9
US-09-770-601-6/c
; Sequence 6, Application US/09770601
; Patent No. US20020104110A1
; GENERAL INFORMATION:
; APPLICANT: Lipes, Myra A.
; APPLICANT: Chen, Qian
; TITLE OF INVENTION: IMMUNOLOGICALLY PRIVILEGED CELLS AND
; FILE REFERENCE: 10276-015002
; CURRENT APPLICATION NUMBER: US/09/770,601
; CURRENT FILING DATE: 2001-01-26
```

;; PRIOR APPLICATION NUMBER: 09/127,276  
;; PRIOR FILING DATE: 1998-07-30  
;; PRIOR APPLICATION NUMBER: 60/054,730  
;; PRIOR FILING DATE: 1997-08-05  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 13  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: primer for PCR  
US-09-770-601-6

Query Match 100.0%; Score 7; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.7e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 7 GCTTCAG 1

RESULT 10  
US-10-146-058-41/c  
;; Sequence 41, Application US/10146058  
;; Publication No. US20030040499A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Schlengersien, Georg-Ferdinand  
;; APPLICANT: Brysch, Wolfgang  
;; APPLICANT: Schlengersien, Karl-Hermann  
;; APPLICANT: Schlengersien, Reimar  
;; APPLICANT: Bogdahn, Ulrich  
;; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
;; NUMBER OF SEQUENCES: 137  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Jacobson, Price, Holman & Stern  
;; STREET: 400 Seventh St. N.W.  
;; CITY: Washington D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION NUMBER: US/10/146,058  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/535,249  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93 107 089.0  
;; FILING DATE: 30-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93 107 849.7  
;; FILING DATE: 13-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Player, William E.  
;; REGISTRATION NUMBER: 31,409  
;; REFERENCE/DOCKET NUMBER: 10577/P58418  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)539-6666  
;; TELEFAX: (202)393-5350  
;; TELEX: RCA 248593 IDEA UR  
;; INFORMATION FOR SEQ ID NO: 41:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: unknown

;; TOPOLOGY: unknown  
;; MOLECULE TYPE: DNA (genomic)  
;; ANTI-SENSE: YES  
US-10-146-058-41  
Query Match 100.0%; Score 7; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.7e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 11 GCTTCAG 5

RESULT 11  
US-10-146-575-21/c  
;; Sequence 21, Application US/10146575  
;; Publication No. US20030059800A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Lichter, Jay  
;; APPLICANT: Guido, Marco  
;; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4  
;; FILE REFERENCE: SEQ-12P  
;; CURRENT APPLICATION NUMBER: US/10/146,575  
;; PRIOR FILING DATE: 2002-05-14  
;; PRIOR APPLICATION NUMBER: US/09/144,367  
;; PRIOR FILING DATE: 1998-08-31  
;; NUMBER OF SEQ ID NOS: 58  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 21  
;; LENGTH: 15  
;; TYPE: DNA  
;; ORGANISM: H. sapiens  
US-10-146-575-21

Query Match 100.0%; Score 7; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.7e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 8 GCTTCAG 2

RESULT 12  
US-10-145-289-2  
;; Sequence 2, Application US/10145289  
;; Publication No. US20030077812A1  
;; GENERAL INFORMATION:  
;; APPLICANT: James G. McArthur  
;; APPLICANT: Dale John Talbot  
;; APPLICANT: Andrew D. Simmons  
;; APPLICANT: Ryan McGuinness  
;; APPLICANT: Michael Kelly  
;; APPLICANT: Lisa V. Tsui  
;; APPLICANT: Thomas Dull  
;; TITLE OF INVENTION: LENTIVIRAL VECTORS ENCODING CLOTTING  
;; FILE REFERENCE: 131.2USU1  
;; CURRENT APPLICATION NUMBER: US/10/145,289  
;; PRIOR FILING DATE: 2002-05-14  
;; PRIOR APPLICATION NUMBER: 60/291,083  
;; PRIOR FILING DATE: 2001-05-14  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 15  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: primer  
US-10-145-289-2

Query Match 100.0%; Score 7; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
 |||||  
 Db 9 GCTTCAG 15

RESULT 13  
 US-09-922-261-10/c  
 ; Sequence 10, Application US/09922261  
 ; Patent No. US2002011471A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.  
 ; APPLICANT: Lo, Donald C.  
 ; APPLICANT: Barney, Shawn  
 ; APPLICANT: Thomas, Mary Beth  
 ; APPLICANT: Portbury, Stuart D.  
 ; APPLICANT: Puranam, Kasturi  
 ; APPLICANT: Katz, Lawrence C.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
 ; TITLE OF INVENTION: CELL DEATH  
 ; FILE REFERENCE: 10001-005-999  
 ; CURRENT APPLICATION NUMBER: US/09/922,261  
 ; CURRENT FILING DATE: 2001-08-03  
 ; PRIOR APPLICATION NUMBER: US/09/461,697  
 ; PRIOR FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 466  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 15  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-922-261-10

Query Match 100.0%; Score 7; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
 |||||  
 Db 11 GCTTCAG 5

RESULT 14  
 US-10-146-058-39/c  
 ; Sequence 39, Application US/10146058  
 ; Publication No. US2003004099A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlingsiepen, Georg-Ferdinand  
 ; APPLICANT: Brysch, Wolfgang  
 ; APPLICANT: Schlingsiepen, Karl-Hermann  
 ; APPLICANT: Schlingsiepen, Reimar  
 ; APPLICANT: Bogdahn, Ulrich  
 ; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
 ; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
 ; NUMBER OF SEQUENCES: 137  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Jacobson, Price, Holman & Stern  
 ; STREET: 400 Seventh St. N.W.  
 ; CITY: Washington D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/146,058  
 ; FILING DATE:

CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/535,249  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 93 107 089.0  
 ; FILING DATE: 30-APR-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 93 107 849.7  
 ; FILING DATE: 13-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Player, William E.  
 ; REGISTRATION NUMBER: 31,409  
 ; REFERENCE/DOCKET NUMBER: 10577/P58418  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 638-6666  
 ; TELEFAX: (202) 393-5350  
 ; TELEX: RCA 248593 IDEA UR  
 ; INFORMATION FOR SEQ ID NO: 39:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 16 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: DNA (genomic)  
 ; ANTI-SENSE: YES  
 US-10-146-058-39

Query Match 100.0%; Score 7; DB 9; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
 |||||  
 Db 7 GCTTCAG 1

RESULT 15  
 US-09-879-813-51/c  
 ; Sequence 51, Application US/09879813  
 ; Patent No. US20020155453A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sale, Julian E.  
 ; APPLICANT: Neuberger, Michael S.  
 ; APPLICANT: Cumbers, Sarah J.  
 ; TITLE OF INVENTION: Method of Generating Diversity  
 ; FILE REFERENCE: 18396/2005  
 ; CURRENT APPLICATION NUMBER: US/09/879,813  
 ; CURRENT FILING DATE: 2001-06-11  
 ; PRIOR APPLICATION NUMBER: 09/828,717  
 ; PRIOR FILING DATE: 2001-06-04  
 ; PRIOR APPLICATION NUMBER: PCT/GB99/03358  
 ; PRIOR FILING DATE: 1999-10-08  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 51  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (7)..(12)  
 ; OTHER INFORMATION: D3  
 ; OTHER INFORMATION: The sequence GACCC between positions 7 and 12 replace the sequence  
 ; OTHER INFORMATION: e AGGACTGT  
 US-09-879-813-51

Query Match 100.0%; Score 7; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
 |||||

Fri Jun 27 07:41:14 2003

us-08-770-564a-12.oligo.rnpb

Page 6

Db 17 GCTTCAG 11

Search completed: June 23, 2003, 20:01:33  
Job time : 56.251 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 10.9602 Seconds  
(without alignments)  
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Title: US-08-770-564A-12

Perfect score: 7  
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*  
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3: /cgn2\_6/prodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	8	3 US-08-859-954-86	Sequence 86, Appl
2	7	100.0	10	1 US-08-235-503B-28	Sequence 28, Appl
3	7	100.0	10	1 US-07-951-715A-49	Sequence 49, Appl
4	7	100.0	10	2 US-08-459-448A-49	Sequence 49, Appl
5	7	100.0	10	3 US-08-899-786-10	Sequence 10, Appl
6	7	100.0	10	3 US-08-459-595A-49	Sequence 49, Appl
7	7	100.0	10	3 US-08-459-504B-49	Sequence 49, Appl
8	7	100.0	10	3 US-08-459-444-49	Sequence 49, Appl
9	7	100.0	10	4 US-09-424-518-1	Sequence 1, Appl
10	7	100.0	10	4 US-09-547-422-49	Sequence 49, Appl
11	7	100.0	10	5 PCT-US95-05265-28	Sequence 28, Appl
12	7	100.0	11	1 US-08-093-383-16	Sequence 16, Appl
13	7	100.0	11	2 US-08-811-949-9	Sequence 9, Appl
14	7	100.0	12	4 US-09-281-418-93	Sequence 93, Appl
15	7	100.0	12	4 US-09-404-430-3	Sequence 3, Appl
16	7	100.0	13	1 US-08-254-811D-10	Sequence 10, Appl
17	7	100.0	13	4 US-08-981-988A-39	Sequence 39, Appl
18	7	100.0	13	6 5182195-35	Patent No. 5182195
19	7	100.0	14	1 US-08-332-747-4	Sequence 4, Appl
20	7	100.0	14	1 US-08-332-747-12	Sequence 12, Appl
21	7	100.0	14	3 US-08-904-871-14	Sequence 14, Appl
22	7	100.0	14	4 US-08-535-249-41	Sequence 41, Appl
23	7	100.0	15	1 US-08-365-189-10	Sequence 10, Appl
24	7	100.0	15	1 US-08-311-760A-72	Sequence 72, Appl
25	7	100.0	15	1 US-08-311-760A-233	Sequence 233, Appl
26	7	100.0	15	1 US-08-363-240A-610	Sequence 610, Appl
27	7	100.0	15	1 US-08-471-033-34	Sequence 34, Appl

Query Match 100.0%; Score 7; DB 3; Length 8;

#### ALIGNMENTS

##### RESULT 1

US-08-859-954-86  
; Sequence 86, Application US/08859954  
; Patent No. 6083695  
; GENERAL INFORMATION:  
; APPLICANT: Hardin, Susan H.  
; APPLICANT: Homayouni, Ramin  
; APPLICANT: Hardin, Paul E.  
; TITLE OF INVENTION: Design and Optimized Primer Library for  
; TITLE OF INVENTION: Gene Sequencing and Method Thereof  
; NUMBER OF SEQUENCES: 566  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,954  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/632,782  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5900  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/651-5325  
; TELEFAX: 713/651-5246  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "oligonucleotide"  
; HYPOTHETICAL: YES  
; ANTI-SENSE: YES  
US-08-859-954-86

28	7	100.0	15	2 US-08-471-044-34	Sequence 34, Appl
29	7	100.0	15	2 US-08-463-483A-34	Sequence 34, Appl
30	7	100.0	15	2 US-08-471-046A-34	Sequence 34, Appl
31	7	100.0	15	2 US-08-470-566B-34	Sequence 34, Appl
32	7	100.0	15	2 US-08-585-684B-73	Sequence 73, Appl
33	7	100.0	15	2 US-08-585-684B-681	Sequence 681, Appl
34	7	100.0	15	2 US-08-585-684B-682	Sequence 682, Appl
35	7	100.0	15	2 US-08-585-684B-683	Sequence 683, Appl
36	7	100.0	15	2 US-08-585-684B-1815	Sequence 1815, Appl
37	7	100.0	15	2 US-08-774-310-72	Sequence 72, Appl
38	7	100.0	15	2 US-08-774-310-233	Sequence 233, Appl
39	7	100.0	15	2 US-08-469-334-34	Sequence 34, Appl
40	7	100.0	15	3 US-09-289-750-8	Sequence 8, Appl
41	7	100.0	15	3 US-09-300-529-34	Sequence 34, Appl
42	7	100.0	15	4 US-09-038-073-73	Sequence 73, Appl
43	7	100.0	15	4 US-09-038-073-681	Sequence 681, Appl
44	7	100.0	15	4 US-09-038-073-682	Sequence 682, Appl
45	7	100.0	15	4 US-09-038-073-683	Sequence 683, Appl

Best Local Similarity 100.0%; Pred. No. 3.6e+07;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 1 GCTTCAG 7

RESULT 2  
US-08-235-503B-28  
; Sequence 28, Application US/08235503B  
; Patent No. 5563036  
; GENERAL INFORMATION:  
; APPLICANT: Peterson, Michael G  
; APPLICANT: Baichwal, Vijay R  
; APPLICANT: Strulovici, Berta  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,503B  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oeman, Richard A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: A-59332/RAO  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 28:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-235-503B-28

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 1 GCTTCAG 7

RESULT 3  
US-07-951-715A-49  
; Sequence 49, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "primer C1 - second half"  
; HYPOTHETICAL: NO  
US-07-951-715A-49

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 2 GCTTCAG 8

RESULT 4  
US-08-459-448A-49  
; Sequence 49, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5859336artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,448A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer C1 - second half"  
HYPOTHETICAL: NO  
US-08-459-448A-49

Query Match 100.0%; Score 7; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 2 GCTTCAG 8

RESULT 5  
US-08-899-786-10/c  
Sequence 10, Application US/08899786  
Patent No. 6001572  
GENERAL INFORMATION:  
APPLICANT: Toothman, Penelope  
TITLE OF INVENTION: Method of Identifying Aloe Using  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM pc compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,786  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/022,611  
FILING DATE: 26-JULY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: UNI.07  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-899-786-10

Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 7 GCTTCAG 1

RESULT 6  
US-08-459-595A-49  
Sequence 49, Application US/08459595A  
Patent No. 6018104  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6018104artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/459,595A
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
; US-08-459-595A-49

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 2 GCTTCAG 8

RESULT 7
US-08-459-504B-49
; Sequence 49, Application US/08459504B
; Patent No. 6073185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/459,504B
; APPLICATION NUMBER: US/08/459,504B
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
; US-08-459-504B-49

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 2 GCTTCAG 8

RESULT 8
US-08-459-444-49
; Sequence 49, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-JUN-1995
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CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer C1 - second half"  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
US-08-459-444-49

Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 2 GCTTCAG 8

RESULT 9  
US-09-424-518-1/C  
Sequence 1, Application US/09424518  
Patent No. 6260034  
GENERAL INFORMATION:  
APPLICANT: Bjorkesten, Lennart  
TITLE OF INVENTION: A Method and a System for Nucleic Acid Sequence Analysis  
Patent No. 6260034  
FILE REFERENCE: 45687-00004  
CURRENT APPLICATION NUMBER: US/09/424,518  
CURRENT FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: PCT/SE98/01005  
PRIOR FILING DATE: 1998-05-27  
PRIOR APPLICATION NUMBER: 9702008-5  
PRIOR FILING DATE: 1997-05-28  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-424-518-1

Query Match 100.0%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 8 GCTTCAG 2

RESULT 10  
US-09-547-422-49  
Sequence 49, Application US/09547422  
Patent No. 6320100  
GENERAL INFORMATION:  
APPLICANT: Kozziel, Michael G.  
Desai, Nalini M.

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauris, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/547,422  
FILING DATE: 11-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer C1 - second half"  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
US-09-547-422-49

Query Match 100.0%; Score 7; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 2 GCTTCAG 8

RESULT 11  
PCT-US95-05265-28  
Sequence 28, Application PC/TUS9505265  
GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05265  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,503  
FILING DATE: 29-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
PCT-US95-05265-28

Query Match 100.0%; Score 7; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 1 GCTTCAG 7

RESULT 12  
US-08-093-383-16  
Sequence 16, Application US/08093383  
Patent No. 5489529  
GENERAL INFORMATION:  
APPLICANT: DeBoer, Herman A.  
APPLICANT: Heyneker, Herbert L.  
APPLICANT: Seeburg, Peter H.  
TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,383  
FILING DATE: 14-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/619827  
FILING DATE: 28-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/198824  
FILING DATE: 05-APR-1988

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/632361  
FILING DATE: 19-JUL-1984  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/303687  
FILING DATE: 18-SEP-1981  
ATTORNEY/AGENT INFORMATION:  
NAME: Johnston, Sean A.  
REGISTRATION NUMBER: P35,910  
REFERENCE/DOCKET NUMBER: 46C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-3562  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-093-383-16

Query Match 100.0%; Score 7; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 2 GCTTCAG 8

RESULT 13  
US-08-811-949-9  
Sequence 9, Application US/08811949  
Patent No. 5840533  
GENERAL INFORMATION:  
APPLICANT: NIWA, MINEO  
APPLICANT: SAITO, YOSHIMASA  
APPLICANT: SASAKI, HITOSHI  
APPLICANT: HAYASHI, MASAKO  
APPLICANT: NOTANI, JOUJI  
APPLICANT: KOBAYASHI, MASAKAZU  
TITLE OF INVENTION: TISSUE FLASMINOGEN ACTIVATOR  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/811,949  
FILING DATE: 05-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 18-966-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
;; DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"  
US-08-811-949-9

Query Match 100.0%; Score 7; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
Db 2 GCTTCAG 8

## RESULT 14

US-09-281-418-93  
; Sequence 93, Application US/09281418  
; Patent No. 6287769  
; GENERAL INFORMATION:  
; APPLICANT: Inoue, Takakazu  
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F  
; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi  
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant  
; FILE REFERENCE: 9982-7  
; CURRENT APPLICATION NUMBER: US/09/281,418  
; CURRENT FILING DATE: 1999-03-30  
; EARLIER APPLICATION NUMBER: JP/1998/87651  
; EARLIER FILING DATE: 1998-03-31  
; EARLIER APPLICATION NUMBER: JP/1999/69694  
; EARLIER FILING DATE: 1999-03-16  
; NUMBER OF SEQ ID NOS: 216  
; SEQ ID NO 93  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-281-418-93

Query Match 100.0%; Score 7; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
Db 4 GCTTCAG 10

## RESULT 15

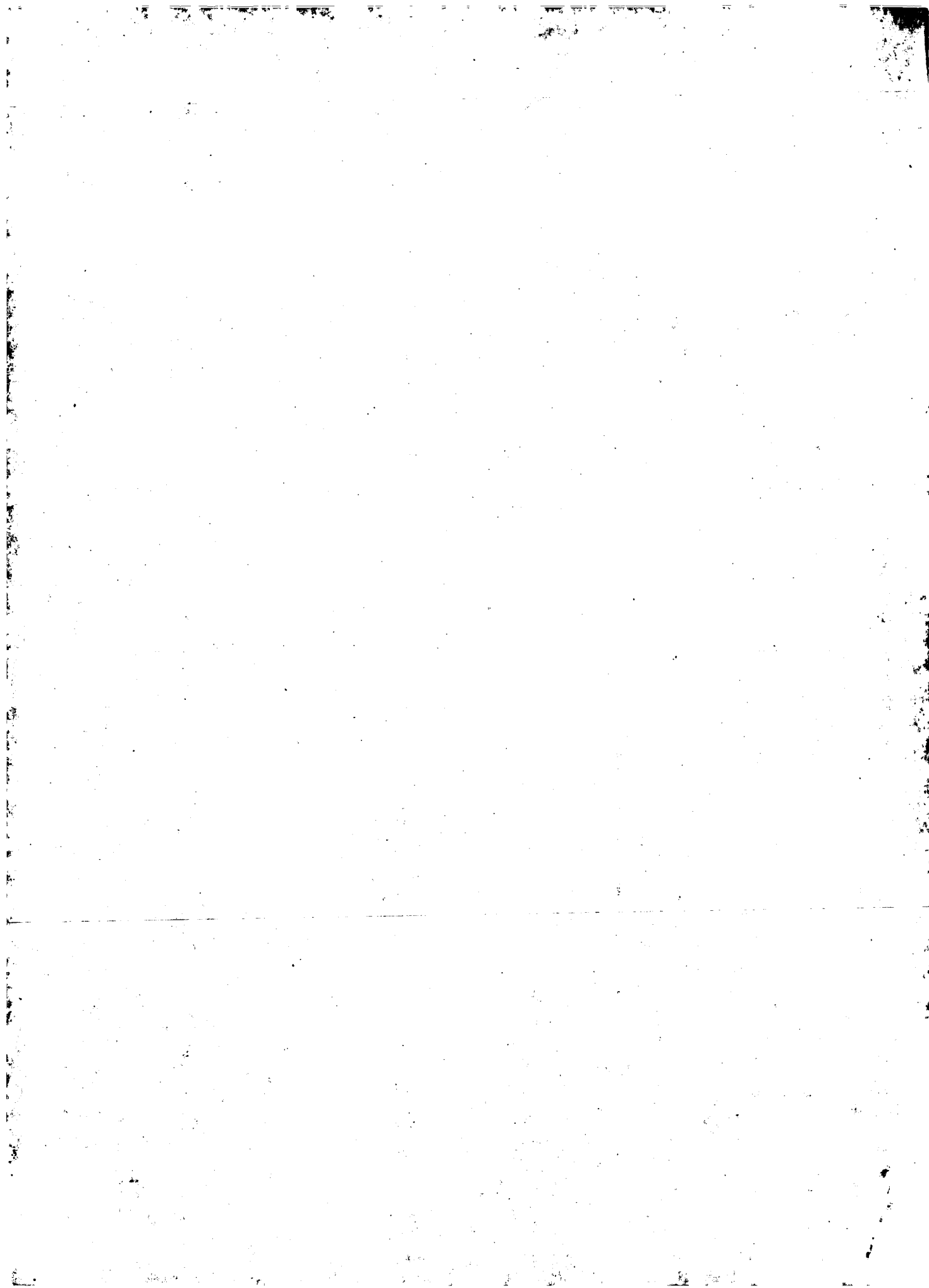
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; Sequence 3, Application US/09404430  
; Patent No. 6350853  
; GENERAL INFORMATION:  
; APPLICANT: Neilsen, Peter  
; APPLICANT: Knudsen, Helle  
; TITLE OF INVENTION: Conjugated Peptide Nucleic Acids Having Enhanced  
; TITLE OF INVENTION: Cellular Uptake  
; FILE REFERENCE: ISIS4181  
; CURRENT APPLICATION NUMBER: US/09/404,430  
; CURRENT FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US08/564,765  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6350853el Sequence  
US-09-404-430-3

Query Match 100.0%; Score 7; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
Db 5 GCTTCAG 11

Search completed: June 23, 2003, 10:17:08  
Job time : 11.9602 secs





### Characterisation of nucleotide sequences using primer pairs - by PCR

PT amplification and indexing of amplification prods. w.r.t. primers  
 XX used for genome mapping and disease diagnosis  
 PS Disclosure, Page 19; 72pp; English.  
 CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which  
 CC target human protein coding regions, together comprise a PCR primer  
 CC kit with 1361 possible primer pairs. The kit is used in a new method  
 CC for the characterisation of nucleic acid sequences obtd. from human  
 CC biological samples, which comprises PCR amplification and indexing of  
 CC the prods. w.r.t the primer pair that hybridised to its delineating  
 CC subsequences. The method may be used in the identification, cloning  
 CC and analysis of genes, e.g. in genome mapping, and disease  
 CC diagnosis.  
 XX  
 SQ Sequence 8 BP; 1 A; 3 C; 2 G; 2 T; 0 other;  
 Query Match 100.0%; Score 7; DB 17; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 DB 1 GCTTCAG 7  
 RESULT 2  
 AAT09466/c  
 ID AAT09466 standard; DNA; 8 BP.  
 XX  
 AC AAT09466;  
 XX  
 DT 21-JUN-1996 (first entry)  
 DE  
 DE 5'-primer used for characterisation of human biological samples.  
 XX  
 XX 5'-primer; human; protein coding region; PCR primer kit;  
 KW characterisation; biological samples; PCR amplification; indexing;  
 KW identification; cloning; analysis; genes; genome mapping;  
 KW disease diagnosis; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9531574-A1.  
 PN  
 XX  
 XX 23-NOV-1995.  
 XX  
 PF 12-MAY-1995; 95WO-US06032.  
 XX  
 PR 16-MAY-1994; 94US-0242887.  
 XX  
 PA (BCHM ) BRIGHAM & WOMENS HOSPITAL.  
 XX  
 XX Lopez-Nieto CE, Nigam SK;  
 PI  
 XX WPI; 1996-010958/01.  
 DR  
 XX Characterisation of nucleotide sequences using primer pairs - by PCR  
 PT amplification and indexing of amplification prods. w.r.t. primers  
 PT used for genome mapping and disease diagnosis  
 XX  
 PS Claim 5; Page 44; 72pp; English.  
 XX  
 CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which  
 CC target human protein coding regions, together comprise a PCR primer  
 CC kit with 1361 possible primer pairs. The kit is used in a new method  
 CC for the characterisation of nucleic acid sequences obtd. from human  
 CC biological samples, which comprises PCR amplification and indexing of  
 CC the prods. w.r.t the primer pair that hybridised to its delineating  
 CC subsequences. The method may be used in the identification, cloning  
 CC and analysis of genes, e.g. in genome mapping, and disease  
 CC diagnosis.  
 XX

SQ Sequence 8 BP; 2 A; 2 C; 3 G; 1 T; 0 other;  
 Query Match 100.0%; Score 7; DB 17; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 DB 8 GCTTCAG 2  
 RESULT 3  
 AAA80773  
 ID AAA80773 standard; DNA; 8 BP.  
 XX  
 AC AAA80773;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE A. thaliana primer walking octamer SEQ ID NO: 86.  
 DE  
 KW Primer walking; octamer; primer; DNA sequencing; PCR; ss.  
 XX  
 XX Arabidopsis thaliana.  
 OS  
 XX US6083695-A.  
 PN  
 XX  
 PD 04-JUL-2000.  
 XX  
 PF 21-MAY-1997; 97US-0859954.  
 XX  
 PR 15-APR-1996; 96US-0632782.  
 XX  
 PA (UVHO-) UNIV HOUSTON.  
 PA (HARD/) HARDIN S H.  
 XX  
 PI Hardin PE, Hardin SH, Homayouni R;  
 XX  
 DR WPI; 2000-474852/41.  
 XX  
 PT Sequencing an unknown DNA molecule for the polymerase chain reaction  
 PT and other primer processes comprises primer walking of octamer  
 PT oligonucleotides -  
 XX  
 XX Example 8; Column 67-68; 161pp; English.  
 PS  
 CC This invention describes a novel method for sequencing an unknown DNA  
 CC molecule which comprises selecting a library primer from an octamer  
 CC oligonucleotide library consisting of 48 8-bp sequences and  
 CC corresponding complementary sequences, where the library primer is  
 CC complementary to a known sequence adjacent to the unknown sequence or  
 CC is complementary to a sequence in a known extension product. The method  
 CC is useful for DNA nucleotide sequencing, in PCR, and in other processes  
 CC which make use of primers. The octamers are used to identify coding  
 CC sequences. Primer walking using the octamer libraries is advantageous  
 CC over other sequencing methods because it does not require multiple  
 CC cloning steps nor subsequent template preparations, and it is a  
 CC directed and methodical approach. AAA80698-A81253 represent the octamer  
 CC primers used in the primer walking method of the invention.  
 XX  
 SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;  
 Query Match 100.0%; Score 7; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 DB 1 GCTTCAG 7  
 RESULT 4  
 AAV20924/c

ID AAV20924 standard; DNA; 10 BP.  
 XX AC AAV20924;  
 XX DT 07-JUL-1998 (first entry)  
 XX DE Aloe specific universal PCR primer OPAB-10.  
 XX KW Aloe; detection; identification; PCR primer; antioxidant;  
 KW differentiation; anti-tumour; anti-diabetic; tyrosine inhibiting; ss.  
 XX OS Synthetic.  
 XX OS Aloe sp.  
 XX PN WO9804741-A1.  
 XX PD 05-FEB-1998.  
 XX PF 24-JUL-1997; 97WO-US13001.  
 XX PR 26-JUL-1996; 96US-0022611.  
 XX PA (UNIV-) UNIVERA PHARM INC.  
 XX PI Toothman P;  
 XX PI WPI; 1998-159152/14.  
 XX DR Detection and assay of Aloe - by extraction of DNA from a sample and  
 PT amplification by polymerase chain reaction using primers specific  
 PT for Aloe.  
 XX PS Claim 3; Page 15; 37pp; English.  
 XX CC The present sequence represents an Aloe specific universal PCR primer  
 CC from the present invention. The present invention describes a method for  
 CC identifying Aloe using polymerase chain reaction (PCR). The method  
 CC comprises: (a) extracting DNA from a sample containing Aloe; (b)  
 CC amplifying the DNA using PCR, and (c) comparing the sequence of the  
 CC amplified DNA obtained from PCR with the sequence of DNA obtained from  
 CC a known sample of Aloe. Also described are: (1) a nucleotide sequence  
 CC comprising sequences given in the specification or a fragment; (2) a  
 CC method for differentiating between different species of Aloe comprising:  
 CC (a) extracting DNA from an unknown sample containing Aloe, and (b)  
 CC amplifying the DNA by PCR using primers specific for a particular  
 CC species of Aloe, and (3) a method for determining the amount of Aloe  
 CC present in a mixture comprising: (a) extracting DNA from an unknown  
 CC sample with internal controls for recovery of DNA, and (b) simultaneous  
 CC amplification of DNA with primers specific to a particular Aloe species  
 CC and amplification of non-homologous DNA added to a sample to internally  
 CC quantify the amplification. The methods can be used for detecting and  
 CC assaying Aloe in samples and for differentiating between different  
 CC species of Aloe. The Aloe compounds have diverse biological activities,  
 CC including anti-tumour activity, anti-acid activity, anti-diabetic  
 CC activity, tyrosine inhibiting activity and antioxidant activity.  
 XX SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;  
 Query Match 100.0%; Score 7; DB 19; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 Db 7 GCTTCAG 1  
 RESULT 5  
 AAA95165/c  
 ID AAA95165 standard; DNA; 10 BP.  
 XX AC AAA95165;  
 XX KW

DT 12-JAN-2001 (first entry)  
 XX DE Primer #12 for detection of TNFR1 polymorphism by primer extension.  
 XX KW TNFR1; tumour necrosis factor receptor; polymorphism; human;  
 KW tumour; cancer; apoptosis; bacterial infection; primer;  
 KW primer extension; ss.  
 XX OS Homo sapiens.  
 XX PN WO200050436-A1.  
 XX PD 31-AUG-2000.  
 XX PF 23-FEB-2000; 2000WO-US04606.  
 XX PR 23-FEB-1999; 99US-0121314.  
 XX PA (GENA-) GENAISSANCE PHARM INC.  
 PA (NAND/) NANDABALAN K.  
 PA (SCHU/) SCHULZ V P.  
 PA (STEP/) STEPHENS J C.  
 PA (CHEW/) CHEW A.  
 XX PI Nandabalan K, Schulz VP, Stephens JC, Chew A;  
 XX PI WPI; 2000-543909/49.  
 XX PT Polynucleotides comprising polymorphic variants of a reference sequence  
 PT for tumour necrosis factor receptor 1 (TNFR1), useful for studying the  
 PT biological function of TNFR1 and identifying drugs targeting the  
 PT protein for treating disorders -  
 XX PS Claim 15; Page 21; 79pp; English.  
 XX CC The present invention relates to polymorphic variants of the tumour  
 CC necrosis factor receptor 1 (TNFR1) gene. The sequence of the gene is  
 CC given in AAA95102, AAA95103 and AAA95104. The polymorphisms were  
 CC identified by amplifying and sequencing regions of the gene. Twelve  
 CC polymorphic loci were discovered. Of these twelve polymorphisms, four can  
 CC cause a change in the TNFR1 protein. The present sequence is the  
 CC terminal sequence of a primer used for detection of a TNFR1 gene  
 CC polymorphism by primer extension. The TNFR1 polymorphisms may be useful  
 CC for studying the biological function of TNFR1 as well as for  
 CC identifying drugs targeting the protein for treatment of disorders  
 CC related to its abnormal expression or function such as tumours,  
 CC apoptosis related disorders and bacterial infection.  
 XX SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 other;  
 Query Match 100.0%; Score 7; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 Db 9 GCTTCAG 3  
 RESULT 6  
 AAZ77798/c  
 ID AAZ77798 standard; DNA; 10 BP.  
 XX AC AAZ77798;  
 XX DT 10-APR-2000 (first entry)  
 XX DE Human dendritic cell SAGE tag, SEQ ID NO:226.  
 XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
 KW APC; monocyte-derived dendritic cell; differential gene expression;  
 KW immunostimulatory cofactor; costimulatory factor; CTL;  
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.  
 XX PN WO9965924-A2.  
 XX PD 23-DEC-1999.  
 XX PF 18-JUN-1999; 99WO-US13800.  
 XX PR 19-JUN-1998; 98US-0089833.  
 XX PR 19-JUN-1998; 98US-0089844.  
 XX PR 19-JUN-1998; 98US-0089853.  
 XX PR 19-JUN-1998; 98US-0089878.  
 XX PR 19-JUN-1998; 98US-0089991.  
 XX PR 19-JUN-1998; 98US-0089992.  
 XX PR 19-JUN-1998; 98US-0089993.  
 XX PR 19-JUN-1998; 98US-0089994.  
 XX PR 19-JUN-1998; 98US-0089997.  
 XX PR 19-JUN-1998; 98US-0089999.  
 XX PR 19-JUN-1998; 98US-0090000.  
 XX PR 19-JUN-1998; 98US-0090035.  
 XX PR 19-JUN-1998; 98US-0090036.  
 XX PR 19-JUN-1998; 98US-0090039.  
 XX PR 19-JUN-1998; 98US-0090040.  
 XX PR 19-JUN-1998; 98US-0090041.  
 XX PR 19-JUN-1998; 98US-0090042.  
 XX PR 19-JUN-1998; 98US-0090043.  
 XX PR 19-JUN-1998; 98US-0090044.  
 XX PR 19-JUN-1998; 98US-0090045.  
 XX PR 19-JUN-1998; 98US-0090047.  
 XX PR 19-JUN-1998; 98US-0090048.  
 XX PR 19-JUN-1998; 98US-0090072.  
 XX PR 19-JUN-1998; 98US-0090076.  
 XX PR 19-JUN-1998; 98US-0090077.  
 XX PR 19-JUN-1998; 98US-0090078.  
 XX PR 19-JUN-1998; 98US-0090079.  
 XX PR 19-JUN-1998; 98US-0090080.  
 XX PR 08-DEC-1998; 98US-0111715.  
 XX (GENZ ) GENZYME CORP.  
 XX (ROSE/) ROBERTS B L.  
 XX (SHAN/) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 XX WPI; 2000-106077/09.  
 XX Isolated polynucleotides differentially expressed in antigen-presenting  
 XX cells, useful in gene vaccines against cancer -  
 XX Claim 1; Page 70; 130pp: English.  
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene  
 XX expression) tags used to identify mRNA transcripts encoding  
 XX immunostimulatory cofactor proteins which are preferentially or  
 XX differentially expressed in monocyte-derived dendritic cells compared  
 XX with monocytes. Some of the transcripts correspond to known genes or  
 XX ESTs (expressed sequence tags) which were previously unknown to be  
 XX preferentially or differentially expressed in dendritic cells, while  
 XX other transcripts correspond to novel genes. Antigen-presenting cell  
 XX (APC)-associated costimulatory factors play an important role in the  
 XX activation of the cytotoxic immune response, particularly against tumour  
 XX cells. Tumour antigen presentation via the MHC (major histocompatibility  
 XX complex) and subsequent recognition by T-cell receptors is alone  
 XX insufficient to activate a robust cytotoxic immune response that can  
 XX lyse the tumour cells; immunostimulatory cofactors also being required  
 XX for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
 XX sequences identified using the SAGE tags have several potential uses.  
 XX They may be used in vaccines to induce an immune response, particularly  
 XX against a tumour antigen; to modulate the genotype of an APC; to screen  
 XX for agents that modulate expression of differentially expressed genes in  
 XX an APC; and as hybridisation probes/amplification primers for the  
 XX diagnosis, prognosis and monitoring of diseases related to abnormal

CC expression of these genes. Detection of the dendritic cell  
 CC differentially expressed genes, or of their encoded proteins, can be used  
 CC to identify cells as belonging to the monocyte lineage. Cells containing  
 CC these genes can be used in active immunotherapy (or to stimulate  
 CC production of a population of antigen-specific effector cells) and  
 CC vectors containing them are used in gene therapy. Co-administration of  
 CC tumour antigens and APC-associated stimulatory factors ensures adequate  
 CC antigen presentation to endogenous APCs and upregulates the APCs for the  
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
 CC recruitment of T cell growth factors and secretion of chemokines for  
 CC recruitment of immune effector cells.  
 XX SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 other;  
 Query Match 100.0%; Score 7; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCCTCAG 7  
 DB 9 GCCTCAG 3  
 RESULT 7  
 AAZ79021/c  
 ID AAZ79021 standard; DNA; 10 BP.  
 XX AC AAZ79021;  
 XX DT 10-APR-2000 (first entry)  
 XX DE Human dendritic cell SAGE tag, SEQ ID NO.1449.  
 XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
 XX KW APC; monocyte-derived dendritic cell; differential gene expression;  
 XX KW immunostimulatory cofactor; costimulatory factor; CTL; anticancer; ss.  
 XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy;  
 XX OS Homo sapiens.  
 XX WO9965924-A2.  
 XX 23-DEC-1999.  
 XX 18-JUN-1999; 99WO-US13800.  
 XX PR 19-JUN-1998; 98US-0089833.  
 XX PR 19-JUN-1998; 98US-0089844.  
 XX PR 19-JUN-1998; 98US-0089853.  
 XX PR 19-JUN-1998; 98US-0089878.  
 XX PR 19-JUN-1998; 98US-0089991.  
 XX PR 19-JUN-1998; 98US-0089992.  
 XX PR 19-JUN-1998; 98US-0089993.  
 XX PR 19-JUN-1998; 98US-0089994.  
 XX PR 19-JUN-1998; 98US-0089997.  
 XX PR 19-JUN-1998; 98US-0089999.  
 XX PR 19-JUN-1998; 98US-0090000.  
 XX PR 19-JUN-1998; 98US-0090035.  
 XX PR 19-JUN-1998; 98US-0090036.  
 XX PR 19-JUN-1998; 98US-0090039.  
 XX PR 19-JUN-1998; 98US-0090040.  
 XX PR 19-JUN-1998; 98US-0090041.  
 XX PR 19-JUN-1998; 98US-0090042.  
 XX PR 19-JUN-1998; 98US-0090043.  
 XX PR 19-JUN-1998; 98US-0090044.  
 XX PR 19-JUN-1998; 98US-0090045.  
 XX PR 19-JUN-1998; 98US-0090047.  
 XX PR 19-JUN-1998; 98US-0090048.  
 XX PR 19-JUN-1998; 98US-0090072.  
 XX PR 19-JUN-1998; 98US-0090076.  
 XX PR 19-JUN-1998; 98US-0090077.  
 XX PR 19-JUN-1998; 98US-0090078.  
 XX PR 19-JUN-1998; 98US-0090079.  
 XX PR 19-JUN-1998; 98US-0090079.

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PR 19-JUN-1998; 98US-0090080.
XX 08-DEC-1998; 98US-0111715.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer -
XX
XX Claim 1; Page 106; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or
XX ESTs (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can
XX lyse the tumour cells. Immunostimulatory cofactors also being required
XX for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen; to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell
XX differentially expressed genes, or of their encoded proteins, can be used
XX to identify cells as belonging to the monocyte lineage. Cells containing
XX these genes can be used in active immunotherapy (or to stimulate
XX production of a population of antigen-specific effector cells) and
XX vectors containing them are used in gene therapy. Co-administration of
XX tumour antigens and APC-associated costimulatory factors ensures adequate
XX antigen presentation to endogenous APCs and upregulates the APCs for the
XX presentation of co-stimulatory signals, migration to T cell-rich sites,
XX secretion of T cell growth factors and secretion of chemokines for
XX recruitment of immune effector cells.
XX
XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 other;
XX
XX Query Match 100.0%; Score 7; DB 21; Length 10;
XX Best Local Similarity 100.0%; Pred No. 9.6e+04;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCTTCAG 7
XX |||||
XX Db 10 GCTTCAG 4
XX
XX RESULT 8
XX AA282243/c
XX ID AA282243 standard; DNA; 10 BP.
XX AC
XX AA282243;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell upregulated transcript tag #1477.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.

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XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US13647.
XX
XX PR 19-JUN-1998; 98US-0089853.
XX PR 19-JUN-1998; 98US-0089997.
XX PR 19-JUN-1998; 98US-0090039.
XX PR 19-JUN-1998; 98US-0090040.
XX PR 19-JUN-1998; 98US-0090041.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic
XX and non-metastatic breast cancer cells, useful for diagnosis,
XX prevention and treatment of cancer -
XX
XX Claim 1; Page 98; 219pp; English.
XX
XX AA280767 to AA283941 represent tags corresponding to distinct
XX transcripts that are preferentially transcribed in the metastatic breast
XX tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
XX AA283942 to AA286677 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the primary or non-metastatic
XX breast tumour tissue (i.e. are downregulated in metastatic breast tumour
XX cells). These transcripts can be used for diagnosis, prognosis,
XX monitoring and treatment of breast cancer, particularly where metastatic.
XX Diagnosis is by standard immunoassays or hybridisation/amplification
XX reactions. Compounds that modulate expression of the transcripts are
XX potentially useful for treatment of (metastatic) breast cancer, while
XX promoters from the transcripts are used to direct expression, in selected
XX cell types, of e.g. therapeutic genes (also ribozymes or antisense
XX sequences), particularly an antigen-encoding sequence for use in gene or
XX cell-based vaccines. Polypeptides encoded by the transcripts are also
XX useful in vaccines; for diagnosing breast cancer and for raising
XX specific antibodies (Ab). Ab are used to detect the polypeptides or as
XX therapeutic agents. Host cells that produce the polypeptides can be used
XX to expand and isolate populations of educated, antigen-specific immune
XX effector cells, e.g. cytotoxic T lymphocytes, and these used for
XX adoptive immunotherapy.
XX
XX Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;
XX
XX Query Match 100.0%; Score 7; DB 21; Length 10;
XX Best Local Similarity 100.0%; Pred No. 9.6e+04;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCTTCAG 7
XX |||||
XX Db 9 GCTTCAG 3
XX
XX RESULT 9
XX AA283879
XX ID AA283879 standard; DNA; 10 BP.
XX AC
XX AA283879;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell upregulated transcript tag #3113.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX

```

KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 XX Homo sapiens.  
 OS WO9965928-A2.  
 PN 23-DEC-1999.  
 XX 18-JUN-1999; 99WO-US13647.  
 XX 19-JUN-1998; 98US-0089853.  
 PR 19-JUN-1998; 98US-0089897.  
 PR 19-JUN-1998; 98US-0090039.  
 PR 19-JUN-1998; 98US-0090040.  
 PR 19-JUN-1998; 98US-0090041.  
 XX (GENZ ) GENZYME CORP.  
 PA (ROBE//) ROBERTS B L.  
 PA (SHAN//) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 XX WPI; 2000-106079/09.  
 XX Isolated polynucleotides differentially expressed between metastatic  
 PT and non-metastatic breast cancer cells, useful for diagnosis,  
 PT prevention and treatment of cancer -  
 XX Claim 1; Page 142; 219pp; English.  
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct  
 CC transcripts that are preferentially transcribed in the metastatic breast  
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).  
 CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the primary or non-metastatic  
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour  
 CC cells). These transcripts can be used for diagnosis, prognosis  
 CC monitoring and treatment of breast cancer, particularly where metastatic.  
 CC Diagnosis is by standard immunoassays or hybridisation/amplification  
 CC reactions. Compounds that modulate expression of the transcripts are  
 CC potentially useful for treatment of (metastatic) breast cancer, while  
 CC promoters from the transcripts are used to direct expression, in selected  
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense  
 CC sequences), particularly an antigen-encoding sequence for use in gene or  
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also  
 CC useful in vaccines; for diagnosing breast cancer and for raising  
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as  
 CC therapeutic agents. Host cells that produce the polypeptides can be used  
 CC to expand and isolate populations of educated, antigen-specific immune  
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for  
 CC adoptive immunotherapy.  
 XX Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 other;  
 SQ Query Match 100.0%; Score 7; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 |||||  
 Db 3 GCTTCAG 9  
 RESULT 10  
 AAZ85548  
 ID AAZ85548 standard; DNA; 10 BP.  
 XX  
 AC AAZ85548;  
 XX  
 DT 07-APR-2000 (first entry)  
 XX  
 DE Metastatic breast tumour cell downregulated transcript tag #4782.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 XX Homo sapiens.  
 OS WO9965928-A2.  
 PN 23-DEC-1999.  
 XX 18-JUN-1999; 99WO-US13647.  
 XX 19-JUN-1998; 98US-0089853.  
 PR 19-JUN-1998; 98US-0089897.  
 PR 19-JUN-1998; 98US-0090039.  
 PR 19-JUN-1998; 98US-0090040.  
 PR 19-JUN-1998; 98US-0090041.  
 XX (GENZ ) GENZYME CORP.  
 PA (ROBE//) ROBERTS B L.  
 PA (SHAN//) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 XX WPI; 2000-106079/09.  
 XX Isolated polynucleotides differentially expressed between metastatic  
 PT and non-metastatic breast cancer cells, useful for diagnosis,  
 PT prevention and treatment of cancer -  
 XX Claim 1; Page 186; 219pp; English.  
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct  
 CC transcripts that are preferentially transcribed in the metastatic breast  
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).  
 CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the primary or non-metastatic  
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour  
 CC cells). These transcripts can be used for diagnosis, prognosis  
 CC monitoring and treatment of breast cancer, particularly where metastatic.  
 CC Diagnosis is by standard immunoassays or hybridisation/amplification  
 CC reactions. Compounds that modulate expression of the transcripts are  
 CC potentially useful for treatment of (metastatic) breast cancer, while  
 CC promoters from the transcripts are used to direct expression, in selected  
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense  
 CC sequences), particularly an antigen-encoding sequence for use in gene or  
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also  
 CC useful in vaccines; for diagnosing breast cancer and for raising  
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as  
 CC therapeutic agents. Host cells that produce the polypeptides can be used  
 CC to expand and isolate populations of educated, antigen-specific immune  
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for  
 CC adoptive immunotherapy.  
 XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 other;  
 SQ Query Match 100.0%; Score 7; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 |||||  
 Db 1 GCTTCAG 7  
 RESULT 11  
 AAF33630/c  
 ID AAF33630 standard; DNA; 10 BP.  
 XX  
 AC AAF33630;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:369.  
 DE  
 XX  
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 XX Saccharomyces cerevisiae.  
 OS  
 XX WO200077214-A2.  
 XX  
 XX 21-DEC-2000.  
 PD  
 XX  
 XX 14-JUN-2000; 2000WO-US16223.  
 PF  
 XX  
 XX 16-JUN-1999; 99US-0335032.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI  
 XX WPI; 2001-061874/07.  
 DR  
 XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis  
 PT of gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle -  
 XX  
 XX Claim 1; Page 388; 419pp; English.  
 PS  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a  
 CC yeast cell; and (b) monitoring expression of a NORF gene whose  
 CC expression varies as in M1, where a test substance which modifies the  
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method  
 CC (M3) for identifying human genes which are involved in cell cycle  
 CC progression comprising contacting human DNA with a probe which comprises  
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies  
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a  
 CC member of a class of drugs having a characteristic effect on gene  
 CC expression in a yeast cell comprising contacting a yeast cell with a  
 CC candidate drug and monitoring expression in the yeast cell of at least 1  
 CC NORF gene whose expression is affected by the class of drugs. The NORF  
 CC genes may be used to study, monitor and affect phases of the cell cycle,  
 CC the differentially expressed genes may be used as markers of phases of  
 CC the cell cycle. The methods may be used to identify candidate drugs which  
 CC affect the cell cycle and for identification of antifungal drugs.  
 CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of  
 CC the present invention. AAF33262 to AAF33267 represent linkers and PCR  
 CC primers used in the SAGE method, in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 DB 7 GCTTCAG 1  
 RESULT 12  
 AAF35902/c  
 ID AAF35902 standard; DNA; 10 BP.

XX AAF35902;  
 AC  
 XX 23-MAR-2001 (first entry)  
 DT  
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2641.  
 DE  
 XX  
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 XX Saccharomyces cerevisiae.  
 OS  
 XX WO200077214-A2.  
 XX  
 XX 21-DEC-2000.  
 PD  
 XX  
 XX 14-JUN-2000; 2000WO-US16223.  
 PF  
 XX  
 XX 16-JUN-1999; 99US-0335032.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI  
 XX WPI; 2001-061874/07.  
 DR  
 XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis  
 PT of gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle -  
 XX  
 XX Example; Page 94; 419pp; English.  
 PS  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a  
 CC yeast cell; and (b) monitoring expression of a NORF gene whose  
 CC expression varies as in M1, where a test substance which modifies the  
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method  
 CC (M3) for identifying human genes which are involved in cell cycle  
 CC progression comprising contacting human DNA with a probe which comprises  
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies  
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a  
 CC member of a class of drugs having a characteristic effect on gene  
 CC expression in a yeast cell comprising contacting a yeast cell with a  
 CC candidate drug and monitoring expression in the yeast cell of at least 1  
 CC NORF gene whose expression is affected by the class of drugs. The NORF  
 CC genes may be used to study, monitor and affect phases of the cell cycle,  
 CC the differentially expressed genes may be used as markers of phases of  
 CC the cell cycle. The methods may be used to identify candidate drugs which  
 CC affect the cell cycle and for identification of antifungal drugs.  
 CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of  
 CC the present invention. AAF33262 to AAF33267 represent linkers and PCR  
 CC primers used in the SAGE method, in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTTCAG 7  
 DB 7 GCTTCAG 1

RESULT 13  
 AAF36192  
 ID AAF36192 standard; DNA; 10 BP.  
 XX AC AAF36192;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2931.  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 XX KW serial analysis of gene expression; antifungal; tag; identification;  
 XX KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX PN WO200077214-A2.  
 XX PD 21-DEC-2000.  
 XX PF 14-JUN-2000; 2000WO-US16223.  
 XX PR 16-JUN-1999; 99US-0335032.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX DR WPI; 2001-061874/07.  
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis  
 XX PT of gene expression (SAGE) tags, useful for studying, monitoring and  
 XX PT affecting phases of the cell cycle -  
 XX PS Example; Page 104; 419pp; English.  
 XX CC The present invention describes an isolated DNA molecule comprising a  
 XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 XX CC previously assigned open reading frame; or nonannotated ORF) genes  
 XX CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 XX CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 XX CC cycle comprising administering a NORF gene whose expression varies by at  
 XX CC least 10% between any two phases of the cell cycle selected from log  
 XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 XX CC antifungal drugs comprising: (a) contacting a test substance with a  
 XX CC yeast cell; and (b) monitoring expression of a NORF gene whose  
 XX CC expression varies as in M1, where a test substance which modifies the  
 XX CC expression of the yeast gene is a candidate antifungal drug; (3) a method  
 XX CC (M3) for identifying human genes which are involved in cell cycle  
 XX CC progression comprising contacting human DNA with a probe which comprises  
 XX CC at least 10 contiguous nucleotides of a NORF gene whose expression varies  
 XX CC as in M1; and (4) a method (M4) for identifying a candidate drug as a  
 XX CC member of a class of drugs having a characteristic effect on gene  
 XX CC expression in a yeast cell comprising contacting a yeast cell with a  
 XX CC candidate drug and monitoring expression in the yeast cell of at least 1  
 XX CC NORF gene whose expression is affected by the class of drugs. The NORF  
 XX CC genes may be used to study, monitor and affect phases of the cell cycle,  
 XX CC the differentially expressed genes may be used as markers of phases of  
 XX CC the cell cycle. The methods may be used to identify candidate drugs which  
 XX CC affect the cell cycle and for identification of antifungal drugs.  
 XX CC AAF3268 to AAF44064 represent SAGE tags used in the exemplification of  
 XX CC the present invention. AAF3262 to AAF3267 represent linkers and PCR  
 XX CC primers used in the SAGE method, in the exemplification of the present  
 XX CC invention.  
 XX SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 other;  
 Query Match 100.0%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. NO. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTCAG 7.  
 DB |||||  
 4 GCTTCAG 10  
 RESULT 14  
 AAF37634/C  
 ID AAF37634 standard; DNA; 10 BP.  
 XX AC AAF37634;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4373.  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 XX KW serial analysis of gene expression; antifungal; tag; identification;  
 XX KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX PN WO200077214-A2.  
 XX PD 21-DEC-2000.  
 XX PF 14-JUN-2000; 2000WO-US16223.  
 XX PR 16-JUN-1999; 99US-0335032.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX DR WPI; 2001-061874/07.  
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis  
 XX PT of gene expression (SAGE) tags, useful for studying, monitoring and  
 XX PT affecting phases of the cell cycle -  
 XX PS Example; Page 156; 419pp; English.  
 XX CC The present invention describes an isolated DNA molecule comprising a  
 XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 XX CC previously assigned open reading frame; or nonannotated ORF) genes  
 XX CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 XX CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 XX CC cycle comprising administering a NORF gene whose expression varies by at  
 XX CC least 10% between any two phases of the cell cycle selected from log  
 XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 XX CC antifungal drugs comprising: (a) contacting a test substance with a  
 XX CC yeast cell; and (b) monitoring expression of a NORF gene whose  
 XX CC expression varies as in M1, where a test substance which modifies the  
 XX CC expression of the yeast gene is a candidate antifungal drug; (3) a method  
 XX CC (M3) for identifying human genes which are involved in cell cycle  
 XX CC progression comprising contacting human DNA with a probe which comprises  
 XX CC at least 10 contiguous nucleotides of a NORF gene whose expression varies  
 XX CC as in M1; and (4) a method (M4) for identifying a candidate drug as a  
 XX CC member of a class of drugs having a characteristic effect on gene  
 XX CC expression in a yeast cell comprising contacting a yeast cell with a  
 XX CC candidate drug and monitoring expression in the yeast cell of at least 1  
 XX CC NORF gene whose expression is affected by the class of drugs. The NORF  
 XX CC genes may be used to study, monitor and affect phases of the cell cycle,  
 XX CC the differentially expressed genes may be used as markers of phases of  
 XX CC the cell cycle. The methods may be used to identify candidate drugs which  
 XX CC affect the cell cycle and for identification of antifungal drugs.  
 XX CC AAF3268 to AAF44064 represent SAGE tags used in the exemplification of  
 XX CC the present invention. AAF3262 to AAF3267 represent linkers and PCR  
 XX CC primers used in the SAGE method, in the exemplification of the present  
 XX CC invention.  
 XX SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 other;



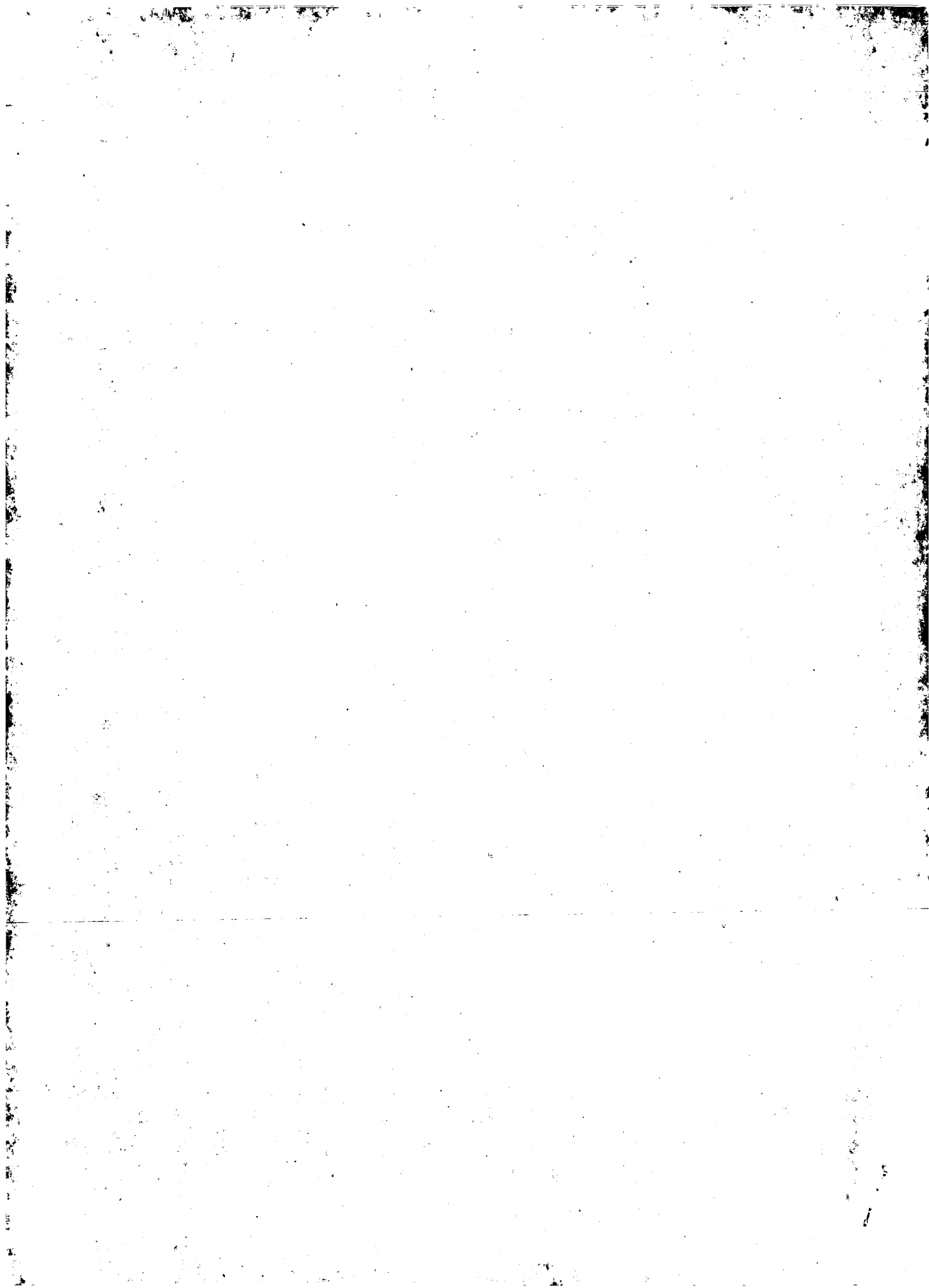
Query Match 100.0%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC invention.  
 XX  
 SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 other;

Query Match 100.0%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
 |||||  
 Db 9 GCTTCAG 3

RESULT 15  
 AAF41438/c  
 ID AAF41438 standard; DNA; 10 BP.  
 XX  
 AC AAF41438;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8177.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 FN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US16223.  
 XX  
 PR 16-JUN-1999; 99US-0335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX  
 DR WPI; 2001-061874/07.  
 XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis  
 of gene expression (SAGE) tags, useful for studying, monitoring and  
 affecting phases of the cell cycle -  
 XX  
 PS Example; Page 292; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 coding sequence of a yeast gene selected from a group of 745 NORF (not  
 previously assigned open reading frame; or nonannotated ORF) genes  
 comprising a SAGE (serial analysis of gene expression) tag. Also  
 described are: (1) a method (M1) of using NORF genes to affect the cell  
 cycle comprising administering a NORF gene whose expression varies by at  
 least 10% between any two phases of the cell cycle selected from log  
 phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 antifungal drugs comprising: (a) contacting a test substance with a  
 yeast cell; and (b) monitoring expression of a NORF gene whose  
 expression varies as in M1, where a test substance which modifies the  
 expression of the yeast gene is a candidate antifungal drug; (3) a method  
 (M3) for identifying human genes which are involved in cell cycle  
 progression comprising contacting human DNA with a probe which comprises  
 at least 10 contiguous nucleotides of a NORF gene whose expression varies  
 as in M1; and (4) a method (M4) for identifying a candidate drug as a  
 member of a class of drugs having a characteristic effect on gene  
 expression in a yeast cell comprising contacting a yeast cell with a  
 candidate drug and monitoring expression in the yeast cell of at least 1  
 NORF gene whose expression is affected by the class of drugs. The NORF  
 genes may be used to study, monitor and affect phases of the cell cycle,  
 the differentially expressed genes may be used as markers of phases of  
 the cell cycle. The methods may be used to identify candidate drugs which  
 affect the cell cycle and for identification of antifungal drugs.  
 CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of  
 the present invention. AAF33262 to AAF33267 represent linkers and PCR  
 primers used in the SAGE method, in the exemplification of the present



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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 81.4064 Seconds  
(without alignments)  
2502.502 Million cell updates/sec

Title: US-08-770-564A-12  
Perfect score: 7  
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl:

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_cm:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7	100.0	10	6	AR029539	Sequence
2	7	100.0	10	6	AR093732	Sequence
3	7	100.0	10	6	AR098492	Sequence
4	7	100.0	10	6	AR162919	Sequence
5	7	100.0	10	6	AX301417	Sequence
6	7	100.0	10	6	AX377325	Sequence
7	7	100.0	10	6	AX441418	Sequence
8	7	100.0	10	6	AX453914	Sequence
9	7	100.0	10	6	I41452	Sequence 49
10	7	100.0	10	6	A27401	Sequence
11	7	100.0	10	6	AR059962	Sequence
12	7	100.0	10	6	AX339224	Sequence
13	7	100.0	10	6	AX471563	Sequence
14	7	100.0	10	6	AX471563	Sequence
15	7	100.0	10	6	HSOLIGON	Sequence 16
16	7	100.0	10	6	I17488	Sequence
17	7	100.0	10	6	AR167729	Sequence
18	7	100.0	10	6	AR195296	Sequence
19	7	100.0	10	6	AX027028	Sequence
20	7	100.0	10	6	E29613	Sequence
21	7	100.0	10	6	E38719	Sequence
22	7	100.0	10	6	E64145	Sequence
23	7	100.0	10	6	S57113S2	Sequence
24	7	100.0	10	6	A11076	Sequence
25	7	100.0	10	6	A59446	Sequence 39
26	7	100.0	10	6	AR013809	Sequence
27	7	100.0	10	6	AR182199	Sequence
28	7	100.0	10	6	AX003113	Sequence
29	7	100.0	10	6	AX146661	Sequence
30	7	100.0	10	6	A40504	Sequence 41
31	7	100.0	10	6	A44356	Sequence 4
32	7	100.0	10	6	A89031	Sequence 11
33	7	100.0	10	6	AX316400	Sequence
34	7	100.0	10	6	BD005920	Sequence
35	7	100.0	10	6	I95576	Sequence 4
36	7	100.0	10	6	I95584	Sequence 12
37	7	100.0	10	6	A04761	Sequence
38	7	100.0	10	6	A11089	Sequence
39	7	100.0	10	6	A35086	Sequence
40	7	100.0	10	6	A64168	Sequence 34
41	7	100.0	10	6	A68354	Sequence
42	7	100.0	10	6	A88036	Sequence 18
43	7	100.0	10	6	A90003	Sequence
44	7	100.0	10	6	AR031280	Sequence
45	7	100.0	10	6	AR036402	Sequence

# ALIGNMENTS

RESULT 1	AR029539	Sequence 49 from patent US 5859336.	10 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR029539	Sequence 49 from patent US 5859336.	10 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	AR029539	Sequence 49 from patent US 5859336.	10 bp	DNA	linear	PAT 29-SEP-1999
ACCESSION	AR029539	Sequence 49 from patent US 5859336.	10 bp	DNA	linear	PAT 29-SEP-1999
VERSION	AR029539.1	GI:5941512				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 10)					
AUTHORS	Kozziel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launius,K.I., Bowman,C.G., Dawson,J.L., Dunder,E.M., Pace,G.M. and Suttie,J.L.					
TITLE	Synthetic DNA sequence having enhanced activity in maize					

JOURNAL Patent: US 5859336-A 49 12-JAN-1999;  
 FEATURES Location/Qualifiers  
 1. .10  
 BASE COUNT 1 a 3 c 3 g 3 t  
 ORIGIN

Query Match 100.0%; Score 7; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
 Db 2 GCTTCAG 8

RESULT 2  
 LOCUS AR093732/c 10 bp DNA linear PAT 08-SEP-2000  
 DEFINITION Sequence 10 from patent US 6001572.  
 ACCESSION AR093732  
 VERSION AR093732.1 GI:10020481  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Toothman,P.  
 TITLE Method of identifying Aloo using PCR  
 JOURNAL Patent: US 6001572-A 10 14-DEC-1999;  
 FEATURES Location/Qualifiers  
 1. .10  
 BASE COUNT 3 a 3 c 3 g 1 t  
 ORIGIN

Query Match 100.0%; Score 7; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
 Db 7 GCTTCAG 1

RESULT 3  
 LOCUS AR098492 10 bp DNA linear PAT 14-FEB-2001  
 DEFINITION Sequence 49 from patent US 6075185.  
 ACCESSION AR098492  
 VERSION AR098492.1 GI:12807749  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Kozel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V., Wright,M.S., Laisi,K.L., Rothstein,S.J., Bowman,C.G., Dawson,J.L., Dunder,E.M., Pace,G.M., and Suttie,J.L.  
 TITLE Synthetic DNA sequence having enhanced insecticidal activity in maize  
 JOURNAL Patent: US 6075185-A 49 13-JUN-2000;  
 FEATURES Location/Qualifiers  
 1. .10  
 BASE COUNT 1 a 3 c 3 g 3 t  
 ORIGIN

Query Match 100.0%; Score 7; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7

Db 2 GCTTCAG 8

RESULT 4  
 LOCUS AR162919/c 10 bp DNA linear PAT 17-OCT-2001  
 DEFINITION Sequence 1 from patent US 6260034.  
 ACCESSION AR162919  
 VERSION AR162919.1 GI:16230279  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Bjorksten,L.  
 TITLE Method and a system for nucleic acid sequence analysis  
 JOURNAL Patent: US 6260034-A 1 10-JUL-2001;  
 FEATURES Location/Qualifiers  
 1. .10  
 BASE COUNT 2 a 4 c 2 g 2 t  
 ORIGIN

Query Match 100.0%; Score 7; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
 Db 8 GCTTCAG 2

RESULT 5  
 LOCUS AX301417/c 10 bp DNA linear PAT 30-NOV-2001  
 DEFINITION Sequence 131 from Patent WO0185941.  
 ACCESSION AX301417  
 VERSION AX301417.1 GI:17382500  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Versteeg,R. and Caron,H.N.  
 TITLE Myc targets  
 JOURNAL Patent: WO 0185941-A 131 15-NOV-2001;  
 Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)  
 FEATURES Location/Qualifiers  
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 BASE COUNT 3 a 3 g 2 t  
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Query Match 100.0%; Score 7; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
 Db 10 GCTTCAG 4

RESULT 6  
 LOCUS AX377325/c 10 bp DNA linear PAT 18-MAR-2002  
 DEFINITION Sequence 63 from Patent WO0212498.  
 ACCESSION AX377325  
 VERSION AX377325.1 GI:19573612  
 KEYWORDS  
 SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Klem,S.E., Koshy,B. and Tanguay,D.A.  
TITLE Haplotypes of the is11 gene  
JOURNAL Patent: WO 0212498-A 63 14-FEB-2002;  
Genaisance Pharmaceuticals, Inc. (US)

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DEFINITION Sequence 49 from Patent EP1209237.  
ACCESSION AX441418  
VERSION AX441418.1 GI:21690399  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Koziel,M.G., Desai,N.M., Lewis,K.S., Kramer,V.C., Warren,G.W.,  
Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L.  
and Rothstein,S.J.  
TITLE Synthetic dna sequence having enhanced insecticidal activity in  
maize  
JOURNAL Patent: EP 1209237-A 49 29-MAY-2002;  
Syngenta Participations AG (CH)

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Db 2 GCTTCAG 8

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AX453914  
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DEFINITION Sequence 49 from Patent EP1213356.  
ACCESSION AX453914  
VERSION AX453914.1 GI:21713572  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Koziel,M.G., Desai,N.M., Lewis,K.S., Kramer,V.C., Warren,G.W.,  
Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L.  
and Rothstein,S.J.

TITLE Synthetic dna sequence having enhanced insecticidal activity in  
maize  
JOURNAL Patent: EP 1213356-A 49 12-JUN-2002;  
Syngenta Participations AG (CH)

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QY 1 GCTTCAG 7  
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Db 2 GCTTCAG 8

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I41452  
LOCUS I41452 10 bp DNA linear PAT 13-MAY-1997  
DEFINITION Sequence 49 from patent US 5625136.  
ACCESSION I41452  
VERSION I41452.1 GI:2082042  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Koziel,M.G., Desai,N.M., Lewis,K.S., Kramer,V.C., Warren,G.W.,  
Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L.,  
Rothstein,S.J., Bowman,C.G., Dawson,J.L., Dunder,E.M., Pace,G.M.  
and Suttie,J.H.  
TITLE Synthetic DNA sequence having enhanced insecticidal activity in  
maize  
JOURNAL Patent: US 5625136-A 49 29-APR-1997;  
Syngenta Participations AG (CH)

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Db 2 GCTTCAG 8

RESULT 10  
A27401  
LOCUS A27401 11 bp DNA linear PAT 09-JUL-2002  
DEFINITION Oligonucleotide HP10.  
ACCESSION A27401  
VERSION A27401.1 GI:21727210  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and  
Kobayashi,M.  
TITLE New tissue plasminogen activator  
JOURNAL Patent: EP 0302456-A 1 08-FEB-1989;  
FUJISAWA PHARMACEUTICAL CO., LTD

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Db 2 GCTTCAG 8

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DEFINITION      Sequence 9 from patent US 5840533.
ACCESSION      AR059962
VERSION      AR059962.1 GI:5986412
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1. (bases 1 to 11)
AUTHORS      Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and Kobayashi,M.
TITLE      Tissue plasminogen activator
JOURNAL      Patent: US 5840533-A 9 24-NOV-1998;
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Db 2 GCTTCAG 8

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DEFINITION      Sequence 18 from Patent WO0196602.
ACCESSION      AX339224
VERSION      AX339224.1 GI:18135485
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Yang,A.L. and Festing,M.
JOURNAL      Methods and materials to determine the p53 status of a sample by determining the binding of p53 to a vector
MEDICAL RESEARCH COUNCIL (GB)
PATENT: WO 0196602-A 18 20-DEC-2001;
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BASE COUNT      2 a      2 c      5 g      2 t
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
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Db 2 GCTTCAG 8

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LOCUS      AX471563/c      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION      Sequence 1140 from Patent WO02053773.
ACCESSION      AX471563
VERSION      AX471563.1 GI:22206688
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Hofmann,K., Conradt,M. and Petersohn,D.
JOURNAL      Method for determining skin stress or skin ageing in vitro
PATENT: WO 02053773-A 1140 11-JUL-2002;
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Qy 1 GCTTCAG 7
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Db 9 GCTTCAG 3

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LOCUS      HSOLIGON      11 bp      DNA      linear      PAT 02-MAR-1995
DEFINITION      oligonucleotide.
ACCESSION      A22481
VERSION      A22481.1 GI:833691
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Brownlee,G.G. and Choo,K.H.
TITLE      Molecular cloning of the gene for human anti-haemophilic factor IX
JOURNAL      Patent: EP 0107278-A 16 02-MAY-1984;
NATIONAL RESEARCH DEVELOPMENT CORPORATION
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Qy 1 GCTTCAG 7
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Db 2 GCTTCAG 8

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LOCUS      IL17488      11 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION      Sequence 16 from patent US 5485529.
ACCESSION      IL17488
VERSION      IL17488.1 GI:1597843
KEYWORDS

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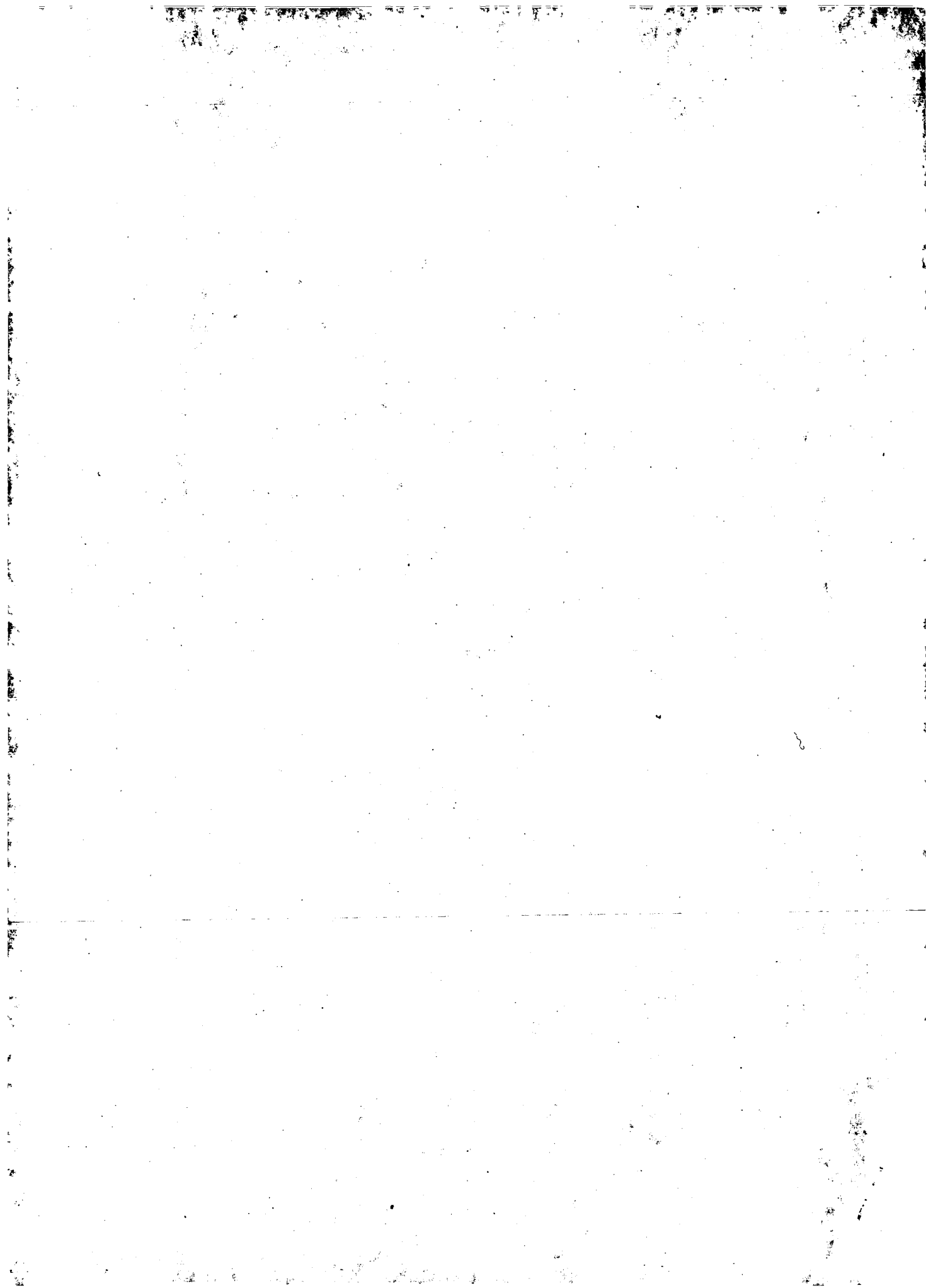
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ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 11)
AUTHORS      de Boer H.A., Heyneker, H.L. and Seeburg, P.H.
TITLE        DNA for expression of bovine growth hormone
JOURNAL      Patent: US 5489529-A 16 06-FEB-1996;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
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Db 2 GCTTCAG 8

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-08-770-564A-13

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	18	90.0	19	1	PCT-US03-04088-279
C 3	18	90.0	28	6	US-09-690-885-5
4	16.4	82.0	25	12	US-60-427-808-561675
5	15.4	77.0	18	9	US-10-310-188-7112
6	15.4	77.0	25	12	US-60-427-808-774039
7	15.2	76.0	25	9	US-10-355-577-692202
8	15.2	76.0	25	12	US-60-427-808-799814
9	15.2	76.0	25	12	US-60-427-836-660522
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11	15	75.0	25	9	US-10-355-577-635066
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13	14.8	74.0	25	12	US-60-427-836-561672
14	14.4	72.0	18	9	US-10-310-188-64333
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C 16	14.2	71.0	25	7	US-09-954-445A-48478
17	14.2	71.0	25	12	US-60-427-808-291699
18	14.2	71.0	25	12	US-60-427-808-401732
19	14.2	71.0	25	12	US-60-427-836-242577
C 20	14.2	71.0	25	12	US-60-427-836-563632

C	21	14.2	71.0	40	6	US-09-765-272A-253	Sequence 253, App
	22	14	70.0	25	12	US-60-427-808-525499	Sequence 525499,
	23	14	70.0	25	12	US-60-427-808-982397	Sequence 982397,
	24	13.8	69.0	21	9	US-10-349-143-7670	Sequence 7670, Ap
	25	13.8	69.0	25	9	US-10-355-577-252936	Sequence 252936,
	26	13.8	69.0	25	9	US-10-355-577-288031	Sequence 288031,
	27	13.8	69.0	25	12	US-60-427-808-325661	Sequence 325661,
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	29	13.8	69.0	25	12	US-60-427-808-638319	Sequence 638319,
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	32	13.8	69.0	25	12	US-60-427-808-762709	Sequence 762709,
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	36	13.6	68.0	25	9	US-10-355-577-396446	Sequence 396446,
	37	13.6	68.0	25	9	US-10-355-577-692201	Sequence 692201,
	38	13.6	68.0	25	12	US-60-417-190-112697	Sequence 112697,
	39	13.6	68.0	25	12	US-60-417-190-112698	Sequence 112698,
	40	13.6	68.0	25	12	US-60-417-190-112699	Sequence 112699,
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ALIGNMENTS

RESULT 1

PCT-US03-04088-15/c  
; Sequence 15, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 15  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
; OTHER INFORMATION: region  
PCT-US03-04088-15

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DB 19 TTTTGTGCTCTAGA 2

RESULT 2
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; Sequence 279, Application PCT/US0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-279

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Best Local Similarity 38.9%; Pred. No. 1.2e+03;
Matches 7; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

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DB 1 UUUUUUUUUUCUAGA 18

RESULT 3
US-09-690-885-5/c
; Sequence 5, Application US/09690885
; GENERAL INFORMATION:
; APPLICANT: SAGAWA, HIROAKI
; APPLICANT: UENO, HARUMI
; APPLICANT: OSHIMA, ATSUSHI
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/690,885
FILING DATE: 18-Oct-2000
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0319P
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-690-885-5

Query Match 90.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGCTCTCTAGA 20
DB 21 TTTTGTGCTCTCTAGA 4

RESULT 4
US-60-427-836-561675
; Sequence 561675, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 561675
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-561675

Query Match 82.0%; Score 16.4; DB 12; Length 25;
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTTTGTGCTCTCTAGA 20
DB 6 TTTTGTGCTCTCTAGA 23

RESULT 5
US-10-310-188-7112
; Sequence 7112, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN:
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7112
; LENGTH: 18
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-7112

Query Match      77.0%; Score 15.4; DB 9; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAG 19
   ||||| ||||| |||||
Db 1 TTTTGTGTTGCTCTAG 17

RESULT 6
US-60-427-808-774039
; Sequence 774039, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 774039
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-774039

Query Match      77.0%; Score 15.4; DB 12; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCT 17
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Db 4 CATTGTTGTTGCTCT 20

RESULT 7
US-10-355-577-692202
; Sequence 692202, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 692202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-692202

Query Match      76.0%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
   ||||| ||||| |||||
Db 6 CATTGTTGTTGCTCAG 25

RESULT 8
US-60-427-808-799814
; Sequence 799814, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
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; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 799814
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-799814

Query Match      76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
   ||||| ||||| |||||
Db 4 CATTGTTGTTGCTCTAGA 23

RESULT 9
US-60-427-836-660522
; Sequence 660522, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 660522
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-660522

Query Match      76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
   ||||| ||||| |||||
Db 6 CATTGTTGTTGCCNAGA 25

RESULT 10
US-10-310-695-12/c
; Sequence 12, Application US/10310695
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: ENENKEL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEB:019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-310-695-12

Query Match      76.0%; Score 15.2; DB 9; Length 27;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
   ||||| ||||| |||||
Db 25 CATTATTGATTCTCTAGA 6
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RESULT 11
US-10-355-577-635066
; Sequence 635066 Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635066
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-635066

Query Match          75.0%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTGTTGCTCTA 18
DB 4 TTTTGTGTTGCTCTA 18

RESULT 12
US-60-427-836-281208
; Sequence 281208 Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 281208
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-281208

Query Match          74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAGA 20
DB 5 TTTTGTGTTGCTCTGGA 22

RESULT 13
US-60-427-836-561672
; Sequence 561672 Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 561672
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-561672

Query Match          74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
US-10-310-188-64233
; Sequence 64233 Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN-
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64233
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-64233

Query Match          72.0%; Score 14.4; DB 9; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTC 16
DB 3 CCTTTTGTGTTGCTC 18

RESULT 15
US-10-355-577-85332
; Sequence 85332 Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 85332
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-85332

Query Match          72.0%; Score 14.4; DB 9; Length 25;
Best Local Similarity 93.8%; Pred. No. 3.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTC 16
DB 5 CATTGTTGTTGCTC 20

Search completed: June 26, 2003, 04:15:22
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-08-770-564A-13

Perfect score: 20

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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# SUMMARIES

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4	19	95.0	20	21	US-09-540-119B-16
5	17	85.0	22	22	US-09-587-662A-5
6	16	80.0	22	13	US-08-973-589-18
7	16	80.0	25	36	US-09-954-427-58350
8	16	80.0	25	67	US-60-233-166-58350
9	15.2	76.0	25	79	US-60-353-987-69202
10	15	75.0	25	36	US-09-956-584-317896
11	15	75.0	25	67	US-60-233-166-58351
12	15	75.0	25	79	US-60-353-987-635066
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14	14.4	72.0	25	36	US-09-956-584-317896
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16	14.4	72.0	25	36	US-09-956-584-450078
17	14.4	72.0	25	36	US-09-956-584-450079
18	14.4	72.0	25	36	US-09-956-584-450083
19	14.4	72.0	25	36	US-09-956-584-450085
20	14.4	72.0	25	67	US-60-234-017-323013
21	14.4	72.0	25	67	US-60-234-017-452894



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; Sequence 10, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,634
; FILING DATE: 31-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-521-634-10

Query Match      100.0%; Score 20; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATTGTTGTTGCTCTAGA 20
      |||||||
DB      28 CATTGTTGTTGCTCTAGA 9

RESULT 4
US-09-540-1198-16
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-1198-16

Query Match      95.0%; Score 19; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATTGTTGTTGCTCTAG 19
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DB      2 CATTGTTGTTGCTCTAG 20

RESULT 5
US-09-587-662A-5
; Sequence 5, Application US/09587662A
; GENERAL INFORMATION:
; APPLICANT: Au, Jessie L.-S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING DRUG ACTIVITY
; TITLE OF INVENTION: THROUGH TELOMERE DAMAGE
; FILE REFERENCE: JAG-004
; CURRENT APPLICATION NUMBER: US/09/587,662A
; CURRENT FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/137,549
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-09-587-662A-5

Query Match      85.0%; Score 17; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATTGTTGTTGCTCT 17
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DB      8 CATTGTTGTTGCTCT 24

RESULT 6
US-08-973-589-18
; Sequence 18, Application US/08973589
; GENERAL INFORMATION:
; APPLICANT: Greider, Carol
; APPLICANT: Autexier, Chantal
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: ESSENTIAL OLIGONUCLEOTIDES OF VERTEBRATE
; TITLE OF INVENTION: TELOMERASE
; FILE REFERENCE: CSHL95-02A
; CURRENT APPLICATION NUMBER: US/08/973,589
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US96/09517
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/478,352
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-08-973-589-18
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Query Match 80.0%; Score 16; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0;  
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATTGTTGTTGCTC 16  
DB 7 CATTGTTGTTGCTC 22

RESULT 7  
US-09-954-427-58350/c  
; Sequence 58350, Application US/09954427  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/09/954,427  
; CURRENT FILING DATE: 2001-09-17  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 58350  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-09-954-427-58350

Query Match 80.0%; Score 16; DB 16; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0;  
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 4 TTTTGTGTTGCTCTAG 19  
DB 25 TTTTGTGTTGCTCTAG 10

RESULT 8  
US-60-233-166-58350/c  
; Sequence 58350, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 58350  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-60-233-166-58350

Query Match 80.0%; Score 16; DB 67; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0;  
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 4 TTTTGTGTTGCTCTAG 19  
DB 25 TTTTGTGTTGCTCTAG 10

RESULT 9  
US-60-353-987-692202  
; Sequence 692202, Application US/60353987

GENERAL INFORMATION:  
; APPLICANT: Mittmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133  
; FILE REFERENCE: 3121  
; CURRENT APPLICATION NUMBER: US/60/353,987  
; CURRENT FILING DATE: 2002-02-01  
; NUMBER OF SEQ ID NOS: 997516  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 692202  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-60-353-987-692202

Query Match 76.0%; Score 15.2; DB 79; Length 25;  
Best Local Similarity 85.0%; Pred. No. 2.6e+04; Indels 0;  
Matches 17; Conservative 0; Mismatches 3; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20  
DB 6 CATTGTTGTTGCTCTAGA 25

RESULT 10  
US-09-954-427-58351/c  
; Sequence 58351, Application US/09954427  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/09/954,427  
; CURRENT FILING DATE: 2001-09-17  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 58351  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-09-954-427-58351

Query Match 75.0%; Score 15; DB 36; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04; Indels 0;  
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 5 TTTTGTGTTGCTCTAG 19  
DB 25 TTTTGTGTTGCTCTAG 11

RESULT 11  
US-60-233-166-58351/c  
; Sequence 58351, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 58351  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-60-233-166-58351



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Query Match      75.0%; Score 15; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TTTTGTGTTGCTCTAG 19
        |||
Db      25 TTTTGTGTTGCTCTAG 11

RESULT 12
US-60-353-987-635066
; Sequence 635066, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635066
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-635066

Query Match      75.0%; Score 15; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TTTTGTGTTGCTCTA 18
        |||
Db      4 TTTTGTGTTGCTCTA 18

RESULT 13
US-09-953-198-241
; Sequence 241, Application US/09953198
; GENERAL INFORMATION:
; APPLICANT: COMPUGEN LTD
; TITLE OF INVENTION: DATA BASE OF SNP
; FILE REFERENCE: 1351253
; CURRENT APPLICATION NUMBER: US/09/953,198
; CURRENT FILING DATE: 2001-08-12
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-953-198-241

Query Match      74.0%; Score 14.8; DB 36; Length 41;
Best Local Similarity 88.9%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 ATTTTGTGTTGCTCTAG 19
        |||
Db      2 ATTTTGTGTTGCTTTG 19

RESULT 14
US-09-956-584-317896
; Sequence 317896, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 450073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-450073

Query Match      72.0%; Score 14.4; DB 36; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 ATTTTGTGTTGCTCT 17
        |||
Db      24 ATTTTGTGTTGCTCT 9

Search completed: June 25, 2003, 06:20:29
Job time : 1698.67 secs

; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 317896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-317896

Query Match      72.0%; Score 14.4; DB 36; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 ATTTTGTGTTGCTCT 17
        |||
Db      1 ATTTTGTGTTGCTCT 16

RESULT 15
US-09-956-584-450073/c
; Sequence 450073, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 450073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-450073

Query Match      72.0%; Score 14.4; DB 36; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 ATTTTGTGTTGCTCT 17
        |||
Db      24 ATTTTGTGTTGCTCT 9

Search completed: June 25, 2003, 06:20:29
Job time : 1698.67 secs
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 60.7968 Seconds  
(without alignments)  
482.732 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20

Sequence: 1 CATTTCCTGCTCTAGA 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	14.2	71.0	40	10	US-09-765-272-253
C 3	14.2	71.0	42	9	US-09-769-787-375
C 4	13.6	68.0	20	9	US-09-971-894-8
C 5	13.4	67.0	26	10	US-09-815-171A-27
C 6	13.4	67.0	30	7	US-08-978-635-38
C 7	13.4	67.0	30	7	US-08-978-636-29
C 8	13.4	67.0	30	8	US-08-978-633-38
C 9	13.4	67.0	30	8	US-08-978-634-38
C 10	13.4	67.0	30	8	US-08-978-637-38
C 11	13.4	67.0	30	8	US-08-978-632-38
C 12	13.2	66.0	21	9	US-09-997-868-13
C 13	13.2	66.0	40	9	US-10-093-335-6
C 14	12.8	64.0	25	9	US-10-215-112-870
C 15	12.8	64.0	29	9	US-09-863-040-49
C 16	12.6	63.0	25	9	US-10-098-263B-32778
C 17	12.6	63.0	36	9	US-10-091-135-32
C 18	12.6	63.0	45	10	US-09-922-261-124
C 19	12.4	62.0	25	9	US-10-098-263B-67431

## ALIGNMENTS

### RESULT 1

US-10-032-924-8/c

; Sequence 8, Application US/10032924

; Publication No. US20030022190A1

; GENERAL INFORMATION:

; APPLICANT: Shipman, Robert

; Leushner, James M.

; Dunn, James M.

; TITLE OF INVENTION: METHOD AND REAGENTS FOR TESTING FOR

; MUTATIONS IN THE BRCA1 GENE

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oppedahl & Larson

; STREET: 1992 Commerce Street Suite 309

; CITY: Yorktown

; STATE: NY

; COUNTRY: US

; ZIP: 10598

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS DOS

; SOFTWARE: Word Perfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/032,924

; FILING DATE: 26-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/649,950

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Larson, Marina T.

; REGISTRATION NUMBER: 32,038

; REFERENCE/DOCKET NUMBER: VGEN.P-028-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (914) 245-3252

; TELEFAX: (914) 962-4330

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21

; TYPE: nucleic acid

Sequence 109459,  
Sequence 116952,  
Sequence 133, App  
Sequence 370, App  
Sequence 285, App  
Sequence 15, Appl  
Sequence 19, Appl  
Sequence 18, Appl  
Sequence 204, App  
Sequence 1024, Ap  
Sequence 16847, A  
Sequence 72375, A  
Sequence 9, Appli  
Sequence 9, Appli  
Sequence 45, Appl  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 7, Appli  
Sequence 10137, A  
Sequence 312, App  
Sequence 312, App  
Sequence 23, Appl  
Sequence 19, Appl  
Sequence 5, Appli  
Sequence 7, Appli  
Sequence 5, Appli

20 12.4 62.0 25 9 US-10-098-263B-109459  
21 12.4 62.0 25 9 US-10-098-263B-116952  
22 12.4 62.0 26 10 US-09-426-548-133  
23 12.4 62.0 33 10 US-09-765-272-370  
24 12.4 62.0 38 9 US-10-085-906-285  
25 12.4 62.0 40 9 US-10-084-553-15  
26 12.4 62.0 40 9 US-10-084-553-19  
27 12.4 62.0 43 9 US-10-084-553-18  
28 12.2 61.0 20 9 US-10-067-125-204  
29 12.2 61.0 23 10 US-09-263-959-1024  
30 12.2 61.0 25 9 US-10-098-263B-16847  
31 12.2 61.0 25 9 US-10-098-263B-72375  
32 12.2 61.0 29 9 US-09-841-513-9  
33 12.2 61.0 29 9 US-10-038-718-9  
34 12.2 61.0 32 9 US-10-045-631A-45  
35 12.2 61.0 39 9 US-09-846-430A-4  
36 12.2 61.0 48 9 US-10-179-046-4  
37 12 60.0 20 10 US-09-839-136-7  
38 12 60.0 25 9 US-10-098-263B-10137  
39 12 60.0 26 9 US-10-044-692-312  
40 12 60.0 26 9 US-10-044-539-312  
41 12 60.0 26 10 US-09-057-351-23  
42 12 60.0 27 9 US-10-199-024-19  
43 12 60.0 30 9 US-10-263-766-5  
44 12 60.0 30 9 US-10-263-766-7  
45 12 60.0 30 10 US-09-272-162-5



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RESULT 5
US-09-815-171A-27
; Sequence 27, Application US/09815171A
; Patent No. US20020064780A1
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Zichi, Dominic
; APPLICANT: Jenison, Robert D
; APPLICANT: Schneider, Daniel J
; TITLE OF INVENTION: Method and Apparatus for the Automated Generation of
; FILE REFERENCE: SML.03
; CURRENT APPLICATION NUMBER: US/09/815,171A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/616,284
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/356,233
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/232,946
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 08/792,075
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: 09/143,190
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 08/469,609
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-815-171A-27

Query Match 67.0%; Score 13.4; DB 10; Length 26;
Best Local Similarity 93.3%; Pred. No. 7.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTTTGTGCTCT 17
Db 3 TTTTGTGCTCT 17

RESULT 6
US-08-978-635-38/c
; Sequence 38, Application US/08978635A
; Publication No. US20030087434A1
; GENERAL INFORMATION:
; APPLICANT: Rabbani, Elazar
; APPLICANT: Donegan, James J.
; APPLICANT: Liu, Dekai
; APPLICANT: Kelker, No. US20030087434A1man E.
; APPLICANT: Engelhardt, Dean L.
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING
; FILE REFERENCE: ENZ-53D4.032499
; CURRENT APPLICATION NUMBER: US/08/978,635A
; CURRENT FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence:oligo
US-08-978-635-38

Query Match 67.0%; Score 13.4; DB 7; Length 30;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTGCTCTAGA 20
Db 17 TTTGTTAGCTCTAGA 3

RESULT 7
US-08-978-636-29/c
; Sequence 29, Application US/08978636
; Publication No. US20030104620A1
; GENERAL INFORMATION:
; APPLICANT: ELAZAR RABBANI
; APPLICANT: JANNIS G. STAVRIANOPOULOS
; APPLICANT: JAMES J. DONEGAN
; APPLICANT: DAKAI LIU
; APPLICANT: NORMAN E. KELKER
; APPLICANT: DEAN L. ENGELHARDT
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING
; TITLE OF INVENTION: AND/OR PROPERTY EXHIBITING COMPOSITIONS FOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ENZO THERAPEUTICS, INC.
; STREET: C/O ENZO BIOCHEM, INC.
; STREET: 527 MADISON AVENUE,
; CITY: 9TH FLOOR
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Micro Floppy Disk. 1.44 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM PC/XT/AT, IBM PS/2 OR COMPATIBLES
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: MICROSOFT WORD - ASCII TEXT (DOS)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,636
; FILING DATE: 25-NOVEMBER-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FEDUS, RONALD C.
; REGISTRATION NUMBER: 32,567
; REFERENCE/DOCKET NUMBER: ENZ-53 (D3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 583-0100
; TELEFAX: (212) 583-0150
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: TER-1
US-08-978-636-29

Query Match 67.0%; Score 13.4; DB 7; Length 30;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTGCTCTAGA 20
Db 17 TTTGTTAGCTCTAGA 3

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RESULT 8  
US-08-978-633-38/c  
; Sequence 38, Application US/08978633  
; Patent No. US20010006814A1  
; GENERAL INFORMATION:  
; APPLICANT: Rabbani, Elazar  
; APPLICANT: Stavrianopoulos, Jannis G.  
; APPLICANT: Donegan, James J.  
; APPLICANT: Liu, Dakai  
; APPLICANT: Kelker, No. US20010006814A1man E.  
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING  
; FILE REFERENCE: ENZ-53 (D1).081299  
; CURRENT APPLICATION NUMBER: US/08/978,633  
; CURRENT FILING DATE: 1997-11-25  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:oligo  
US-08-978-633-38

Query Match 67.0%; Score 13.4; DB 8; Length 30;  
Best Local Similarity 93.3%; Pred. No. 7.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTTGGCTCTAGA 20  
|||||  
DB 17 TTTGTTAGCTCTAGA 3

RESULT 9  
US-08-978-634-38/c  
; Sequence 38, Application US/08978634A  
; Patent No. US20010006815A1  
; GENERAL INFORMATION:  
; APPLICANT: Rabbani, Elazar  
; APPLICANT: Stavrianopoulos, Jannis G.  
; APPLICANT: Donegan, James J.  
; APPLICANT: Liu, Dakai  
; APPLICANT: Kelker, No. US20010006815A1man E.  
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING  
; FILE REFERENCE: ENZ-53 (D2).081299  
; CURRENT APPLICATION NUMBER: US/08/978,634A  
; CURRENT FILING DATE: 1997-11-25  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:oligo  
US-08-978-634-38

Query Match 67.0%; Score 13.4; DB 8; Length 30;  
Best Local Similarity 93.3%; Pred. No. 7.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTTGGCTCTAGA 20  
|||||  
DB 17 TTTGTTAGCTCTAGA 3

RESULT 10

US-08-978-637-38/c  
; Sequence 38, Application US/08978637A  
; Patent No. US20010006816A1  
; GENERAL INFORMATION:  
; APPLICANT: Rabbani, Elazar  
; APPLICANT: Stavrianopoulos, Jannis G.  
; APPLICANT: Donegan, James J.  
; APPLICANT: Liu, Dakai  
; APPLICANT: Kelker, No. US20010006816A1man E.  
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING  
; FILE REFERENCE: ENZ-53 (D5).081299  
; CURRENT APPLICATION NUMBER: US/08/978,637A  
; CURRENT FILING DATE: 1997-11-25  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:oligo  
US-08-978-637-38

Query Match 67.0%; Score 13.4; DB 8; Length 30;  
Best Local Similarity 93.3%; Pred. No. 7.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTTGGCTCTAGA 20  
|||||  
DB 17 TTTGTTAGCTCTAGA 3

RESULT 11  
US-08-978-632-38/c  
; Sequence 38, Application US/08978632A  
; Patent No. US20010007767A1  
; GENERAL INFORMATION:  
; APPLICANT: Rabbani, Elazar  
; APPLICANT: Stavrianopoulos, Jannis G.  
; APPLICANT: Donegan, James J.  
; APPLICANT: Liu, Dakai  
; APPLICANT: Kelker, No. US20010007767A1man E.  
; APPLICANT: Engelhardt, Dean L.  
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING  
; FILE REFERENCE: ENZ-53 (C)Sequence.073099  
; CURRENT APPLICATION NUMBER: US/08/978,632A  
; CURRENT FILING DATE: 1997-11-25  
; EARLIER APPLICATION NUMBER: 08/574,443  
; EARLIER FILING DATE: 1995-12-15  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:oligo  
US-08-978-632-38

Query Match 67.0%; Score 13.4; DB 8; Length 30;  
Best Local Similarity 93.3%; Pred. No. 7.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTTGGCTCTAGA 20  
|||||  
DB 17 TTTGTTAGCTCTAGA 3

RESULT 12  
US-09-997-868-13/c

```

; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial DNA Sequence
US-10-093-365-6

Query Match 66.0%; Score 13.2; DB 9; Length 40;
Best Local Similarity 83.3%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAGA 20
   ||||| ||| |||||
DB 24 TTTTGTGTTTCTCTAGA 7

RESULT 14
US-10-215-112-870
; Sequence 870, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 870
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-870

Query Match 64.0%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATTTTGTGTTGCTCT 17
   ||||| |||||
DB 10 ACTTTTGTGCTCT 25

RESULT 15
US-09-863-040-49/c
; Sequence 49, Application US/09863040
; Patent No. US20020155517A1
; GENERAL INFORMATION:
; APPLICANT: Rupp, Steffan
; APPLICANT: Robertson, Laura
; APPLICANT: Summers, Eric F.
; APPLICANT: Hecht, Peter
; APPLICANT: Roberts, Radclyffe
; APPLICANT: Madhani, Hiren
; APPLICANT: Styles, Cora Ann
; APPLICANT: Lo, Hsiu-Jung
; APPLICANT: Sherman, Amir
; APPLICANT: Cali, Brian
; APPLICANT: Pink, Gerald R.
; TITLE OF INVENTION: Regulation of Fungal Gene Expression
; FILE REFERENCE: 109272.152
; CURRENT APPLICATION NUMBER: US/09/863,040
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/066,129
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: US 60/066,308
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/066,462
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: US 60/078,510

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; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/094,523
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: #6R primer
US-09-863-040-49

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Query Match      64.0%; Score 12.8; DB 9; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      4 TTTTGTGCTCTAG 19
Db      19 TTTTCTTGTCTGAG 4

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Search completed: June 25, 2003, 22:25:09  
 Job time : 61.7968 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 30.3586 Seconds  
(without alignments)  
202.036 Million cell updates/sec

Title: US-08-770-564A-13  
Perfect score: 20  
Sequence: 1 CATTGTTGTTGCTCTAGA 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	28	2	US-08-770-565-13
C 2	18	90.0	28	1	US-08-318-867A-19
C 3	18	90.0	28	4	US-08-352-089A-5
C 4	14.2	71.0	21	4	US-08-649-950-8
C 5	14.2	71.0	40	3	US-08-961-083-253
C 6	13.8	69.0	27	2	US-08-766-439-17
C 7	13.8	69.0	30	2	US-08-766-439-89
C 8	13.8	69.0	30	2	US-08-766-439-91
C 9	13.6	68.0	20	4	US-09-472-035A-8
C 10	13.6	68.0	29	1	US-08-153-071-17
C 11	13.6	68.0	29	1	US-08-609-271-24
C 12	13.6	68.0	29	2	US-08-438-511-17
C 13	13.6	68.0	29	3	US-08-487-431-20
C 14	13.6	68.0	29	3	US-08-188-374-24
C 15	13.4	67.0	20	1	US-08-403-866-16
C 16	13.2	66.0	21	4	US-08-026-143B-13
C 17	13.2	66.0	21	5	PCT-US92-10621-13
C 18	13.2	66.0	21	5	PCT-US94-02233-13
C 19	13.2	66.0	30	1	US-07-862-831A-15
C 20	13.2	66.0	30	1	US-08-126-564A-15
C 21	13.2	66.0	30	5	PCT-US94-09143-15
C 22	13.2	66.0	36	2	US-08-928-692-33
C 23	13.2	66.0	36	4	US-09-339-972-33
C 24	13.2	66.0	38	1	US-08-510-215A-11
C 25	13.2	66.0	40	4	US-09-605-192-4
C 26	13.2	66.0	42	1	US-08-639-256-6
C 27	12.8	64.0	25	4	US-09-387-341-207

C 28	12.8	64.0	29	4	US-09-189-462-49	Sequence 49, Appl
C 29	12.8	64.0	33	1	US-08-741-881-110	Sequence 110, App
C 30	12.8	64.0	33	1	US-08-739-158-110	Sequence 110, App
C 31	12.8	64.0	33	2	US-08-739-167-110	Sequence 110, App
C 32	12.8	64.0	33	3	US-08-404-796-110	Sequence 110, App
C 33	12.8	64.0	33	3	US-08-931-869-110	Sequence 110, App
C 34	12.8	64.0	33	4	US-09-350-399-110	Sequence 110, App
C 35	12.8	64.0	33	4	US-09-236-140A-110	Sequence 110, App
C 36	12.8	64.0	37	2	US-08-702-572-11	Sequence 11, Appl
C 37	12.8	64.0	41	1	US-08-332-420-57	Sequence 57, Appl
C 38	12.8	64.0	45	4	US-09-387-341-192	Sequence 192, App
C 39	12.6	63.0	30	4	US-07-661-370-4	Sequence 4, Appl
C 40	12.6	63.0	35	1	US-07-958-133-3	Sequence 3, Appl
C 41	12.6	63.0	35	1	US-08-412-913-3	Sequence 3, Appl
C 42	12.6	63.0	45	4	US-09-461-697-124	Sequence 124, App
C 43	12.6	63.0	48	4	US-09-225-990-13	Sequence 13, Appl
C 44	12.6	63.0	48	4	US-09-225-990-14	Sequence 14, Appl
C 45	12.4	62.0	33	3	US-08-961-083-370	Sequence 370, App

## ALIGNMENTS

RESULT 1  
US-08-770-565-13  
; Sequence 13, Application US/08770565  
; Patent No. 5846723  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; TITLE OF INVENTION: Telomerase  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-00230005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-565-13

Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred.No. 2.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20

Db 1 CATTTCCTGCTCTAGA 20

RESULT 2  
US-08-318-867A-19/c  
; Sequence 19, Application US/08318867A  
; Patent No. 5714323  
; GENERAL INFORMATION:  
; APPLICANT: ATUSHI OHSHIMA  
; APPLICANT: SUMIKO INOUE  
; APPLICANT: MASAYORI INOUE  
; TITLE OF INVENTION: OVER EXPRESSION OF SINGLE-STRANDED  
; MOLECULES  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WEISER & ASSOCIATES, P.C.  
; STREET: 230 S. 15th ST.  
; CITY: PHILADELPHIA, PA  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,867A  
; FILING DATE: MAY 4, 1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GERARD J. WEISER  
; REFERENCE/DOCKET NUMBER: 377.6120P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 875-8383  
; TELEFAX: (215) 875-8394  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-318-867A-19

Query Match 90.0%; Score 18; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTTCCTGCTCTAGA 20  
DB 21 TTTTTCCTGCTCTAGA 4

RESULT 3  
US-08-952-089A-5/c  
; Sequence 5, Application US/08952089A  
; Patent No. 6165749  
; GENERAL INFORMATION:  
; APPLICANT: SAGAWA, HIROAKI  
; APPLICANT: UENO, HARUMI  
; APPLICANT: OSHIMA, ATSUSHI  
; APPLICANT: KATO, IKUNOSHIN  
; TITLE OF INVENTION: PLASMID  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/952,089A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEINER, MARC S.  
; REGISTRATION NUMBER: 32,181  
; REFERENCE/DOCKET NUMBER: 1422-0319P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-205-8000  
; TELEFAX: 703-205-8050  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic DNA"  
US-08-952-089A-5  
Query Match 90.0%; Score 18; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTTCCTGCTCTAGA 20  
DB 21 TTTTTCCTGCTCTAGA 4

RESULT 4  
US-08-649-950-8/c  
; Sequence 8, Application US/08649950  
; Patent No. 6403303  
; GENERAL INFORMATION:  
; APPLICANT: Shipman, Robert  
; APPLICANT: Leushner, James  
; APPLICANT: Dunn, James M.  
; TITLE OF INVENTION: METHOD AND REAGENTS FOR TESTING FOR  
; TITLE OF INVENTION: MUTATIONS IN THE BRCA1 GENE  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oppedahl & Larson  
; STREET: 1992 Commerce Street Suite 309  
; CITY: Yorktown  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10598  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/649,950  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Larson, Marina T.  
; REGISTRATION NUMBER: 32,038  
; REFERENCE/DOCKET NUMBER: VGEN.P-028-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 245-3252  
; TELEFAX: (914) 962-4330  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 21  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 HYPOTHETICAL: no  
 ANTI-SENSE: yes  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 ORGANISM: human  
 FEATURE:  
 OTHER INFORMATION: amplification primer for BRCA1 gene  
 US-08-649-950-8

Query Match 71.0%; Score 14.2; DB 4; Length 21;  
 Best Local Similarity 84.2%; Pred. No. 6.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATTTTGTGTTGCTCTAG 20  
 DB 20 ATTTGTTGTTTCTGTAGA 2

RESULT 5  
 US-08-961-083-253/c  
 ; Sequence 253, Application US/08961083  
 ; Patent No. 6159469  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Choi et. al.  
 ; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
 ; NUMBER OF SEQUENCES: 452  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: Maryland  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 ; COMPUTER: HP Vectra 486/33  
 ; OPERATING SYSTEM: MSDOS version 6.2  
 ; SOFTWARE: ASCII Text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/961,083  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Brookes, A. Anders  
 ; REGISTRATION NUMBER: 36,373  
 ; REFERENCE/DOCKET NUMBER: PB340P2  
 ; TELEPHONE: (301) 309-8504  
 ; TELEFAX: (301) 309-8512  
 ; INFORMATION FOR SEQ ID NO: 253:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 40 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; US-08-961-083-253

Query Match 71.0%; Score 14.2; DB 3; Length 40;  
 Best Local Similarity 84.2%; Pred. No. 6.6e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTTTGTGTTGCTCTAG 19  
 DB 33 CATTTTGTGTTTCTCTG 15

RESULT 6  
 US-08-766-439-17  
 ; Sequence 17, Application US/08766439  
 ; Patent No. 5922538  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HAZEL, JAMES WILLIAM  
 ; APPLICANT: JENSEN, MARK ANTON  
 ; TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR  
 ; TITLE OF INVENTION: THE DETECTION OF LISTERIA  
 ; TITLE OF INVENTION: MONOCYTOGENES AND LISTERIA SPP.  
 ; NUMBER OF SEQUENCES: 110  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
 ; STREET: 1007 MARKET STREET  
 ; CITY: WILMINGTON  
 ; STATE: DELAWARE  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19898

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.50 INCH DISKETTE  
 ; COMPUTER: IBM PC COMPATIBLE  
 ; OPERATING SYSTEM: MICROSOFT WINDOWS 3.1  
 ; SOFTWARE: MICROSOFT WORD 2.0C  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/766,439  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/745,228  
 ; FILING DATE: NOVEMBER 8, 1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FLOYD, LINDA AXAMETHY  
 ; REGISTRATION NUMBER: 33,692  
 ; REFERENCE/DOCKET NUMBER: MD-1065-A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 302-892-8112  
 ; TELEFAX: 302-773-0164  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 27 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-766-439-17

Query Match 69.0%; Score 13.8; DB 2; Length 27;  
 Best Local Similarity 88.2%; Pred. No. 9.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAG 19  
 DB 4 TGTGTTGTTGCTCTAG 20

RESULT 7  
 US-08-766-439-89  
 ; Sequence 89, Application US/08766439  
 ; Patent No. 5922538  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HAZEL, JAMES WILLIAM  
 ; APPLICANT: JENSEN, MARK ANTON  
 ; TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR  
 ; TITLE OF INVENTION: THE DETECTION OF LISTERIA  
 ; TITLE OF INVENTION: MONOCYTOGENES AND LISTERIA SPP.  
 ; NUMBER OF SEQUENCES: 110  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
 ; STREET: 1007 MARKET STREET  
 ; CITY: WILMINGTON  
 ; STATE: DELAWARE  
 ; COUNTRY: U.S.A.

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ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,439
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,228
FILING DATE: NOVEMBER 8, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: MD-1065-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear DNA (genomic)
US-08-766-439-89

Query Match 69.0%; Score 13.8; DB 2; Length 30;
Best Local Similarity 89.2%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAG 19
DB 4 TGTTGGTTTGCTCTAG 20

RESULT 8
US-08-766-439-91
; Sequence 91, Application US/08766439
; Patent No. 5922538
; GENERAL INFORMATION:
; APPLICANT: HAZEL, JAMES WILLIAM
; APPLICANT: JENSEN, MARK ANTON
; TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR
; TITLE OF INVENTION: THE DETECTION OF LISTERIA
; TITLE OF INVENTION: MONOCYTOGENES AND LISTERIA SPP.
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 INCH DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
; SOFTWARE: MICROSOFT WORD 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,439
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/745,228
; FILING DATE: NOVEMBER 8, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: MD-1065-A
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear DNA (genomic)
US-08-766-439-91

Query Match 69.0%; Score 13.8; DB 2; Length 30;
Best Local Similarity 88.2%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAG 19
DB 4 TGTTGGTTTGCTCTAG 20

RESULT 9
US-09-472-035A-8/C
; Sequence 8, Application US/09472035A
; Patent No. 6322985
; GENERAL INFORMATION:
; APPLICANT: Yechezkel Kashi et al.
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
; TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
; TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/472,035A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 74/77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: linear
US-09-472-035A-8

Query Match 68.0%; Score 13.6; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATTTTGTGTTGCTCTAGA 20
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Db 20 CATTTGTTCAATTCCTCTAGA 1  
||||| || ||||||| |||||

RESULT 10  
US-08-153-071-17/c  
; Sequence 17, Application US/08153071  
; Patent No. 5665869  
; GENERAL INFORMATION:  
; APPLICANT: Ryland, James R.  
; APPLICANT: Matthews, Maura-Ann H.  
; APPLICANT: Ernst, Ulrich P.  
; APPLICANT: Houk, Daniel E.  
; APPLICANT: Traylor, David W.  
; APPLICANT: Williams, Lee R.  
; APPLICANT: Mitchell, David J.  
; APPLICANT: Chivers, Mark L.  
; APPLICANT: Belval, Thomas K.  
; TITLE OF INVENTION: Method for the Rapid Removal of  
; TITLE OF INVENTION: Protoporphyrin IX from Protoporphyrin IX-Containing Solutions  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Somatogen, Inc.  
; STREET: 5797 Central Avenue  
; CITY: Boulder  
; STATE: Colorado  
; ZIP: 80301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7.0.1  
; SOFTWARE: Microsoft Word 5.0a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/153,071  
; FILING DATE: No. 5665869ember 15, 1993  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5665869ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 120  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-541-3322  
; TELEFAX: 303-444-3013  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: beta gene fragment  
; HYPOTHETICAL: no  
US-08-153-071-17

Query Match 68.0%; Score 13.6; DB 1; Length 29;  
Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATTTTTCCTCTCTAGA 20  
||||| || ||||||| |||||

Db 26 CATATATTATTCCTCTAGA 7

RESULT 11  
US-08-609-271-24/c  
; Sequence 24, Application US/08609271  
; Patent No. 5811264  
; GENERAL INFORMATION:  
; APPLICANT: Aitken, Jacqueline F.  
; APPLICANT: Apostol, Izidor Z.  
; APPLICANT: Lippincott, Julie A.  
; APPLICANT: Levine, Joseph D.  
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation  
; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Somatogen, Inc.  
; STREET: 2545 Central Avenue, Site FD-1  
; CITY: Boulder  
; STATE: Colorado  
; ZIP: 80301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7.0.1  
; SOFTWARE: Microsoft Word 5.0a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/609,271  
; FILING DATE: 28 February 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/188,374  
; FILING DATE: 1/27/94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5811264elli, Marianne F.  
; REGISTRATION NUMBER: 38571  
; NAME: Brown, Theresa A.  
; REGISTRATION NUMBER: 32547  
; REFERENCE/DOCKET NUMBER: 170/Div  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-541-3324  
; TELEFAX: 303-444-3013  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: beta gene fragment  
; HYPOTHETICAL: no  
US-08-609-271-24

Query Match 68.0%; Score 13.6; DB 1; Length 29;  
Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATTTTTCCTCTCTAGA 20

Db 26 CATATATTATTCCTCTAGA 7

RESULT 12  
US-08-438-511-17/c  
; Sequence 17, Application US/08438511  
; Patent No. 5840851  
; GENERAL INFORMATION:  
; APPLICANT: Plomer, J. Jeffrey  
; APPLICANT: Ryland, James R.  
; APPLICANT: Matthews, Maura-Ann H.  
; APPLICANT: Traylor, David W.  
; APPLICANT: Milne, Erin E.  
; APPLICANT: Durfee, Steven L.  
; APPLICANT: Mathews, Antony J.  
; APPLICANT: Neway, Justin O.  
; TITLE OF INVENTION: Purification of Hemoglobin  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Somatogen, Inc.  
; STREET: 2545 Central Avenue, Suite FDI  
; CITY: Boulder  
; STATE: Colorado  
; ZIP: 80301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7.0.1  
; SOFTWARE: Microsoft Word 5.0a  
; CURRENT APPLICATION DATA:



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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,866
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30, 727
; REFERENCE/DOCKET NUMBER: 20747/30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1600
; TELEFAX: (716) 263-1487
; TELEX: 978450 (WUT)
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-403-866-16

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Query Match      67.0%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      4 TTTTGTGTTGCTCTA 18
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Db       6 TTTTGTGTTGCTCTA 20

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Search completed: June 25, 2003, 00:24:42  
Job time : 32.3586 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1031.16 Seconds

(without alignments)  
314.123 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20  
Sequence: 1 CATTTTGTGTTGCTCTAGA 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_nam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
c 1	13	65.0	37	17	BH790191
c 2	12	60.0	23	17	AZ488263
c 3	12	60.0	47	17	AL764740
4	12	60.0	50	9	AUI07157
5	11	55.0	19	17	AZ323986
6	11	55.0	23	17	AZ468097

7	11	55.0	23	17	AZ609822
8	11	55.0	24	17	AZ308225
c 9	11	55.0	24	17	AZ333171
10	11	55.0	25	10	AW245275
11	11	55.0	27	17	AZ591593
12	11	55.0	27	17	AZ807733
13	11	55.0	29	17	AZ827060
14	11	55.0	30	17	AZ808163
c 15	11	55.0	31	9	AA929219
16	11	55.0	31	14	R77576
c 17	11	55.0	33	10	BE267796
c 18	11	55.0	34	9	AA911862
19	11	55.0	34	17	AZ626219
20	11	55.0	35	9	AL641482
c 21	11	55.0	35	9	AU007015
c 22	11	55.0	35	9	AU007016
23	11	55.0	35	17	AZ785723
24	11	55.0	35	17	AZ788667
25	11	55.0	36	17	AZ446375
26	11	55.0	36	17	AZ512567
27	11	55.0	37	9	AA972505
28	11	55.0	39	14	C02027
29	11	55.0	40	9	AI318679
30	11	55.0	41	17	AZ793496
c 31	11	55.0	42	17	AZ807193
32	11	55.0	43	9	AI266869
c 33	11	55.0	45	12	BE896253
c 34	11	55.0	46	17	AZ345913
c 35	11	55.0	49	9	AI267816
c 36	11	55.0	49	9	AI687910
37	11	55.0	50	9	AU105307
c 38	11	55.0	50	9	AA607953
39	10	50.0	17	10	AW247165
40	10	50.0	17	10	AW248574
c 41	10	50.0	19	9	AA934303
c 42	10	50.0	19	17	AZ650252
c 43	10	50.0	20	17	AZ579122
44	10	50.0	21	17	AZ308846
45	10	50.0	21	17	AZ627840

## ALIGNMENTS

### RESULT 1

BH790191/c

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BH790191 37 bp DNA linear GSS 02-APR-2002  
SALK\_056569.17.50.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_056569.17.50.x, DNA

BH790191.1 GI:19883289

GSS,

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 37)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckero@salk.edu

This is single pass sequence recovered from the left border of

TDNA.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1. 37  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_056569.17.50.x"  
 /notes="lib=Arabidopsis thaliana TDNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

BASE COUNT 11 a 8 c 11 g 7 t  
 ORIGIN  
 Query Match 65.0%; Score 13; DB 17; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 TTTTGTTCCTC 16  
 |||||  
 Db 36 TTTTGTTCCTC 24

RESULT 2  
 AZ488263/c  
 LOCUS  
 DEFINITION  
 clone UUGC1M0318N21 F, DNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus  
 house mouse.  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0318 row: N column: 21  
 Seq primer: CGTTGTAACAGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 23.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0318N21"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 4 c 3 g 3 t  
 ORIGIN  
 Query Match 60.0%; Score 12; DB 17; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 TTTTGTTCCTC 15  
 |||||  
 Db 20 TTTTGTTCCTC 9

RESULT 3  
 AL764740  
 LOCUS  
 DEFINITION  
 Arabidopsis thaliana T-DNA flanking sequence GK-130E02-012667, genomic survey sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1  
 Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Siedler, H. and Weisshaar, B.  
 A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines  
 Unpublished  
 2  
 Rosso, M., Strizhov, N., Li, Y., Rosso, M. and Weisshaar, B.  
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics  
 Unpublished  
 3 (bases 1 to 47)  
 Strizhov, N., Li, Y., Rosso, M. and Weisshaar, B.  
 Direct Submission  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 COMMENT

FEATURES  
 source  
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 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-130E02-012667"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from

vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequences were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 10 a 5 c 10 g 22 t  
ORIGIN  
Query Match 60.0%; Score 12; DB 17; Length 47;  
Best Local Similarity 100.0%; Pred. No. 8.6e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTGTTGTTG 12  
|||||  
Db 20 CATTGTTGTTG 31

RESULT 4  
AUI07157  
LOCUS  
DEFINITION AUI07157 Sugano Homo sapiens cDNA library EST 30-AUG-2001  
LNG02840, mRNA sequence.

ACCESSION AUI07157  
VERSION AUI07157.1 GI:13556678  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
JOURNAL ENBO Rep. 2 (5), 388-393 (2001)  
MEDLINE 21270072  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
FEATURES  
source  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="LNG02840"  
/clone\_lib="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and dimethylformate treated U937 cells"

BASE COUNT 7 a 10 c 8 g 25 t  
ORIGIN  
Query Match 60.0%; Score 12; DB 9; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.6e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATTGTTGTTG 13  
|||||  
Db 1 ATTGTTGTTG 12

RESULT 5  
AZ323986  
LOCUS  
DEFINITION AZ323986 19 bp DNA linear GSS 29-SEP-2000  
IN0045P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0045P09 R, DNA sequence.  
ACCESSION AZ323986

VERSION AZ323986.1 GI:10379252  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Em. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0045 row: P column: 09

Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 19.

FEATURES  
Location/Qualifiers  
1..19

source

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0045P09"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, P-"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 2 c 3 g 14 t  
ORIGIN  
Query Match 55.0%; Score 11; DB 17; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTTGTGTTG 13  
|||||  
Db 5 TTTTGTGTTG 15

RESULT 6  
AZ468097  
LOCUS  
DEFINITION AZ468097 23 bp DNA linear GSS 04-OCT-2000  
IM0279K22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0279K22 R, DNA sequence.  
ACCESSION AZ468097

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VERSION      AZ4609822.1  GI:10626222
KEYWORDS     GSS.
SOURCE       house mouse.
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 23)
              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
              Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
              M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
              and Wright, D., Weiss, R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0279 row: K column: 22
              Seq primer: CACACAGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 23.
              Location/Qualifiers
FEATURES     1..23
              source
              /organism="Mus musculus"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC1M0279K22"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 Kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWB42 (G14732114|GB|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   0 a 0 c 4 g 19 t
ORIGIN
Query Match 55.0%; Score 11; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTG 13
Db 3 TTTTGTGTTG 13

RESULT 7
AZ609822
LOCUS      23 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0434J13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC1M0434J13 R, DNA sequence.
ACCESSION  AZ609822

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VERSION      AZ609822.1  GI:11732012
KEYWORDS     GSS.
SOURCE       house mouse.
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 23)
              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
              Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
              M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
              and Wright, D., Weiss, R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0434 row: J column: 13
              Seq primer: CACACAGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 23.
              Location/Qualifiers
FEATURES     1..23
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              /organism="Mus musculus"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC1M0434J13"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 Kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWB42 (G14732114|GB|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   0 a 0 c 6 g 17 t
ORIGIN
Query Match 55.0%; Score 11; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTG 13
Db 1 TTTTGTGTTG 11

RESULT 8
AZ308225
LOCUS      24 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0011E08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC1M0011E06 F, DNA sequence.
ACCESSION  AZ308225

```

VERSION KEYWORDS SOURCE ORGANISM	AZ308225.1 GI:10348004 GSS. house mouse. Mus musculus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
REFERENCE AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0011 row: E column: 06 Seq primer: CGTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 24.
FEATURES source	1..24 Location/Qualifiers /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0011E06" /clone_lib="Mouse 10kb plasmid UUGC1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-" /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT ORIGIN	1 a 0 c 4 g 19 t 3 TTTTGTGTTG 13 4 TTTTGTGTTG 14
Query Match Best Local Similarity Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	55.0%; Score 11; DB 17; Length 24; 100.0%; Pred. No. 2.6e+05;
QY	3 TTTTGTGTTG 13 
Db	4 TTTTGTGTTG 14 
RESULT 9 AZ333171/c LOCUS DEFINITION ACCESSION	24 bp DNA linear GSS 29-SEP-2000 1M0062B08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0062B08 F, DNA sequence. AZ333171
VERSION KEYWORDS SOURCE ORGANISM	AZ333171.1 GI:10397528 GSS. house mouse. Mus musculus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
REFERENCE AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0062 row: B column: 08 Seq primer: CGTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 24.
FEATURES source	1..24 Location/Qualifiers /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0062B08" /clone_lib="Mouse 10kb plasmid UUGC1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-" /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT ORIGIN	16 a 4 c 1 g 3 t 55.0%; Score 11; DB 17; Length 24; 100.0%; Pred. No. 2.6e+05;
QY	1 CATTTTGTGT 11 
Db	16 CATTTTGTGT 6 
RESULT 10 AW245275 LOCUS DEFINITION ACCESSION	25 bp mRNA linear EST 07-JAN-2000 2819996.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819996 3', mRNA sequence. AW245275

```

VERSION AW245275.1 GI:6588268
SOURCE EST.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mhc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Other ESTs: 2819996.5prime
Contact: Robert Strausberg, Ph.D.
Email: cga@bte-mail.nih.gov
Tissue Procurement: DCTD/DTA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNI) DNA Sequencing by: Berkeley MGC sequencing
Project Clone Distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNI at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 25 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: L1CM3 row: A column: 21.
Location/Qualifiers
FEATURES
source
1..25
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2819996"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_hosts="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pORF7; Site: 1; XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCGCGG(G) Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 3 a 1 c 3 g 18 t
ORIGIN
Query Match 55.0%; Score 11; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTG 13
| | | | |
Db 5 TTTTGTGTTG 15

RESULT 11
AZ591593 27 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0401115R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM1M0401115 R, DNA sequence.
ACCESSION AZ591593
VERSION AZ591593.1 GI:11713783
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
.M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0401 row: I column: 15
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
FEATURES
source
1..27
/organism="Mus musculus"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM1M0401115"
/clone_lib="Mouse 10kb plasmid UGCM library"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 1 a 0 c 6 g 20 t
ORIGIN
Query Match 55.0%; Score 11; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTG 13
| | | | |
Db 1 TTTTGTGTTG 11

RESULT 12
AZ807733 27 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0070H16R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM2M0070H16 R, DNA sequence.
ACCESSION AZ807733
VERSION AZ807733.1 GI:12972374
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

```

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0070 row: H column: 16  
 Seq primer: CACACAGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers

TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source

1. .27  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0103F17"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTTGTGTTG 13  
 |||||  
 Db 1 TTTTGTGTTG 11

RESULT 13  
 AZ827060  
 LOCUS

AZ827060 2M0103F17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0103F17 F, DNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

AZ827060.1 GI:12996968  
 GSS.

ORGANISM

house mouse.  
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

REFERENCE  
 AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0103 row: F column: 17  
 Seq primer: CGTTGTAACACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 29.  
 Location/Qualifiers

TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source

1. .29  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0103F17"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTTGTGTTG 13  
 |||||  
 Db 5 TTTTGTGTTG 15

RESULT 14  
 AZ808163  
 LOCUS

AZ808163 2M0071N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0071N08 R, DNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

AZ808163.1 GI:12973424  
 GSS.

ORGANISM

house mouse.  
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 30)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

REFERENCE  
 AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

# TITLE JOURNAL COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0071 row: N column: 08

Seq primer: CACACAGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 30.

## FEATURES

Location/Qualifiers

1..30

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0071N08"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMDA2 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

0 a 8 c 3 g 19 t

## BASE COUNT

ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 30;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTG 13

|||||

Db 11 TTTTGTGTTG 21

## RESULT 15

AA929219/C

LOCUS

DEFINITION

vt29e03.r1 Barstead mouse proximal colon MRLRB6 Mus musculus CDNA

clone IMAGE:1164508 5 similar to TR:Q33565 Q33565 EATRO 164

KINETOPLAST CR3. ; mRNA sequence.

AA929219

AA929219.1 GI:3078528

EST.

house mouse.

Mus musculus

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 31)

## REFERENCE

## AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, S., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

## TITLE JOURNAL COMMENT

The WashU-HHMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:630420

Trace considered overall poor quality

Putative full length read

vector to vector length is

Possible reversed clone: similarity on wrong strand

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 1.

## FEATURES

source

1..31

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:1164508"

/clone\_lib="Barstead mouse proximal colon MRLRB6"

/dev\_stage="7 day juvenile"

/lab\_host="DH10B"

/note="Vector: p7T73D-Pac (Pharmacia) with a modified

polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5,

TGTTACGAATCTGAATGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

[AATTCGATCCTTG], digested with Not I and cloned into the

Not I and Eco RI sites of the modified p7T73 vector.

Library constructed by Bob Barstead."

20 a 5 c 5 g 1 t

## BASE COUNT

ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 31;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTGTTGC 14

|||||

Db 11 TTTTGTGTTGC 1

Search completed: June 23, 2003, 10:10:35

Job time : 1034.31 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 877.928 Seconds  
(without alignments)  
158.668 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20

Sequence: 1 CATTGTTGTTGCTCTAGA 20

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Pending Patents\_NA\_New:\*

1: /cgn2\_6/ptodata/1/pna/US06\_PCT\_NEW\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*

7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*

8: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*

9: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*

10: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*

11: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

12: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

13: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	90.0	19	1	PCT-US03-04088-15
2	18	90.0	19	1	PCT-US03-04088-15
3	18	90.0	28	6	US-09-690-885-5
4	15	75.0	25	9	US-10-355-577-635066
5	14	70.0	18	9	US-10-310-188-64233
6	14	70.0	25	12	US-60-427-808-525499
7	14	70.0	22	12	US-60-427-808-982397
8	13	65.0	22	9	US-10-310-188-3317
9	13	65.0	25	9	US-10-355-577-14566
10	13	65.0	25	9	US-10-355-577-226117
11	13	65.0	25	9	US-10-355-577-949348
12	13	65.0	25	12	US-60-427-808-76032
13	13	65.0	25	12	US-60-427-808-523567
14	13	65.0	25	12	US-60-427-808-774039
15	13	65.0	25	12	US-60-427-836-281208
16	13	65.0	25	12	US-60-427-836-392577
17	13	65.0	25	13	US-60-469-545-95571
18	13	65.0	25	13	US-60-469-545-142606
19	12	60.0	18	9	US-10-310-188-51234
20	12	60.0	18	9	US-10-310-188-84760

21	12	60.0	19	9	US-10-310-188-71730	Sequence 71730, A
22	12	60.0	25	1	PCT-US02-10873A-373	Sequence 373, App
23	12	60.0	25	9	US-10-355-577-226115	Sequence 226115,
24	12	60.0	25	9	US-10-355-577-231716	Sequence 231716,
25	12	60.0	25	9	US-10-355-577-300369	Sequence 300369,
26	12	60.0	25	9	US-10-355-577-486926	Sequence 486926,
27	12	60.0	25	9	US-10-355-577-578563	Sequence 578563,
28	12	60.0	25	9	US-10-355-577-583938	Sequence 583938,
29	12	60.0	25	9	US-10-355-577-710151	Sequence 710151,
30	12	60.0	25	9	US-10-355-577-923328	Sequence 923328,
31	12	60.0	25	9	US-10-355-577-949347	Sequence 949347,
32	12	60.0	25	9	US-10-355-577-970825	Sequence 970825,
33	12	60.0	25	9	US-10-355-577-970826	Sequence 970826,
34	12	60.0	25	12	US-60-417-190-101304	Sequence 101304,
35	12	60.0	25	12	US-60-417-190-101305	Sequence 101305,
36	12	60.0	25	12	US-60-417-190-101306	Sequence 101306,
37	12	60.0	25	12	US-60-417-190-101307	Sequence 101307,
38	12	60.0	25	12	US-60-417-190-101311	Sequence 101311,
39	12	60.0	25	12	US-60-417-190-101312	Sequence 101312,
40	12	60.0	25	12	US-60-417-190-101313	Sequence 101313,
41	12	60.0	25	12	US-60-417-190-101314	Sequence 101314,
42	12	60.0	25	12	US-60-427-808-47418	Sequence 47418, A
43	12	60.0	25	12	US-60-427-808-83312	Sequence 83312, A
44	12	60.0	25	12	US-60-427-808-137138	Sequence 137138,
45	12	60.0	25	12	US-60-427-808-148620	Sequence 148620,

ALIGNMENTS

RESULT 1

PCT-US03-04088-15/c  
; Sequence 15, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 15  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
; OTHER INFORMATION: region  
PCT-US03-04088-15

Query Match 90.0%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No. 30;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 TTTTGTGCTCTAGA 20
Db 19 TTTTGTGCTCTAGA 2

RESULT 2
PCT-US03-04088-279
; Sequence 279, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2002-06-06
; PRIOR FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-09-05
; PRIOR FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-279

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 38.9%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGCTCTAGA 20
Db 1 UUUUUUUUCUUA 18

RESULT 3
US-09-690-885-5/c
; Sequence 5, Application US/09690885
; GENERAL INFORMATION:
; APPLICANT: SAGAWA, HIROAKI
; APPLICANT: UENO, HARUMI
; APPLICANT: OSHISHI
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/690,885
; FILING DATE: 18-Oct-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0319P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-690-885-5

Query Match 90.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGCTCTAGA 20
Db 21 TTTTGTGCTCTAGA 4

RESULT 4
US-10-355-577-635066
; Sequence 635066, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635066
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-635066

Query Match 75.0%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTGCTCTA 18
Db 4 TTTTGTGCTCTA 18

RESULT 5
US-10-310-188-64233
; Sequence 64233, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN-
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64233
; LENGTH: 18
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-64233

Query Match      70.0%; Score 14; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTC 16
   |||||
Db 5 TTTTGTGTTGCTC 18
   |||||

RESULT 6
US-60-427-808-525499
; Sequence 525499, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 525499
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-525499

Query Match      70.0%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTTTGTGTTGCTCTA 18
   |||||
Db 3 TTTTGTGTTGCTCTA 16
   |||||

RESULT 7
US-60-427-808-982397
; Sequence 982397, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 982397
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-982397

Query Match      70.0%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTGTTGCTCT 17
   |||||
Db 1 TTTTGTGTTGCTCT 14
   |||||

RESULT 8
US-10-310-188-3317
; Sequence 3317, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3317
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-3317

Query Match      65.0%; Score 13; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCT 15
   |||||
Db 4 TTTTGTGTTGCT 16
   |||||

RESULT 9
US-10-355-577-14566
; Sequence 14566, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 14566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-14566

Query Match      65.0%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTTTGTGTTGCTCT 17
   |||||
Db 10 TTTTGTGTTGCTCT 22
   |||||

RESULT 10
US-10-355-577-226117/C
; Sequence 226117, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 226117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-226117

Query Match      65.0%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTTTGTGTTGC 14
   |||||
Db 25 ATTTTGTGTTGC 13
   |||||

RESULT 11
US-10-355-577-949348/c
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; Sequence 949348, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 949348
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-949348
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Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 25 TGTTCCTCTAGA 13
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RESULT 12
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; Sequence 76032, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76032
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-76032
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Query Match 65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 10 CATTTCCTCTTG 22
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US-60-427-808-523567
; Sequence 523567, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 523567
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-523567
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Query Match 65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 TGTTCCTCTAG 15
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; Sequence 774039, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 774039
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-774039
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Query Match 65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 281208, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 281208
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-281208
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Query Match 65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 7 TTTTCCTCTCT 19
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Search completed: June 23, 2003, 19:12:14
Job time : 878.928 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1677.45 Seconds  
(without alignments)  
299.770 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20  
Sequence: 1 CATTGTTGTTGCTCTAGA 20

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	%				
1	20	100.0	20	1	PCT-US97-23619-13		Sequence 13, Appl
2	20	100.0	20	11	US-08-770-564A-13		Sequence 10, Appl
c	3	20	100.0	30	9	US-08-521-634-10	Sequence 16, Appl
	4	19	95.0	20	21	US-09-540-119B-16	Sequence 18, Appl
	5	17	85.0	24	22	US-09-587-662A-5	Sequence 18, Appl
6	16	80.0	22	13	US-08-973-589-18		Sequence 58350, A
c	7	16	80.0	25	36	US-09-954-427-58350	Sequence 58350, A
c	8	16	80.0	25	67	US-60-233-166-58350	Sequence 58350, A
c	9	15	75.0	25	36	US-09-954-427-58351	Sequence 58351, A
c	10	15	75.0	25	67	US-60-233-166-58351	Sequence 58351, A
c	11	15	75.0	25	79	US-60-353-987-635066	Sequence 635066, A
c	12	14	70.0	25	36	US-09-954-427-58352	Sequence 58352, A
c	13	14	70.0	25	67	US-60-233-166-58352	Sequence 58352, A
14	14	70.0	41	36	US-09-953-198-241		Sequence 241, Appl
15	13	65.0	13	21	US-09-540-119B-19		Sequence 19, Appl
16	13	65.0	13	21	US-09-540-119B-20		Sequence 20, Appl
17	13	65.0	25	36	US-09-954-427-379210		Sequence 379210, A
c	18	13	65.0	25	36	US-09-954-427-408651	Sequence 408651, A
c	19	13	65.0	25	36	US-09-954-427-408670	Sequence 408670, A
20	13	65.0	25	67	US-60-233-166-379210		Sequence 379210, A
c	21	13	65.0	25	67	US-60-233-166-408651	Sequence 408651, A

C 22 13 65.0 25 67 US-60-233-166-408670  
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C 36 12 60.0 19 65 US-60-216-745-9743  
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C 42 12 60.0 25 17 US-09-396-196G-67372  
C 43 12 60.0 25 36 US-09-591-366-62  
C 44 12 60.0 25 36 US-09-954-427-58419  
C 45 12 60.0 25 36 US-09-956-584-317896

## ALIGNMENTS

RESULT 1  
PCT-US97-23619-13  
; Sequence 13, Application PC/TUS9723619  
; GENERAL INFORMATION:  
; APPLICANT: Kealey, James T.  
; APPLICANT: Kealey, James T.  
; APPLICANT: Kealey, James T.  
; APPLICANT: Kealey, James T.  
; APPLICANT: Kealey, James T.  
; APPLICANT: Kealey, James T.  
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
; TITLE OF INVENTION: RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/23619  
; FILING DATE: Not yet assigned  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/770,564  
; FILING DATE: 20-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/770,565  
; FILING DATE: 20-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 15389-27PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0300  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:

Sequence 408670, A  
Sequence 14566, A  
Sequence 226117, A  
Sequence 949348, A  
Sequence 885, App  
Sequence 17, Appl  
Sequence 8256, App  
Sequence 1170, App  
Sequence 1171, App  
Sequence 1172, App  
Sequence 1173, App  
Sequence 1174, App  
Sequence 1175, App  
Sequence 9743, App  
Sequence 9406, App  
Sequence 5, Appl  
Sequence 5, Appl  
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; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..20  
; OTHER INFORMATION: /note="oligo 20/21"  
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Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 CATTTTTGTGCTCTAGA 20  
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US-08-770-564A-13  
; Sequence 13, Application US/08770564A  
; GENERAL INFORMATION:  
; APPLICANT: Kealey, James T.  
; APPLICANT: Kealey, James T.  
; APPLICANT: Kealey, James T.  
; APPLICANT: Kealey, James T.  
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
; TITLE OF INVENTION: Against the RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,564A  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002200US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-564A-13  
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Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 CATTTTTGTGCTCTAGA 20  
RESULT 3  
US-08-521-634-10/c

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; Sequence 10, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,634
; FILING DATE: 31-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-10

Query Match 100.0%; Score 20; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 28 CATTTCCTGTTGCTCTAGA 9

RESULT 4
US-09-540-119B-16
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
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; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-16

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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 CATTTCCTGTTGCTCTAG 20

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; Sequence 5, Application US/09587662A
; GENERAL INFORMATION:
; APPLICANT: Au, Jessie L.-S.
; APPLICANT: Wientjes, M. Guillaume
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING DRUG ACTIVITY
; TITLE OF INVENTION: THROUGH TELOMERE DAMAGE
; FILE REFERENCE: JAG-004
; CURRENT APPLICATION NUMBER: US/09/587,662A
; CURRENT FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/137,549
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-09-587-662A-5

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTTCCTGTTGCTCT 17
Db 8 CATTTCCTGTTGCTCT 24

RESULT 6
US-08-973-589-18
; Sequence 18, Application US/08973589
; GENERAL INFORMATION:
; APPLICANT: Greider, Carol
; APPLICANT: Autexier, Chantal
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: ESSENTIAL OLIGONUCLEOTIDES OF VERTEBRATE
; TITLE OF INVENTION: TELOMERASE
; FILE REFERENCE: CSHL95-02A
; CURRENT APPLICATION NUMBER: US/08/973,589
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US96/09517
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/478,352
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-08-973-589-18
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Query Match 80.0%; Score 16; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTTTGTGCTCTAG 16  
Db 7 CATTTTGTGCTCTAG 22

## RESULT 7

US-09-954-427-58350/c  
; Sequence 58350, Application US/09954427  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/09/954,427  
; CURRENT FILING DATE: 2001-09-17  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58350  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-09-954-427-58350

Query Match 80.0%; Score 16; DB 36; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTTTGTGCTCTAG 19  
Db 25 TTTTGTGCTCTAG 10

## RESULT 8

US-60-233-166-58350/c  
; Sequence 58350, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58350  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-60-233-166-58350

Query Match 80.0%; Score 16; DB 67; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTTTGTGCTCTAG 19  
Db 25 TTTTGTGCTCTAG 10

## RESULT 9

US-09-954-427-58351/c  
; Sequence 58351, Application US/09954427

; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/09/954,427  
; CURRENT FILING DATE: 2001-09-17  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58351  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-09-954-427-58351

Query Match 75.0%; Score 15; DB 36; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTTTGTGCTCTAG 19  
Db 25 TTTTGTGCTCTAG 11

## RESULT 10

US-60-233-166-58351/c  
; Sequence 58351, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58351  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-60-233-166-58351

Query Match 75.0%; Score 15; DB 67; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTTTGTGCTCTAG 19  
Db 25 TTTTGTGCTCTAG 11

## RESULT 11

US-60-353-987-635066  
; Sequence 635066, Application US/60353987  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI133  
; FILE REFERENCE: 3121  
; CURRENT APPLICATION NUMBER: US/60/353,987  
; CURRENT FILING DATE: 2002-02-01  
; NUMBER OF SEQ ID NOS: 997516  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 635066  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-60-353-987-635066



Query Match 75.0%; Score 15; DB 79; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 TTTTGTGTTGCTCTA 18  
|||||  
Db 4 TTTTGTGTTGCTCTA 18

RESULT 12  
US-09-954-427-58352/c  
; Sequence 58352, Application US/09954427  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; TITLE OF INVENTION: Genome  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/09/954,427  
; CURRENT FILING DATE: 2001-09-17  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58352  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-09-954-427-58352

Query Match 70.0%; Score 14; DB 36; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTTGTTTGTCTAG 19  
|||||  
Db 25 TTTGTTTGTCTAG 12

RESULT 13  
US-60-233-166-58352/c  
; Sequence 58352, Application US/60233166  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat  
; TITLE OF INVENTION: Genome  
; FILE REFERENCE: 3112  
; CURRENT APPLICATION NUMBER: US/60/233,166  
; CURRENT FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 420907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58352  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank AA819129  
US-60-233-166-58352

Query Match 70.0%; Score 14; DB 67; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTTGTTTGTCTAG 19  
|||||  
Db 25 TTTGTTTGTCTAG 12

RESULT 14  
US-09-953-198-241  
; Sequence 241, Application US/09953198

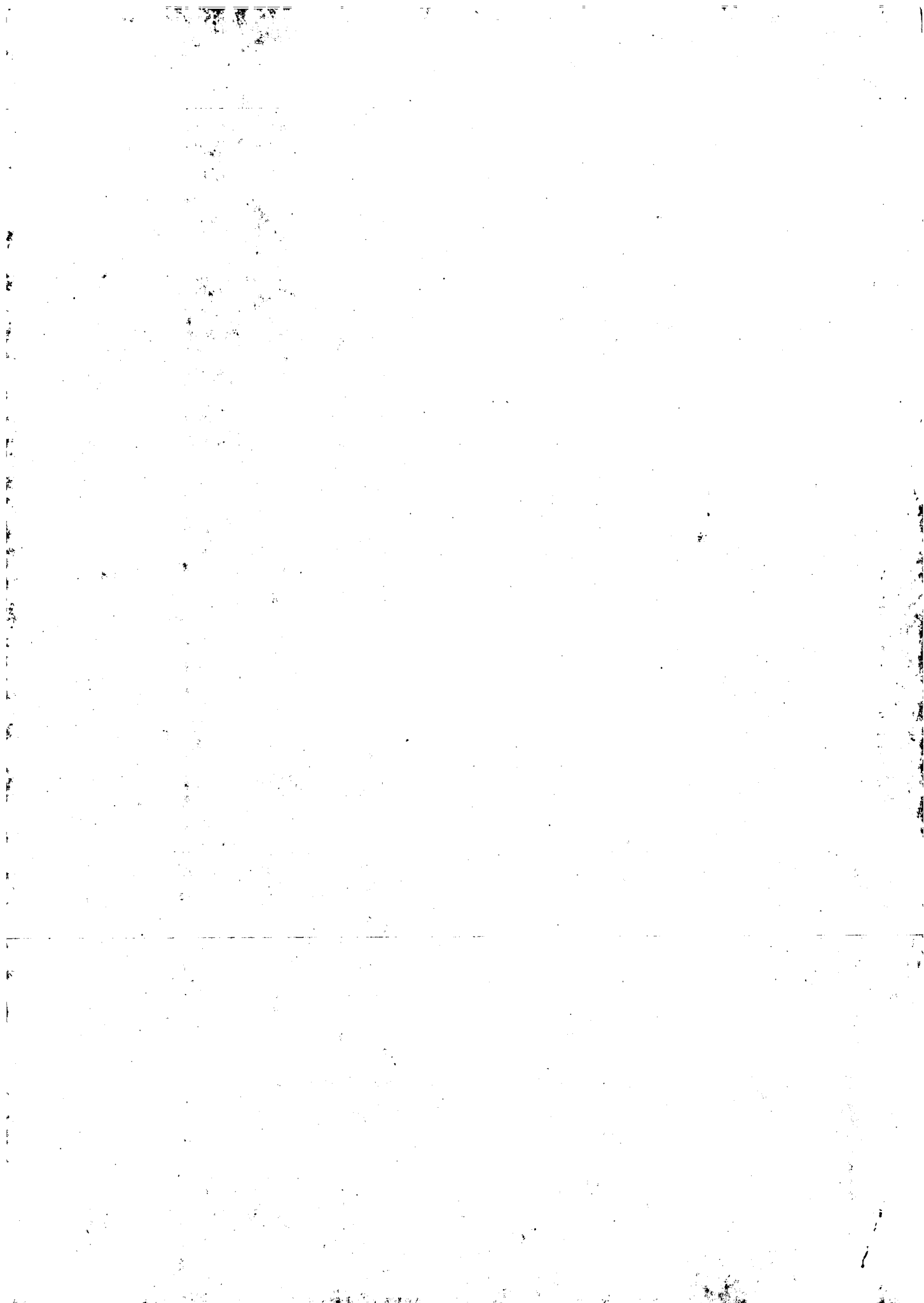
; GENERAL INFORMATION:  
; APPLICANT: COMPUGEN LTD  
; TITLE OF INVENTION: DATA BASE OF SNP  
; FILE REFERENCE: 1351253  
; CURRENT APPLICATION NUMBER: US/09/953,198  
; CURRENT FILING DATE: 2001-08-12  
; NUMBER OF SEQ ID NOS: 979  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 241  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-953-198-241

Query Match 70.0%; Score 14; DB 36; Length 41;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 ATTTTGTGTTGCT 15  
|||||  
Db 2 ATTTTGTGTTGCT 15

RESULT 15  
US-09-540-119B-19  
; Sequence 19, Application US/09540119B  
; GENERAL INFORMATION:  
; APPLICANT: Gryaznov, Sergei  
; APPLICANT: Pruzan, Ronald  
; APPLICANT: Weinrich, Scott  
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides  
; FILE REFERENCE: 029/001  
; CURRENT APPLICATION NUMBER: US/09/540,119B  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-540-119B-19

Query Match 65.0%; Score 13; DB 21; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TTTTGTGTTGCT 15  
|||||  
Db 1 TTTTGTGTTGCT 13

Search completed: June 23, 2003, 16:08:24  
Job time : 1678.53 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model.

Run on: June 23, 2003, 06:41:29 ; Search time 160.717 Seconds  
(without alignments)  
182.610 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20

Sequence: 1 CATTTTGTGCTCTAGA 20

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

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- 2: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	60.0	26	9 US-10-044-692-312	Sequence 312, App
2	12	60.0	26	9 US-10-044-539-312	Sequence 312, App
3	12	60.0	26	10 US-09-057-351-23	Sequence 23, Appl
4	12	60.0	35	10 US-09-765-272-248	Sequence 248, App
5	12	60.0	38	9 US-10-085-906-285	Sequence 285, App
6	12	60.0	40	10 US-09-245-802-103	Sequence 103, App
7	12	60.0	40	10 US-09-245-802-110	Sequence 110, App
8	12	60.0	40	10 US-09-765-272-253	Sequence 253, App
9	12	60.0	42	9 US-09-769-787-375	Sequence 375, App
10	11	55.0	20	9 US-09-403-609-15	Sequence 15, Appl
11	11	55.0	20	9 US-09-918-026A-53	Sequence 53, Appl
12	11	55.0	21	9 US-10-109-728A-15	Sequence 15, Appl
13	11	55.0	21	9 US-09-997-868-13	Sequence 13, Appl
14	11	55.0	21	10 US-09-263-959-969	Sequence 969, App
15	11	55.0	24	9 US-09-940-185-2806	Sequence 2806, App
16	11	55.0	25	9 US-10-098-263B-72610	Sequence 72610, A
17	11	55.0	25	9 US-10-098-263B-92356	Sequence 92356, A
18	11	55.0	25	9 US-10-098-263B-118744	Sequence 118744, App
19	11	55.0	26	10 US-09-426-548-133	Sequence 133, App

c	20	11	55.0	26	10	US-09-870-375-30	Sequence 30, Appl
c	21	11	55.0	27	9	US-09-232-785-359	Sequence 359, App
c	22	11	55.0	28	10	US-09-975-408-41	Sequence 41, Appl
c	23	11	55.0	28	12	US-10-075-579-41	Sequence 41, Appl
c	24	11	55.0	29	10	US-09-887-576-424	Sequence 424, App
c	25	11	55.0	31	9	US-09-815-533-2	Sequence 2, Appl
c	26	11	55.0	33	10	US-09-765-272-370	Sequence 370, App
c	27	11	55.0	39	10	US-09-057-351-12	Sequence 12, Appl
c	28	11	55.0	41	9	US-10-085-906-99	Sequence 99, Appl
c	29	11	55.0	47	9	US-09-853-526-196	Sequence 196, App
c	30	11	55.0	47	10	US-09-901-484A-196	Sequence 196, App
c	31	10	50.0	17	8	US-08-983-605-224	Sequence 224, App
c	32	10	50.0	17	9	US-10-041-856-21	Sequence 21, Appl
c	33	10	50.0	17	9	US-09-825-805-557	Sequence 557, App
c	34	10	50.0	17	9	US-10-163-552-984	Sequence 984, App
c	35	10	50.0	18	9	US-10-198-069-43	Sequence 43, Appl
c	36	10	50.0	20	9	US-09-971-843-22	Sequence 22, Appl
c	37	10	50.0	20	9	US-10-271-887-74	Sequence 74, Appl
c	38	10	50.0	22	9	US-10-133-205-6	Sequence 6, Appl
c	39	10	50.0	22	9	US-10-112-653-55	Sequence 55, Appl
c	40	10	50.0	22	9	US-10-017-995-61	Sequence 61, Appl
c	41	10	50.0	22	9	US-09-776-479-61	Sequence 61, Appl
c	42	10	50.0	23	9	US-10-112-653-767	Sequence 767, App
c	43	10	50.0	23	9	US-10-017-995-794	Sequence 794, App
c	44	10	50.0	23	9	US-09-776-479-794	Sequence 794, App
c	45	10	50.0	23	9	US-09-998-027-52	Sequence 52, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-044-692-312  
: Sequence 312, Application US/10044692  
: Publication No. US20030096344A1

GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.

Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

```

; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-692-312
Query Match 60.0%; Score 12; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20
DB 1 GTTGTCTCTAGA 12

RESULT 2
US-10-044-539-312
; Sequence 312, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; INVENTOR: Nakamura, Toru
; INVENTOR: Lingner, Joachim
; INVENTOR: Chapman, Karen B.
; INVENTOR: Morin, Gregory B.
; INVENTOR: Harley, Calvin
; INVENTOR: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
Query Match 60.0%; Score 12; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20
DB 1 GTTGTCTCTAGA 12

RESULT 3
US-09-057-351-23
; Sequence 23, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-23

Query Match          60.0%; Score 12; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GTTGTCTCTAGA 20
Db 1 GTTGTCTCTAGA 12

RESULT 4
US-09-765-272-248
; Sequence 248, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 248:

US-09-765-272-248

Query Match          60.0%; Score 12; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTTTGTGTTGCT 15
Db 12 TTTTGTGTTGCT 23

RESULT 5
US-10-085-906-285
; Sequence 285, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.

; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-285

Query Match          60.0%; Score 12; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATTTTGTGTTG 13
Db 1 ATTTTGTGTTG 12

RESULT 6
US-09-245-802-103
; Sequence 103, Application US/09245802
; Patent No. US20010049125A1
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,802
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESO., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; TOPOLOGY: circular
; US-09-245-802-103
;
; Query Match 60.0%; Score 12; DB 10; Length 40;
; Best Local Similarity 100.0%; Pred. No. 2.4e+03;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 3 TTTTTCGTTTGC 14
; DB 23 TTTTTCGTTTGC 34
;
; RESULT 7
; US-09-245-802-110/c
; Sequence 110, Application US/09245802
; Patent No. US20010049125A1
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,802
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; US-09-245-802-110
;
; Query Match 60.0%; Score 12; DB 10; Length 40;
; Best Local Similarity 100.0%; Pred. No. 2.4e+03;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 3 TTTTTCGTTTGC 14
; DB 38 TTTTTCGTTTGC 27
;
; RESULT 8
; US-09-765-272-253/c
; Sequence 253, Application US/09765272
; Patent No. US20020061545A1
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; GENERAL INFORMATION:
; APPLICANT: Choi, et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-09-765-272-253
;
; Query Match 60.0%; Score 12; DB 10; Length 40;
; Best Local Similarity 100.0%; Pred. No. 2.4e+03;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CATTTCGTTT 12
; DB 33 CATTTCGTTT 22
;
; RESULT 9
; US-09-769-787-375/c
; Sequence 375, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hanebro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PNC/P21129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2003-01-26
; PRIOR APPLICATION NUMBER: CB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 375
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-769-787-375
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Query Match 60.0%; Score 12; DB 9; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTTGTGTT 12  
|||||  
DB 40 CATTGTTGTTT 29

## RESULT 10

US-09-403-609-15/c  
; Sequence 15, Application US/09403609  
; Publication No. US20030087229A1  
; GENERAL INFORMATION:  
; APPLICANT: HAKENBECK, Regine  
; TITLE OF INVENTION: DNA PROBES, METHOD AND KIT FOR IDENTIFYING  
; FILE REFERENCE: 012627-011  
; CURRENT APPLICATION NUMBER: US/09/403,609  
; CURRENT FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/DE98/01134  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: DE 197 17 346.2  
; PRIOR FILING DATE: 1997-04-24  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Streptococcus pneumoniae  
US-09-403-609-15

Query Match 55.0%; Score 11; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTTGTGTT 11  
|||||  
DB 20 CATTGTTGTT 10

## RESULT 11

US-09-918-026A-53/c  
; Sequence 53, Application US/09918026A  
; Publication No. US20030096772A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosanne M. Crooke  
; APPLICANT: Mark J. Graham  
; APPLICANT: Kristina M. Lemonidis  
; TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COA CHOLESTEROL ACYLTRANSFERASE-2 EX  
; FILE REFERENCE: ISPH-0588  
; CURRENT APPLICATION NUMBER: US/09/918,026A  
; CURRENT FILING DATE: 2001-07-30  
; NUMBER OF SEQ ID NOS: 65  
; SEQ ID NO 53  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-918-026A-53

Query Match 55.0%; Score 11; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGTGCTCTCTA 18  
|||||  
DB 14 TGTGCTCTCTA 4

## RESULT 12

US-10-109-725A-15  
; Sequence 15, Application US/10109725A  
; Patent No. US20020177154A1  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalgo, Mark L.  
; APPLICANT: Jones, Peter A.  
; APPLICANT: Liang, Gangning  
; TITLE OF INVENTION: CANCER DIAGNOSTIC METHOD BASED UPON DNA METHYLATION DIFFERENCES  
; FILE REFERENCE: 47675-21  
; CURRENT APPLICATION NUMBER: US/10/109,725A  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 09/887,941  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: p16 promoter region-specific Ms-SNUPE primer  
US-10-109-725A-15

Query Match 55.0%; Score 11; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTG 13  
|||||  
DB 2 TTTTGTGTTG 12

## RESULT 13

US-09-997-868-13/c  
; Sequence 13, Application US/09997868  
; Publication No. US20030031654A1  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Cornelia M.,  
; Grotskreutz, Debyra J.  
; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/997,868  
; FILING DATE: 12-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/887265  
; FILING DATE: 22-MAY-1992  
; APPLICATION NUMBER: 07/803631  
; FILING DATE: 06-DEC-1992  
; APPLICATION NUMBER: PCT/US92/10621  
; FILING DATE: 04-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0748P3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 13:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-997-868-13

Query Match      55.0%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 TTTGCTCTAGA 20
DB      14 TTTGCTCTAGA 4

RESULT 14
US-09-263-959-969/c
; Sequence 969, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4500
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 969:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-969

Query Match      55.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTTTGTGTTG 13
DB      18 TTTTGTGTTG 8

RESULT 15
US-09-940-185-2806/c
; Sequence 2806, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin

```

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; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2806
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2806

Query Match      55.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TTTGTTTGCTC 16
DB      13 TTTGTTTGCTC 3

Search completed: June 23, 2003, 20:01:34
Job time : 161.717 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 31.3147 Seconds  
(without alignments)  
195.867 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20  
Sequence: 1 CATTGTTGTTGCTCTAGA 20

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/prodata/2/ina/5B-COMB.seq.\*
- 3: /cgn2\_6/prodata/2/ina/6A-COMB.seq.\*
- 4: /cgn2\_6/prodata/2/ina/6B-COMB.seq.\*
- 5: /cgn2\_6/prodata/2/ina/6C-COMB.seq.\*
- 6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	US-08-770-565-13
2	18	90.0	28	1	US-08-318-867A-19
3	18	90.0	28	4	US-08-952-089A-5
4	12	60.0	26	1	US-08-330-123A-23
5	12	60.0	26	1	US-08-482-115B-23
6	12	60.0	26	2	US-08-660-678A-23
7	12	60.0	26	2	US-08-710-249-26
8	12	60.0	26	2	US-08-485-778-19
9	12	60.0	26	2	US-08-472-802C-24
10	12	60.0	26	3	US-08-520-550A-19
11	12	60.0	26	3	US-08-998-443-23
12	12	60.0	26	4	US-08-974-549A-598
13	12	60.0	26	4	US-09-060-523-23
14	12	60.0	26	4	US-09-220-157A-26
15	12	60.0	26	4	US-09-286-959B-4
16	12	60.0	26	4	US-09-580-517-23
17	12	60.0	27	2	US-08-770-565-26
18	12	60.0	30	3	US-08-833-377-5
19	12	60.0	35	3	US-08-961-083-248
20	12	60.0	40	2	US-08-425-684-103
21	12	60.0	40	2	US-08-425-684-103
22	12	60.0	40	2	US-08-425-684-110
23	12	60.0	40	2	US-08-675-502-103
24	12	60.0	40	3	US-08-675-502-110
25	12	60.0	40	3	US-08-961-083-253
26	12	60.0	41	1	US-08-332-420-57
27	12	60.0	42	1	US-08-639-256-6
28	12	60.0	43	1	US-08-639-256-7

28	11	55.0	21	4	US-09-094-207A-15	Sequence 15, Appl
29	11	55.0	21	4	US-09-311-912-51	Sequence 51, Appl
c 30	11	55.0	21	4	US-08-026-143B-13	Sequence 13, Appl
c 31	11	55.0	21	5	PCT-US92-10621-13	Sequence 13, Appl
c 32	11	55.0	21	5	PCT-US94-02233-13	Sequence 13, Appl
c 33	11	55.0	24	2	US-08-529-190B-44	Sequence 44, Appl
34	11	55.0	24	2	US-08-859-998-119	Sequence 119, Appl
35	11	55.0	24	4	US-09-225-928-119	Sequence 119, Appl
c 36	11	55.0	25	3	US-09-010-641-15	Sequence 15, Appl
c 37	11	55.0	25	4	US-09-356-281-15	Sequence 15, Appl
38	11	55.0	27	2	US-08-766-439-17	Sequence 17, Appl
c 39	11	55.0	28	4	US-09-710-200-41	Sequence 41, Appl
40	11	55.0	30	2	US-08-766-439-89	Sequence 89, Appl
41	11	55.0	30	2	US-08-766-439-91	Sequence 91, Appl
42	11	55.0	33	3	US-08-961-083-370	Sequence 370, Appl
43	11	55.0	37	2	US-08-702-572-11	Sequence 11, Appl
c 44	11	55.0	39	1	US-08-330-123A-12	Sequence 12, Appl
c 45	11	55.0	39	1	US-08-482-115B-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-08-770-565-13  
; Sequence 13, Application US/08770565  
; Patent No. 5846723  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; TITLE OF INVENTION: Telomerase  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770.565  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scorella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-00230005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-565-13

Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20

Db  
1 CATTTTTGTGCTCTAGA 20

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Query Match      90.0%; Score 18; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3      TTTTGTGTTGCTCTAGA 20
        |||||
Db      21      TTTTGTGTTGCTCTAGA 4

```

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RESULT 3
US-08-952-089A-5/C
SEQUENCE 5, APPLICATION US/08952089A
; PAGES 6, 68, 719
; GENERAL INFORMATION:
; APPLICANT: SAGAWA, HIROAKI
; APPLICANT: UENO HARUMI
; APPLICANT: OSHIMA ATSUSHI
; APPLICANT: KATO IKUNOSHIN
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,089A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0319P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-952-089A-5

```

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Query Match      90.0%; Score 18; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTTCGTTTGCTCTAGA 20
    |||||
Db 21 TTTTTCGTTTGCTCTAGA 4
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1  RESULT 4
2  US-08-330-123A-23
3  ; Sequence 23, Application US/08330123A
4  ; Patent No. 583016
5  ; GENERAL INFORMATION:
6  ; APPLICANT: VILLEPONTEAU, Bryant
7  ; APPLICANT: FENG, Junli
8  ; APPLICANT: FUNK, Walter
9  ; APPLICANT: ANDREWS, William H.
10 ; TITLE OF INVENTION: HUMAN TELOMERASE
11 ; NUMBER OF SEQUENCES: 25
12 ; CORRESPONDENCE ADDRESS:
13 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
14 ; STREET: 379 Lytton Avenue
15 ; CITY: Palo Alto
16 ; STATE: California
17 ; COUNTRY: US
18 ; ZIP: 94301
19 ; COMPUTER READABLE FORM:
20 ; MEDIUM TYPE: Floppy disk
21 ; COMPUTER: IBM PC compatible
22 ; OPERATING SYSTEM: PC-DOS/MS-DOS
23 ; SOFTWARE: Patentin Release #1.0, Version #1.25
24 ; CURRENT APPLICATION DATA:
25 ; APPLICATION NUMBER: US/08/330,123A
26 ; FILING DATE: 27-OCT-1994
27 ; CLASSIFICATION: 435
28 ; PRIOR APPLICATION DATA:
29 ; APPLICATION NUMBER: US 08/272,102
30 ; FILING DATE: 07-JUL-1994
31 ; ATTORNEY/AGENT INFORMATION:
32 ; NAME: Smith, William M
33 ; REGISTRATION NUMBER: 30,223
34 ; TELECOMMUNICATION INFORMATION:
35 ; TELEPHONE: (415) 326-2400
36 ; TELEFAX: (415) 326-2422
37 ; INFORMATION FOR SEQ ID NO: 23:
38 ; SEQUENCE CHARACTERISTICS:
39 ; LENGTH: 26 base pairs

```

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-330-123A-23

Query Match 60.0%; Score 12; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GTTTGCTCTAGA 20  
Db 1 GTTTGCTCTAGA 12

## RESULT 5

US-08-482-115B-23  
Sequence 23, Application US/08482115B  
Patent No. 5776679  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Assays for the RNA Component of Human  
TITLE OF INVENTION: Telomerase  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,115B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000830US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-482-115B-23

Query Match 60.0%; Score 12; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GTTTGCTCTAGA 20  
Db 1 GTTTGCTCTAGA 12

## RESULT 6

US-08-660-678A-23  
Sequence 23, Application US/08660678A  
Patent No. 5837857  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,678A  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000811US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-660-678A-23

Query Match 60.0%; Score 12; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GTTTGCTCTAGA 20  
Db 1 GTTTGCTCTAGA 12

## RESULT 7

US-08-710-249-26  
Sequence 26, Application US/08710249  
Patent No. 5858777  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Andrews, William H.  
APPLICANT: Adams, Robert R.  
TITLE OF INVENTION: Methods and Reagents for Regulating  
Telomere Length and Telomerase Activity  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,249  
FILING DATE: 13-SEP-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION NUMBER: US 08/583,808  
FILING DATE: 05-JAN-1996  
APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US 60/003,492  
FILING DATE: 08-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001220US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-710-249-26

Query Match 60.0%; Score 12; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 9 GTTGTCTCTAGA 20  
DB 1 GTTGTCTCTAGA 12

RESULT 8  
US-08-485-778-19  
Sequence 19, Application US/08485778  
Patent No. 5876979  
GENERAL INFORMATION:  
APPLICANT: Andrews, William H.  
APPLICANT: Avilion, Ariel Athena  
APPLICANT: Funk, Junli  
APPLICANT: Greider, Carol  
APPLICANT: Marhuenda, Maria Antonia Blasco  
APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,778

FILING DATE: 07-JE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/387,524  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-778-19  
Query Match 60.0%; Score 12; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 9 GTTGTCTCTAGA 20  
DB 1 GTTGTCTCTAGA 12  
RESULT 9  
US-08-472-802C-24  
Sequence 24, Application US/08472802C  
Patent No. 5958680  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,802C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sich, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000820  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-472-802C-24

Query Match 60.0%; Score 12; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20  
DB 1 GTTGTCTCTAGA 12

## RESULT 10

US-08-520-550A-19  
Sequence 19, Application US/08520550A  
Patent No. 6013468  
GENERAL INFORMATION:  
APPLICANT: Andrews, William H.  
APPLICANT: Avilion, Ariel A.  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Greider, Carol  
APPLICANT: Marhuenda, Maria A. B.  
APPLICANT: Villeponteau, Bryant  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,550A  
FILING DATE: 29-AUG-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/387,524  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A3B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-520-550A-19

Query Match 60.0%; Score 12; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20  
DB 1 GTTGTCTCTAGA 12

## RESULT 11

US-08-998-443-23  
Sequence 23, Application US/08998443  
Patent No. 6054575  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Funk, Junli  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,443  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,678  
FILING DATE: 05-JUN-1996  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000811US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-998-443-23

Query Match 60.0%; Score 12; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20  
DB 1 GTTGTCTCTAGA 12

## RESULT 12

US-08-974-549A-598  
Sequence 598, Application US/08974549A  
Patent No. 6166178

```

; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; NAME/KEY:
; LOCATION: 1..26

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; OTHER INFORMATION: /note= "R3c primer"
; US-08-974-549A-598
; Query Match 60.0%; Score 12; DB 4; Length 26;
; Best Local Similarity 100.0%; Pred. No. 7.6e+02;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 9 GTTTGCTCTAGA 20
; DB 1 GTTTGCTCTAGA 12
;
; RESULT 13
; US-09-060-523-23
; Sequence 23, Application US/09060523
; Patent No. 6258535
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Ferg, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,523
; FILING DATE: 14-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000813US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-060-523-23
;
; Query Match 60.0%; Score 12; DB 4; Length 26;
; Best Local Similarity 100.0%; Pred. No. 7.6e+02;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 9 GTTTGCTCTAGA 20
; DB 1 GTTTGCTCTAGA 12

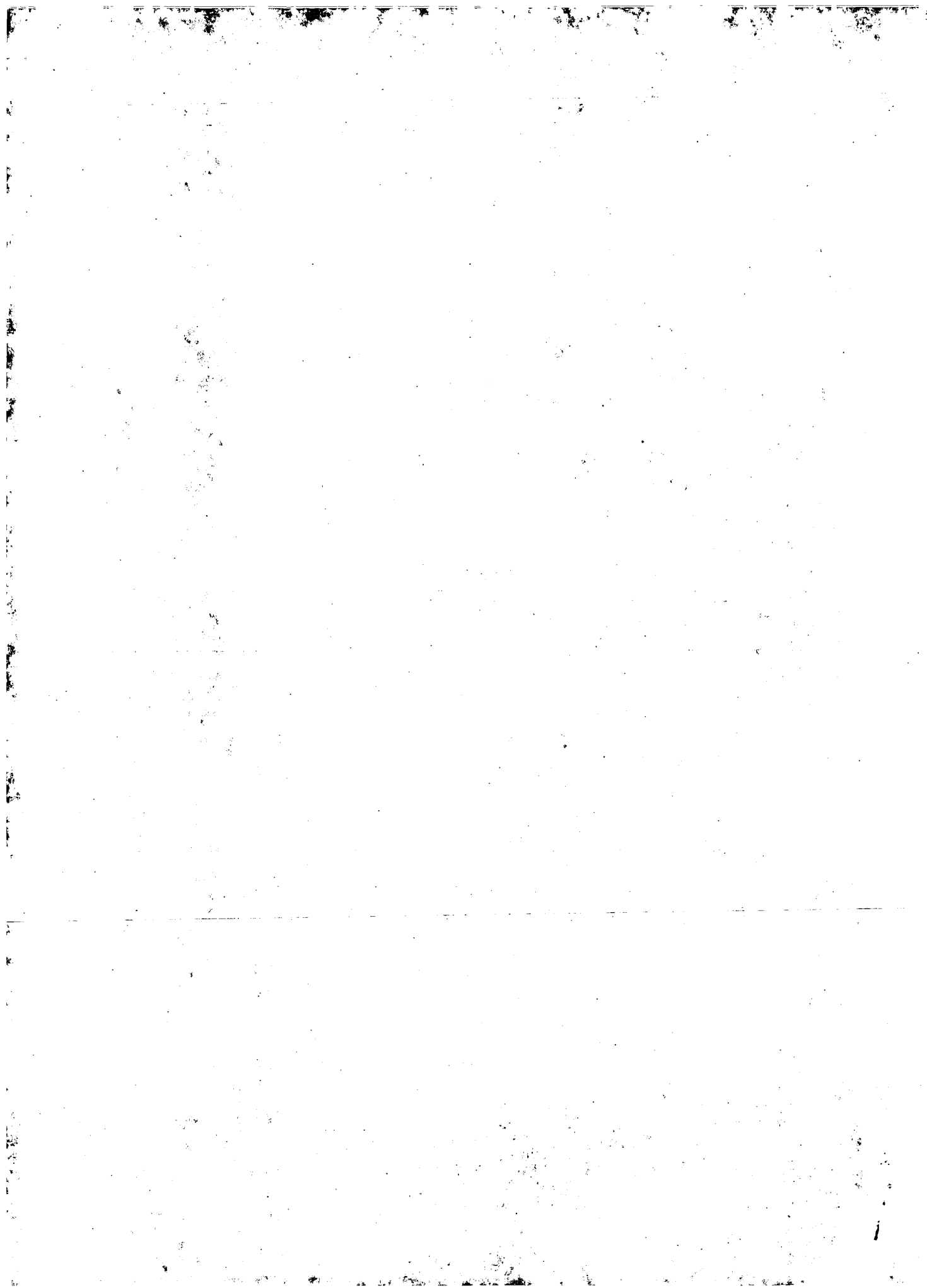
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RESULT 14  
US-09-220-157A-26  
; Sequence 26, Application US/09220157A  
; Patent No. 6300110  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Andrews, William H.  
; APPLICANT: Adams, Robert R.  
; TITLE OF INVENTION: Methods and Reagents for Regulating  
; TITLE OF INVENTION: Telomere Length and Telomerase Activity  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/220,157A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/710,249  
; FILING DATE: 13-SEP-1996  
; APPLICATION NUMBER: US 08/583,808  
; FILING DATE: 05-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/003,492  
; FILING DATE: 08-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-001220US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-220-157A-26

Query Match 60.0%; Score 12; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 GTTTCCTCTAGA 20  
Db 1 GTTTCCTCTAGA 12

RESULT 15  
US-09-286-959B-4  
; Sequence 4, Application US/09286959B  
; Patent No. 6300131  
; GENERAL INFORMATION:  
; APPLICANT: Johns Hopkins University  
; APPLICANT: Greider, Carol W.  
; APPLICANT: Le, Siyuan  
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS  
; FILE REFERENCE: 07265/157001  
; CURRENT APPLICATION NUMBER: US/09/286,959B  
; CURRENT FILING DATE: 1999-04-06

; PRIOR APPLICATION NUMBER: 60/080,783  
; PRIOR FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-286-959B-4  
Query Match 60.0%; Score 12; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 GTTTCCTCTAGA 20  
Db 1 GTTTCCTCTAGA 12  
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Job time : 32.3147 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 132.908 Seconds  
(without alignments)  
338.880 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20

Sequence: 1 CATTTTGTGCTCTAGA 20

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Minimum DB seq length: 0

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24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	19 AAV41180	RNA component of h
2	19	95.0	20	23 AAS15934	Human telomerase p
3	18	90.0	25	22 AAC93100	Human telomerase p
4	18	90.0	28	18 AAT93259	Primer used in pre
5	16	80.0	22	18 AAT58812	Human telomerase p
6	13	65.0	13	23 AAS15937	Human telomerase p
7	13	65.0	13	23 AAS15938	Human telomerase p
8	13	65.0	24	22 AAH39806	SNP specific lower
9	12	60.0	12	23 ABH86386	Oligonucleotide pr

10	12	60.0	13	23 AAS15935	Human telomerase p
11	12	60.0	13	23 ABC09084	Oligonucleotide SE
12	12	60.0	13	23 ABC09085	Oligonucleotide SE
13	12	60.0	13	23 ABH44170	Oligonucleotide SE
14	12	60.0	13	23 ABH44171	Oligonucleotide SE
15	12	60.0	13	23 ABH59432	Oligonucleotide SE
16	12	60.0	13	23 ABH59433	Oligonucleotide SE
17	12	60.0	13	23 AAT32141	Oligonucleotide SE
18	12	60.0	18	17 AAT32141	DNA sequencing "pr
19	12	60.0	21	22 AAH62524	FC fragment of IGG
20	12	60.0	24	20 AAZ39443	SCFV1 DNA sequenci
21	12	60.0	24	20 AAZ39443	Human SCFV1 primer
22	12	60.0	25	22 AAF23878	Human STS tag PCR
23	12	60.0	26	17 AAT10304	RNA component of h
24	12	60.0	26	17 AAT10299	RNA component of h
25	12	60.0	26	17 AAT11044	Primer for product
26	12	60.0	26	18 AAT58811	Human telomerase p
27	12	60.0	26	19 AAV19489	Human hTR gene RT-
28	12	60.0	26	19 AAV17033	Telomerase PCR pri
29	12	60.0	26	20 AAX90788	Human telomerase R
30	12	60.0	26	20 AAX77402	Human telomerase R
31	12	60.0	26	20 AAX01542	PCR primer for Hum
32	12	60.0	26	21 AAH88250	Human telomerase R
33	12	60.0	26	24 ABK48024	Human telomerase-a
34	12	60.0	26	24 AAD24246	Human telomerase (
35	12	60.0	27	19 AAV41193	RNA component of h
36	12	60.0	27	24 ABA95497	Human telomerase R
37	12	60.0	30	19 AAV63648	Antisense oligonuc
38	12	60.0	30	20 AAZ23630	Human clone 28-1 t
39	12	60.0	30	22 AAS09475	Antisense oligonuc
40	12	60.0	33	24 AAL42603	Human serine/threo
41	12	60.0	35	19 AAV27458	Streptococcus pneu
42	12	60.0	35	24 ABQ84926	Streptococcus pneu
43	12	60.0	40	17 AAT69500	Plasmid p182Sfil c
44	12	60.0	40	17 AAT69507	Plasmid p182Sfil c
45	12	60.0	40	19 AAV27463	Streptococcus pneu
			40	20 AAX88932	Circular plasmid e

#### ALIGNMENTS

RESULT 1  
AAV41180  
ID AAV41180 standard; DNA; 20 BP.

XX AC AAV41180;

XX DT 08-OCT-1998 (first entry)

XX RNA component of human telomerase (hTR) antisense oligo 20/21.

XX RNA component; human telomerase; antisense oligonucleotide; infection;  
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;  
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;  
KW immune system down-regulation; anti-inflammatory therapy; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9828442-A1.

XX PD 02-JUL-1998.

XX PF 19-DEC-1997; 97WO-US23619.

XX PR 20-DEC-1996; 96US-0770565.

XX PR 20-DEC-1996; 96US-0770564.

XX PA (GERO-) GERON CORP.

XX PI Kealey JT, Kim NW, Pruzaan R, Weinrich SL, Wu F;

XX WPI; 1998-377670/32.

```

XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 20 BP; 3 A; 3 C; 3 G; 11 T; 0 other;
Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTTTGTGCTCTAGA 20
DB 1 CATTTTGTGCTCTAGA 20

```

```

XX
XX PI Gryaznov SM, Pruzan R, Weinrich SL;
XX WPI; 2001-656955/75.
XX
XX New polynucleotide useful for inhibiting telomerase activity in cells,
PT or for treating telomerase-mediated condition or disease, such as
PT cancers, tumours, Hodgkin's disease, or inflammatory conditions -
XX
XX Claim 8; Page 36; 48pp; English.
XX
XX The invention relates to polynucleotide inhibitors (I) and methods for
CC inhibiting telomerase activity (I) are useful in inhibiting telomerase
CC activity and proliferation of a telomerase positive cell, and in
CC manufacturing a medicament for inhibiting telomerase activity in a cell
CC and in treating telomerase-mediated condition or disease such as
CC adenocarcinoma of breast, prostate of colon, mixed cell leukaemia,
CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also
CC useful in treating a tumour or in manufacturing a medicament for the
CC treatment of tumour. The polynucleotide inhibitors may also be used in
CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
CC activity in cells in vivo is useful in prophylactic and therapeutic
CC methods of treating cancer and other disorders involving inappropriate
CC expression of telomerase, and in treating veterinary proliferative
CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
CC for immunosuppression and for selectively down-regulating specific
CC branches of the immune system. The present sequence represents
CC human telomerase polynucleotide inhibitor #15, as described in the
CC method of the invention.
XX
SQ Sequence 20 BP; 3 A; 3 C; 3 G; 11 T; 0 other;
Query Match 95.0%; Score 19; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTTTGTGCTCTAG 19
DB 2 CATTTTGTGCTCTAG 20

```

## RESULT 2

## AAS15934

```

ID AAS15934 standard; DNA; 20 BP.
AC AAS15934;
XX
XX 27-FEB-2002 (first entry)
XX
XX Human telomerase polynucleotide inhibitor #15.
XX
XX Human; telomerase; hTR; cytotatic; anti-inflammatory; adenocarcinoma;
KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;
KW fertility; inflammatory condition; tumour; cancer; veterinary;
KW immunosuppression; telomerase inhibitor; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key modified_base 1..20
XX Location/Qualifiers
FT /*tag= a
FT /mod_base= OTHER
FT /note= "N3'-P5' phosphoramidate linkages"
XX
XX WO200174136-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10476.
XX
XX 31-MAR-2000; 2000US-0540119.
XX
XX (GERO-) GERON CORP.

```

## RESULT 3

## AAC93100

```

ID AAC93100 standard; DNA; 25 BP.
AC AAC93100;
XX
XX 23-MAR-2001 (first entry)
XX
XX Human telomerase PCR primer #1.
XX
XX Telomerase; cancer; telomere damage; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200074667-A2.
XX
XX 14-DEC-2000.
XX
XX 05-JUN-2000; 2000WO-US15544.
XX
XX 04-JUN-1999; 99US-0137549.
XX
XX (AUJL/) AU J L.
XX (WIEN/) WIENTJES G.
XX
XX Au JL, Wientjes G;
XX
XX WPI; 2001-071022/08.
XX
XX Inhibiting or reducing growth of cell for treating cancer, comprising
PT administering telomere damage-inducing agent and telomerase inhibitory
PT agent to the cell -

```

```

XX Example 7; Page 62; 97pp; English.
XX
CC The present invention provides a method for inhibiting or reducing the
CC growth of a cell which involves administering to the cell a telomere
CC damage inducing agent and a telomerase inhibitory agent. This can be
CC used in the treatment of aberrant cell growth, including cancers.
XX
SQ Sequence 25 BP; 4 A; 5 C; 4 G; 12 T; 0 other;
    Query Match          90.0%; Score 18; DB 22; Length 25;
    Best Local Similarity 100.0%; Pred. No. 5.1;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTTCCTGCTCTA 18
    |||||||
DB 8 CATTTCCTGCTCTA 25

RESULT 4
AAT93259/c
ID AAT93259 standard; DNA; 28 BP.
XX
AC AAT93259;
XX
DT 27-MAR-1998 (first entry)
XX
DE Primer used in preparation of expression plasmid.
XX
KW Plasmid vector; gene expression; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9734006-A1.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-JP00748.
XX
PR 18-JUL-1996; 96JP-0208897.
XX
PR 13-MAR-1996; 96JP-0085801.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
PI Kato I, Oshima A, Sagawa H, Ueno H;
XX
WPI; 1997-470885/43.
XX
PT Plasmid for expression of heterologous genes in a host - contains a
PT promoter sequence recognised by a non-host RNA polymerase
XX
PS Disclosure; Page 53; 102pp; Japanese.
XX
CC The present sequence was used in the preparation of a plasmid
CC vector for the expression of foreign genes in a host, e.g. E. coli,
CC contains a promoter sequence, which is recognised by a non-host RNA
CC polymerase and a replication origin which increases the number of
CC copies when induced by an extracellular augmentation factor. The
CC use of the plasmid vector allows the efficient expression of
CC proteins which may be fatal or harmful to a host, e.g. the
CC restriction enzyme AccII. The vector allows expression of the
CC restriction enzyme gene even in the absence of a modification
CC enzyme gene.
XX
SQ Sequence 28 BP; 15 A; 7 C; 4 G; 2 T; 0 other;
    Query Match          90.0%; Score 18; DB 18; Length 28;
    Best Local Similarity 100.0%; Pred. No. 5.1;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TTTTTCCTGCTCTAGA 20
    |||||||
DB 21 TTTTTCCTGCTCTAGA 4

```

## RESULT 5

```

AAT58812
ID AAT58812 standard; DNA; 22 BP.
XX
AC AAT58812;
XX
DT 20-NOV-1997 (first entry)
XX
DE Human telomerase PCR 3'-primer hal88.
XX
KW Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;
KW protozoa; tumour; antibody; polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9640868-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09517.
XX
PR 07-JUN-1995; 95US-0478352.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Autexier C, Greider C;
XX
WPI; 1997-099928/09.
XX
PT DNA encoding essential RNA components of human telomerase - also
PT truncated or recombinant telomerase, useful for diagnosis and
PT treatment of cancer and infection by eukaryotic parasites
XX
PS Example 5; Page 32; 48pp; English.
XX
CC The present sequence represents PCR 3'-primer hal88 used for
CC amplifying the human telomerase (hTR). The RNA and DNA can be used in
CC hybridisation assays to detect or quantify telomerase activity in cells,
CC tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites
CC (yeast and protozoa) or tumours. It is also useful as primers for
CC amplification assays. The truncated or recombinant vertebrate telomerase
CC is used therapeutically to increase telomerase activity (also as
CC as antisense molecules, are used to reduce such activity. Typical
CC applications are initiation/restoration of activity to cause senescence
CC or to prevent immortalisation of cells in tumours or parasites. The DNA
CC is also used to produce recombinant telomerase, which can then be used
CC conventionally to raise antibodies for diagnostic detection of
CC telomerase. Detecting telomerase allows early diagnosis of tumour or
CC infection, before clinical signs manifest. Telomerase inhibitors
CC directed against e.g. Trypanosoma should cause fewer side effects than
CC drugs currently used to treat such infections. The DNA encodes those
CC parts of hTR RNA essential for activity but are significantly shorter
CC than the endogenous RNA component.
XX
SQ Sequence 22 BP; 3 A; 4 C; 4 G; 11 T; 0 other;
    Query Match          80.0%; Score 16; DB 18; Length 22;
    Best Local Similarity 100.0%; Pred. No. 48;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTTCCTGCTCTC 16
    |||||||
DB 7 CATTTCCTGCTCTC 22

RESULT 6
AAS15937
ID AAS15937 standard; DNA; 13 BP.
XX
AC AAS15937;

```

```

XX
DI 27-FEB-2002 (first entry)
XX
XX Human telomerase polynucleotide inhibitor #19.
XX
XX Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;
KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;
KW fertility; inflammatory condition; tumour; cancer; veterinary;
KW immunosuppression; telomerase inhibitor; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..13
FT /*tag= a
FT /mod_base= OTHER
FT /note= "N3'-P5' phosphoramidate linkages"
XX
XX WO200174136-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10476.
XX
XX 31-MAR-2000; 2000US-0540119.
XX
XX (GERO-) GERON CORP.
XX
XX Gryaznov SM, Pruzan R, Weinrich SL;
XX WPI; 2001-656955/75.
XX
XX New polynucleotide useful for inhibiting telomerase activity in cells,
PT or for treating telomerase-mediated condition or disease, such as
PT cancers, tumours, Hodgkin's disease, or inflammatory conditions -
XX
XX Example 3; Page 32; 48pp; English.
XX
XX The invention relates to polynucleotide inhibitors (I) and methods for
CC inhibiting telomerase activity. (I) are useful in inhibiting telomerase
CC activity and proliferation of a telomerase positive cell, and in
CC manufacturing a medicament for inhibiting telomerase activity in a cell
CC and in treating telomerase-mediated condition or disease, such as
CC adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,
CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also
CC useful in treating a tumour or in manufacturing a medicament for the
CC treatment of tumour. The polynucleotide inhibitors may also be used in
CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
CC activity in cells in vivo is useful in prophylactic and therapeutic
CC methods of treating cancer and other disorders involving inappropriate
CC expression of telomerase, and in treating veterinary proliferative
CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
CC for immunosuppression and for selectively down-regulating specific
CC branches of the immune system. The present sequence represents
CC human telomerase polynucleotide inhibitor #19, as described in the
CC method of the invention.
XX
XX Sequence 13 BP; 0 A; 1 C; 2 G; 10 T; 0 other;
SQ
Query Match 65.0%; Score 13; DB 23; Length 13;
Best Local Similarity 100.0%; Pred No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTTTGTGTTGCT 15
DB 1 TTTTGTGTTGCT 13

RESULT 7
AAH39806
ID AAS15938 standard; DNA; 13 BP.
XX

```

```

AC AAS15938;
XX
DI 27-FEB-2002 (first entry)
XX
XX Human telomerase polynucleotide inhibitor #19.
XX
XX Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;
KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;
KW fertility; inflammatory condition; tumour; cancer; veterinary;
KW immunosuppression; telomerase inhibitor; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..13
FT /*tag= a
FT /mod_base= OTHER
FT /note= "N3'-P5' phosphoramidate linkages"
XX
XX WO200174136-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10476.
XX
XX 31-MAR-2000; 2000US-0540119.
XX
XX (GERO-) GERON CORP.
XX
XX Gryaznov SM, Pruzan R, Weinrich SL;
XX WPI; 2001-656955/75.
XX
XX New polynucleotide useful for inhibiting telomerase activity in cells,
PT or for treating telomerase-mediated condition or disease, such as
PT cancers, tumours, Hodgkin's disease, or inflammatory conditions -
XX
XX Example 3; Page 32; 48pp; English.
XX
XX The invention relates to polynucleotide inhibitors (I) and methods for
CC inhibiting telomerase activity. (I) are useful in inhibiting telomerase
CC activity and proliferation of a telomerase positive cell, and in
CC manufacturing a medicament for inhibiting telomerase activity in a cell
CC and in treating telomerase-mediated condition or disease, such as
CC adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,
CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also
CC useful in treating a tumour or in manufacturing a medicament for the
CC treatment of tumour. The polynucleotide inhibitors may also be used in
CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
CC activity in cells in vivo is useful in prophylactic and therapeutic
CC methods of treating cancer and other disorders involving inappropriate
CC expression of telomerase, and in treating veterinary proliferative
CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
CC for immunosuppression and for selectively down-regulating specific
CC branches of the immune system. The present sequence represents
CC human telomerase polynucleotide inhibitor #19, as described in the
CC method of the invention.
XX
XX Sequence 13 BP; 1 A; 2 C; 2 G; 8 T; 0 other;
SQ
Query Match 65.0%; Score 13; DB 23; Length 13;
Best Local Similarity 100.0%; Pred No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 TTTGTTTGTCTCTA 18
DB 1 TTTGTTTGTCTCTA 13

RESULT 8
AAH39806
ID AAH39806 standard; DNA; 24 BP.
XX

```

XX AAH39806;  
 XX  
 XX 14-AUG-2001 (first entry)  
 XX  
 XX SNP specific lower PCR primer SEQ ID 2602.  
 XX  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200129262-A2.  
 XX  
 XX 26-APR-2001.  
 XX  
 XX 13-OCT-2000; 2000WO-US28436.  
 XX  
 XX 15-OCT-1999; 99US-0160096.  
 XX  
 XX (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 XX Picoult-Newburg L, Pohl M;  
 XX  
 XX WPI; 2001-290930/30.  
 XX  
 XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample -  
 XX  
 XX Claim 1; Page 63; 83pp; English.  
 XX  
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension. (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a PCR primer specific  
 CC for a human SNP containing DNA sequence.  
 XX  
 XX Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 other;  
 SQ  
 Query Match 65.0%; Score 13; DB 22; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ATTTTGTGTC 14  
 |||||  
 Db 5 ATTTTGTGTC 17  
 |||||  
 RESULT 9  
 ABH86386

ID ABH86386 standard; DNA; 12 BP.  
 XX  
 XX AC ABH86386;  
 XX  
 XX DT 22-FEB-2002 (first entry)  
 XX  
 XX DE Oligonucleotide primer SEQ ID NO 286379 for detecting SNP TSC0012703.  
 XX  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX  
 XX PN 18-OCT-2001.  
 XX  
 XX PD 06-APR-2001; 2001WO-IB00713.  
 XX  
 XX PF 07-APR-2000; 2000DE-1019173.  
 XX  
 XX PR (EPIG-) EPIGENOMICS AG.  
 XX  
 XX PA Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX PI WPI; 2001-657177/75.  
 XX  
 XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single nucleotide polymorphisms and cytosine  
 PT methylation status -  
 XX  
 XX PS Claim 1; SEQ ID 286379; 29pp + Sequence Listing; German.  
 XX  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation.  
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
 CC ABI00010-ABI82073 represent the oligomers described in the invention.  
 CC NOTE: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX SQ Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 other;  
 Query Match 60.0%; Score 12; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ATTTTGTGTC 13  
 |||||  
 Db 1 ATTTTGTGTC 12  
 |||||  
 RESULT 10  
 AAS15935  
 ID AAS15935 standard; DNA; 13 BP.  
 XX  
 XX AC AAS15935;  
 XX  
 XX DT 27-FEB-2002 (first entry)  
 XX  
 XX DE Human telomerase polynucleotide inhibitor #16.  
 XX  
 XX KW Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;  
 KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;  
 KW fertility; inflammatory condition; tumour; cancer; veterinary;  
 KW immunosuppression; telomerase inhibitor; ss.  
 XX

OS Homo sapiens.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT modified\_base 1..13  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "N3'-P5' phosphoramidate linkages"  
 XX  
 XX WO200174136-A2.  
 XX  
 XX 11-OCT-2001.  
 XX  
 XX 30-MAR-2001; 2001WO-US10476.  
 XX  
 XX 31-MAR-2000; 2000US-0540119.  
 XX  
 XX (GERO-) GERON CORP.  
 XX  
 XX Gryaznov SM, Pruzan R, Weinrich SL;  
 XX  
 XX WPI; 2001-656955/75.  
 XX

XX New polynucleotide useful for inhibiting telomerase activity in cells,  
 XX or for treating telomerase-mediated condition or disease, such as  
 XX cancer, tumours, Hodgkin's disease, or inflammatory conditions -  
 XX  
 XX Claim 8; Page 36; 48pp; English.  
 XX  
 XX The invention relates to polynucleotide inhibitors (I) and methods for  
 XX inhibiting telomerase activity. (I) are useful in inhibiting telomerase  
 XX activity and proliferation of a telomerase positive cell, and in  
 XX manufacturing a medicament for inhibiting telomerase activity in a cell  
 XX and in treating telomerase-mediated condition or disease, such as  
 XX adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,  
 XX Hodgkin's disease, fertility and inflammatory conditions. (I) are also  
 XX useful in treating a tumour or in manufacturing a medicament for the  
 XX treatment of tumour. The polynucleotide inhibitors may also be used in  
 XX diagnostic assays for detecting RNA or DNA. Inhibition of telomerase  
 XX activity in cells in vivo is useful in prophylactic and therapeutic  
 XX methods of treating cancer and other disorders involving inappropriate  
 XX expression of telomerase, and in treating veterinary proliferative  
 XX diseases. Inhibition of telomerase in haematopoietic stem cells is useful  
 XX for immunosuppression and for selectively down-regulating specific  
 XX branches of the immune system. The present sequence represents  
 XX human telomerase polynucleotide inhibitor #16, as described in the  
 XX method of the invention.

XX Sequence 13 BP; 2 A; 1 C; 1 G; 9 T; 0 other;  
 XX  
 XX Query Match 60.0%; Score 12; DB 23; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTITTTGTTT 12  
 Db 2 CATTITTTGTTT 13

RESULT 11  
 ABC09084  
 ID ABC09084 standard; DNA; 13 BP.  
 XX  
 XX ABC09084;  
 XX  
 XX 20-FEB-2002 (first entry)  
 XX

DE Oligonucleotide SEQ ID NO 9075 for detecting SNP TSC0002428.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.  
 XX WO200177384-A2.  
 XX  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB00713.  
 XX  
 XX 07-APR-2000; 2000DE-1019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single nucleotide polymorphisms and cytosine  
 XX methylation status -  
 XX  
 XX Claim 1; SEQ ID 9075; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 XX and cytosine methylation status in chemically pretreated genomic DNA. The  
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 XX range of diseases including immune system, gastrointestinal, respiratory,  
 XX central nervous system, cardiovascular and metabolic disorders. The  
 XX oligomers are also used for detecting cell type differentiation.  
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
 XX ABT00010-ABT99989 represent the oligomers described in the invention.  
 XX NOTE: The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 other;

XX Query Match 60.0%; Score 12; DB 23; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATTTTITGTTTG 13  
 Db 1 ATTTTITGTTTG 12

RESULT 12  
 ABC09085/c  
 ID ABC09085 standard; DNA; 13 BP.  
 XX  
 XX ABC09085;  
 XX  
 XX 20-FEB-2002 (first entry)  
 XX

DE Oligonucleotide SEQ ID NO 9076 for detecting SNP TSC0002428.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.  
 XX WO200177384-A2.  
 XX  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB00713.  
 XX  
 XX 07-APR-2000; 2000DE-1019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -  
XX Claim 1; SEQ ID 9076; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 other;  
SQ

Query Match 60.0%; Score 12; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTTTGTGTTG 13  
Db 13 ATTTTGTGTTG 2

RESULT 13  
ABH44170  
ID ABH44170 standard; DNA; 13 BP.  
XX  
AC ABH44170;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 244147 for detecting SNP TSC0059579.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
FN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB00713.  
XX  
PR 07-APR-2000; 2000DE-1019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -  
XX Claim 1; SEQ ID 244147; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 other;  
SQ

CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 other;  
SQ

Query Match 60.0%; Score 12; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTTTGTGTTG 13  
Db 2 ATTTTGTGTTG 13

RESULT 14  
ABH44171/c  
ID ABH44171 standard; DNA; 13 BP.  
XX  
AC ABH44171;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 244148 for detecting SNP TSC0059579;  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
FN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB00713.  
XX  
PR 07-APR-2000; 2000DE-1019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -  
XX Claim 1; SEQ ID 244148; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 other;  
SQ

Query Match 60.0%; Score 12; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ATTTTGTTC 13  
DB 12 ATTTTGTTC 1

RESULT 15  
ABH59432  
ID ABH59432 standard; DNA; 13 BP.  
XX  
AC ABH59432;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 259409 for detecting SNP TSC0063000.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB00713.  
XX  
PR 07-APR-2000; 2000DE-1019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status  
XX  
PS Claim 1; SEQ ID 259409; 29pp + Sequence Listing; German.  
XX

CC This invention describes novel oligonucleotide primers of peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 13 BP; 0 A; 1 C; 3 G; 9 T; 0 other;

Query Match 60.0%; Score 12; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred No. 4.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTTTGTTC 14  
DB 1 TTTTGTTC 12

Search completed: June 23, 2003, 05:43:41  
Job time : 134.216 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 232.59 Seconds  
(without alignments)  
2502.502 Million cell updates/sec

Title: US-08-770-564A-13  
Perfect score: 20  
Sequence: 1 CATTCTTTGTTGCTCTAGA 20

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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- 24: em\_ph:\*
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- 26: em\_ro:\*
- 27: em\_scs:\*
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- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
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- 36: em\_htg\_man:\*
- 37: em\_htg\_vrt:\*
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- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
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# SUMMARIES

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C 3	18	90.0	28	6	BD000545	BD000545 Restricti
C 4	18	90.0	28	6	I83455	I83455 Sequence 19
5	17	85.0	24	6	AX058270	AX058270 Sequence
6	13	65.0	22	6	AX462591	AX462591 Sequence
7	13	65.0	24	6	AX117479	AX117479 Sequence
8	12	60.0	24	6	A24429	A24429 oligonucleo
9	12	60.0	25	6	AX057458	AX057458 Sequence
10	12	60.0	26	6	A94988	A94988 Sequence 2
11	12	60.0	26	6	AR016055	AR016055 Sequence
12	12	60.0	26	6	AR028786	AR028786 Sequence
13	12	60.0	26	6	AR059216	AR059216 Sequence
14	12	60.0	26	6	AR075527	AR075527 Sequence
15	12	60.0	26	6	AR161925	AR161925 Sequence
16	12	60.0	26	6	AX022187	AX022187 Sequence
17	12	60.0	26	6	AX033377	AX033377 Sequence
18	12	60.0	26	6	AX468455	AX468455 Sequence
19	12	60.0	26	6	BD011297	BD011297 Human tel
20	12	60.0	26	6	E36508	E36508 Method for
21	12	60.0	26	6	E37046	E37046 Human telom
22	12	60.0	26	6	I31770	I31770 Sequence 23
23	12	60.0	27	6	AR063850	AR063850 Sequence
24	12	60.0	27	6	AX317989	AX317989 Sequence
25	12	60.0	30	6	A84595	A84595 Sequence 5
26	12	60.0	30	6	AR079892	AR079892 Sequence
27	12	60.0	35	6	AR120372	AR120372 Sequence
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C 29	12	60.0	38	6	A06778	A06778 Nucleotide
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C 32	12	60.0	40	6	AR053686	AR053686 Sequence
C 33	12	60.0	40	6	AR120377	AR120377 Sequence
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C 35	12	60.0	42	6	AR001574	AR001574 Sequence
C 36	12	60.0	43	6	AR001575	AR001575 Sequence
C 37	12	60.0	45	6	A02009	A02009 Artificial
C 38	12	60.0	45	6	A06779	A06779 Nucleotide
C 39	12	60.0	50	6	AX161232	AX161232 Sequence
40	12	60.0	50	6	E23942	E23942 Oligonucleo
41	11	55.0	18	6	AX069089	AX069089 Sequence
C 42	11	55.0	20	6	A83837	A83837 Sequence 15
C 43	11	55.0	20	6	AX487392	AX487392 Sequence
44	11	55.0	21	6	AR159606	AR159606 Sequence
C 45	11	55.0	21	6	AR193717	AR193717 Sequence

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RESULT 1  
AR063837  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

AR063837  
Sequence 13 from patent US 5846723.  
AR063837  
Sequence 13 from patent US 5846723.  
AR063837.1  
GI:5993145

Unknown.  
Unknown.  
Unclassified.  
1 (bases 1 to 20)  
Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.  
Methods for detecting the RNA component of telomerase  
Patent: US 5846723-A 13 08-DEC-1998;  
Location/Qualifiers

20 bp  
DNA  
linear  
PAT 29-SEP-1999

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTGTTGTTGCTCTAGA 20
Db 1 CATTGTTGTTGCTCTAGA 20

RESULT 2
LOCUS AR122661/c 28 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6165749.
ACCESSION AR122661
VERSION AR122661.1 GI:14106978
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
1 (bases 1 to 28)
AUTHORS Sagawa,H., Ueno,H., Oshima,A. and Kato,I.
TITLES Plasmid
JOURNAL Patent: US 6165749-A 5 26-DEC-2000;
FEATURES
Location/Qualifiers
1. .28
source
BASE COUNT 15 a 7 c 4 g 2 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TTTTGTGTTGCTCTAGA 20
Db 21 TTTTGTGTTGCTCTAGA 4

RESULT 3
LOCUS BD000545/c 28 bp DNA linear PAT 31-JAN-2002
DEFINITION Restriction enzyme and gene thereof.
ACCESSION BD000545
VERSION BD000545.1 GI:18623658
KEYWORDS JP 2000325094-A/4.
SOURCE unidentified.
ORGANISM
REFERENCE
1 (bases 1 to 28)
AUTHORS Sagawa,H., Ueno,H., Oshima,A. and Kato,I.
TITLES Restriction enzyme and gene thereof
JOURNAL Patent: JP 2000325094-A 4 28-NOV-2000;
COMMENT TAKARA SHUZO CO LTD
OS Unidentified
PN JP 2000325094-A/4
PD 28-NOV-2000
PF 20-APR-2000 JP 2000120124
PR
PI HIROAKI SAGAWA, HARUMI UENO, ATSUSHI OHSIMA, IKUNOSHIN KATO PC
C12N15/09, C12N9/16//((C12N9/16, C12R1:19), C12N15/00, CC
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CC Topology: Linear;
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 21 TTTTGTGTTGCTCTAGA 4

RESULT 4
LOCUS I83455/c 28 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 19 from patent US 5714323.
ACCESSION I83455
VERSION I83455.1 GI:3406985
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
1 (bases 1 to 28)
AUTHORS Oshima,A., Inouye,S. and Inouye,M.
TITLES Over expression of single-stranded molecules
JOURNAL Patent: US 5714323-A 19 03-FEB-1998;
FEATURES
Location/Qualifiers
1. .28
source
BASE COUNT 15 a 7 c 4 g 2 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 21 TTTTGTGTTGCTCTAGA 4

RESULT 5
LOCUS AX058270 24 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 5 from Patent WO0074667.
ACCESSION AX058270
VERSION AX058270.1 GI:12310769
KEYWORDS
SOURCE synthetic construct.
ORGANISM
REFERENCE
1 (bases 1 to 24)
AUTHORS Au,J.B. and Wientjes,G.
TITLES Compositions active in telomere damage comprising a taxane and
telomerase inhibitor
JOURNAL Patent: WO 0074667-A 5 14-DEC-2000;
Au, Jessie L.S. (US) ; Wientjes, Guillaume (US)
FEATURES
Location/Qualifiers
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source
/organism='synthetic construct'
/db_xref='taxon:32630'
/notes='primer/probe'
BASE COUNT 3 a 5 c 4 g 12 t
ORIGIN
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 8 CATTGTTGTTGCTCTCT 24
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RESULT 6
AX462591
LOCUS
DEFINITION
Sequence 335 from Patent EP1217079.
ACCESSION
AX462591
VERSION
AX462591.1 GI:21885804
KEYWORDS
SOURCE
ORGANISM
Aegilops tauschii.
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poodeae; Triticeae; Aegilops.
1
REFERENCE
AUTHORS
Bernard,M., Sourdil,P. and Guyomarch,H.
TITLE
Microsatellite markers from Triticum tauschii
JOURNAL
Patent: EP 1217079-A 335 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES
Location/Qualifiers
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTGTTTGCTCTA 18
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DB 6 TTGTTTGCTCTA 18

RESULT 7
AX117479
LOCUS
DEFINITION
Sequence 2602 from Patent WO0129262.
ACCESSION
AX117479
VERSION
AX117479.1 GI:14034430
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 24)
REFERENCE
AUTHORS
Picault-Newburg,L. and Pohl,M.
TITLE
Genotyping reagents, kits and methods of use thereof
JOURNAL
Patent: WO 0129262-A 2602 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
Location/Qualifiers
1..24
/organism="synthetic construct"
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BASE COUNT
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTTTGTGTC 14
|||||
DB 5 ATTTTGTGTC 17

RESULT 8
A24429
LOCUS
DEFINITION
oligonucleotide TPI.
ACCESSION
A24429
VERSION
A24429.1 GI:2293585
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
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artificial sequences.
Location/Qualifiers
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 14 ATTTTGTGTC 25

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AX057458
LOCUS
DEFINITION
Sequence 62 from Patent WO0077257.
ACCESSION
AX057458
VERSION
AX057458.1 GI:12310196
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
REFERENCE
AUTHORS
Baidya,N., Chen,Y.D., Holding,J. and Yu,Y.T.
TITLE
Gene specific arrays and the use thereof
JOURNAL
Patent: WO 0077257-A 62 21-DEC-2000;
Clingenix, Inc. (US)
FEATURES
Location/Qualifiers
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ORIGIN
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QY 2 ATTTTGTGTC 13
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DB 3 ATTTTGTGTC 14

RESULT 10
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LOCUS
DEFINITION
Sequence 2 from Patent EP0926245.
ACCESSION
A94988
VERSION
A94988.1 GI:6779168
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
1 (bases 1 to 26)
REFERENCE
AUTHORS
Emrich,T.D.
TITLE
Method for detection of carcinoma of the urinary bladder within a
urine sample
JOURNAL
Patent: EP 0926245-A 2 30-JUN-1999;
ROCHE DIAGNOSTICS GMBH (DE)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32644"
BASE COUNT
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ORIGIN
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Db 1 GTTGGCTCTAGA 12

RESULT 11
LOCUS AR016055 26 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 23 from patent US 5776679.
ACCESSION AR016055
VERSION AR016055.1 GI:3972332
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 23 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTGGCTCTAGA 12

RESULT 12
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DEFINITION Sequence 26 from patent US 5858777.
ACCESSION AR028786
VERSION AR028786.1 GI:5940759
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Andrews,W.H. and Adams,R.R.
TITLE Methode and reagents for regulating telomere length and telomerase activity
JOURNAL Patent: US 5858777-A 26 12-JAN-1999;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 3 c 9 g 7 t
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Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GTTGGCTCTAGA 20
Db 1 GTTGGCTCTAGA 12

RESULT 13
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DEFINITION Sequence 23 from patent US 5837857.
ACCESSION AR059216
VERSION AR059216.1 GI:5984793
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 23 17-NOV-1998;
FEATURES Location/Qualifiers
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BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

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Db 1 GTTGGCTCTAGA 12

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LOCUS AR075527 26 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 24 from patent US 5956680.
ACCESSION AR075527
VERSION AR075527.1 GI:10002275
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5956680-A 24 28-SEP-1999;
FEATURES Location/Qualifiers
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BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1e+05;
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Qy 9 GTTGGCTCTAGA 20
Db 1 GTTGGCTCTAGA 12

RESULT 15
LOCUS AR161925 26 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 23 from patent US 6258535.
ACCESSION AR161925
VERSION AR161925.1 GI:16228953
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 23 10-JUL-2001;
FEATURES Location/Qualifiers
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BASE COUNT 7 a 3 c 9 g 7 t

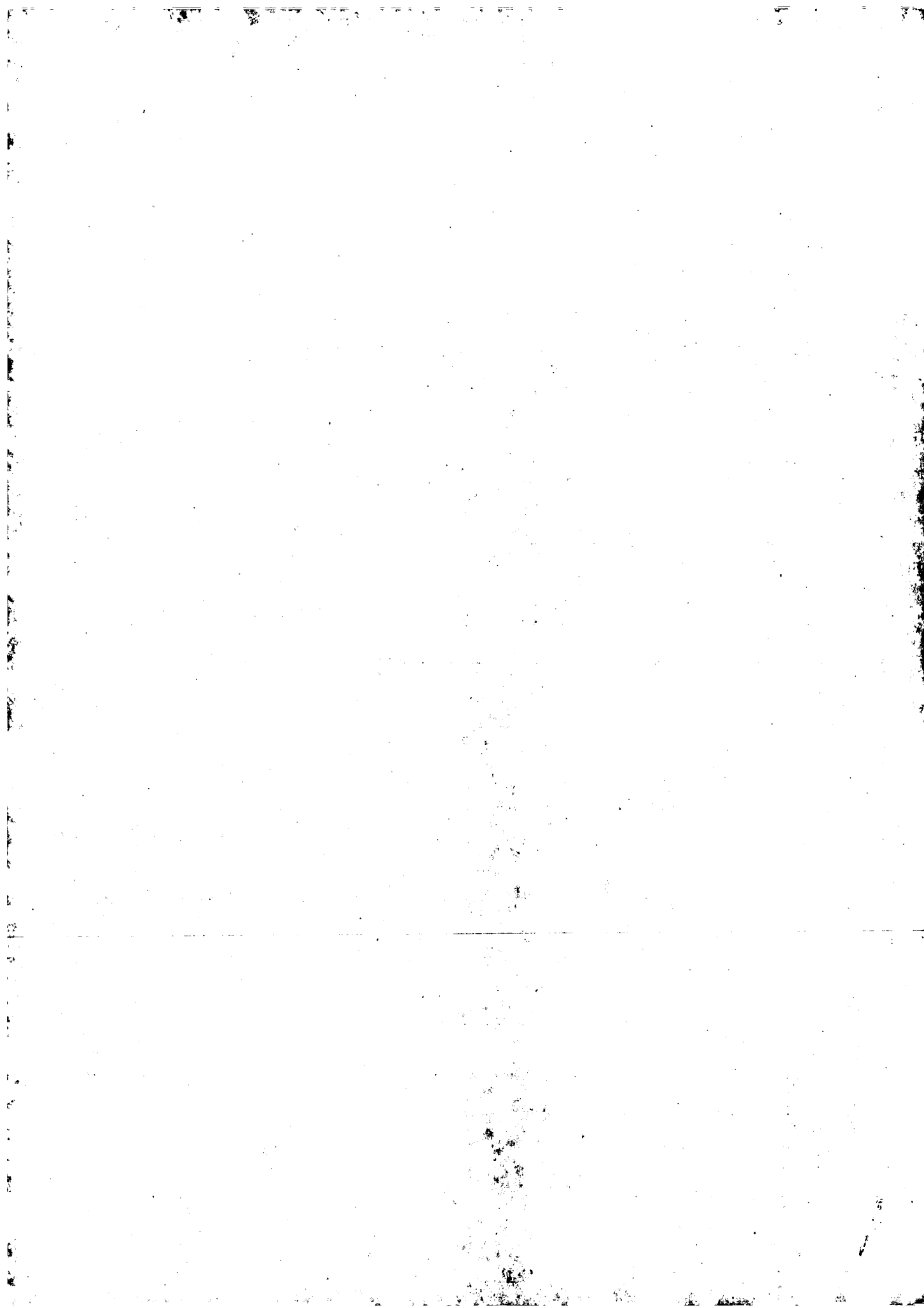
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 Db 1 GTTGGCTCTAGA 12

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 Job time : 234.051 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 406.104 Seconds  
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Title: US-08-770-564A-14  
Perfect score: 17  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 4	17	100.0	30	10	US-10-330-872-4
C 5	17	100.0	30	10	US-10-330-872A-4
C 6	15	88.2	25	9	US-10-359-935-27
C 7	14.4	84.7	25	12	US-60-427-808-681796
C 8	14	82.4	24	6	US-09-536-058D-52
C 9	14	82.4	25	12	US-60-427-808-148950
C 10	13.8	81.2	50	5	US-09-749-280B-6883
C 11	13.4	78.8	25	9	US-10-303-778-7843
C 12	13.4	78.8	25	12	US-60-427-808-12244
C 13	13.4	78.8	25	12	US-60-427-808-16616
C 14	13.4	78.8	25	12	US-60-427-808-153744
C 15	13.4	78.8	25	12	US-60-427-808-834500
C 16	13.4	78.8	25	12	US-60-427-836-193942
C 17	13.4	78.8	25	12	US-60-427-836-599012
C 18	13.4	78.8	50	5	US-09-749-280B-1479
C 19	13	76.5	15	10	US-10-287-787-16506
C 20	13	76.5	15	10	US-10-287-787-18526

C 21	13	76.5	16	9	US-10-310-188-5556	Sequence 5556, Ap
C 22	13	76.5	17	9	US-10-303-778-7849	Sequence 7849, Ap
C 23	13	76.5	17	9	US-10-310-188-14135	Sequence 14135, A
C 24	13	76.5	17	9	US-10-310-188-57644	Sequence 57644, A
C 25	13	76.5	17	10	US-10-299-054A-1993	Sequence 1993, Ap
C 26	13	76.5	17	10	US-10-299-054A-1994	Sequence 1994, Ap
C 27	13	76.5	18	9	US-10-310-188-39627	Sequence 39627, A
C 28	13	76.5	18	10	US-10-287-787-23414	Sequence 23414, A
C 29	13	76.5	18	10	US-10-287-787-23415	Sequence 23415, A
C 30	13	76.5	24	10	US-10-287-787-12803	Sequence 12803, A
C 31	13	76.5	25	12	US-60-427-808-467694	Sequence 467694, A
C 32	13	76.5	25	12	US-60-427-836-391360	Sequence 391360, A
C 33	13	76.5	25	12	US-60-427-836-421414	Sequence 421414, A
C 34	13	76.5	25	12	US-60-427-836-455025	Sequence 455025, A
C 35	13	76.5	39	10	US-10-287-787-12804	Sequence 12804, A
C 36	12.8	75.3	23	9	US-10-310-188-62469	Sequence 62469, A
C 37	12.8	75.3	25	9	US-10-355-577-404464	Sequence 404464, A
C 38	12.8	75.3	25	9	US-10-355-577-700065	Sequence 700065, A
C 39	12.8	75.3	25	12	US-60-427-808-23365	Sequence 23365, A
C 40	12.8	75.3	25	12	US-60-427-808-182757	Sequence 182757, A
C 41	12.8	75.3	25	12	US-60-427-808-249883	Sequence 249883, A
C 42	12.8	75.3	25	12	US-60-427-808-273706	Sequence 273706, A
C 43	12.8	75.3	25	12	US-60-427-808-382705	Sequence 382705, A
C 44	12.8	75.3	25	12	US-60-427-808-496697	Sequence 496697, A
C 45	12.8	75.3	25	12	US-60-427-808-518595	Sequence 518595, A

## ALIGNMENTS

## RESULT 1

PCT-US03-04088-16/c  
; Sequence 16, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 16  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
; OTHER INFORMATION: region  
PCT-US03-04088-16

Query Match 100.0%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
 Db 18 CGGGCCAGCAGCTGACA 2

RESULT 2  
 PCT-US03-04088-280  
 ; Sequence 280, Application PC/TUS0304088  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McSwiggen Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leonid  
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
 ; FILE REFERENCE: Expression Using Short Interfering RNA (siRNA)  
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088  
 ; CURRENT FILING DATE: 2003-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/396,600  
 ; PRIOR FILING DATE: 2002-07-17  
 ; PRIOR APPLICATION NUMBER: US 60/358,580  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: US 60/363,124  
 ; PRIOR FILING DATE: 2002-03-11  
 ; PRIOR APPLICATION NUMBER: US 60/386,782  
 ; PRIOR FILING DATE: 2002-06-06  
 ; PRIOR APPLICATION NUMBER: US 60/406,784  
 ; PRIOR FILING DATE: 2002-08-29  
 ; PRIOR APPLICATION NUMBER: US 60/408,378  
 ; PRIOR FILING DATE: 2002-09-05  
 ; PRIOR APPLICATION NUMBER: US 60/409,293  
 ; PRIOR FILING DATE: 2002-09-09  
 ; PRIOR APPLICATION NUMBER: US 60/440,129  
 ; PRIOR FILING DATE: 2003-01-15  
 ; NUMBER OF SEQ ID NOS: 626  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 280  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense  
 ; OTHER INFORMATION: region  
 PCT-US03-04088-280

Query Match 100.0%; Score 17; DB 1; Length 19;  
 Best Local Similarity 94.18; Pred. No. 1.7e+02;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
 Db 2 CGGGCCAGCAGCTGACA 18

RESULT 3  
 PCT-US02-33146-10  
 ; Sequence 10, Application PC/TUS0233146  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Rochester Medical Center  
 ; APPLICANT: Rowley, Peter  
 ; TITLE OF INVENTION: Telomerase Interference  
 ; FILE REFERENCE: FP-71506-2/RFT/SRN  
 ; CURRENT APPLICATION NUMBER: PCT/US02/33146  
 ; CURRENT FILING DATE: 2002-12-05  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 22  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US02-33146-10

Query Match 100.0%; Score 17; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGGGCCAGCAGCTGACA 17  
 Db 5 CGGGCCAGCAGCTGACA 21

RESULT 4  
 US-10-330-872-4  
 ; Sequence 4, Application US/10330872  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Weinrich, Scott  
 ; APPLICANT: Atkinson III, Edward  
 ; APPLICANT: Lichtsteiner, Serge  
 ; APPLICANT: Vasserot, Alain  
 ; APPLICANT: Pruzan, Ronald  
 ; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and  
 ; TITLE OF INVENTION: Inhibitors  
 ; FILE REFERENCE: 011/006C  
 ; CURRENT APPLICATION NUMBER: US/10/330,872  
 ; CURRENT FILING DATE: 2002-12-24  
 ; PRIOR APPLICATION NUMBER: 08/510,736  
 ; PRIOR FILING DATE: 1995-08-04  
 ; PRIOR APPLICATION NUMBER: 08/833,377  
 ; PRIOR FILING DATE: 1997-04-04  
 ; PRIOR APPLICATION NUMBER: 09/420,056  
 ; PRIOR FILING DATE: 1999-10-18  
 ; PRIOR APPLICATION NUMBER: 09/717,828  
 ; PRIOR FILING DATE: 2000-11-20  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 30  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-330-872-4

Query Match 100.0%; Score 17; DB 10; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
 Db 4 CGGGCCAGCAGCTGACA 20

RESULT 5  
 US-10-330-872A-4  
 ; Sequence 4, Application US/10330872A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Weinrich, Scott  
 ; APPLICANT: Atkinson III, Edward  
 ; APPLICANT: Lichtsteiner, Serge  
 ; APPLICANT: Vasserot, Alain  
 ; APPLICANT: Pruzan, Ronald  
 ; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and  
 ; TITLE OF INVENTION: Inhibitors  
 ; FILE REFERENCE: 011/006C  
 ; CURRENT APPLICATION NUMBER: US/10/330,872A  
 ; CURRENT FILING DATE: 2002-12-24  
 ; PRIOR APPLICATION NUMBER: 08/510,736  
 ; PRIOR FILING DATE: 1995-08-04  
 ; PRIOR APPLICATION NUMBER: 08/833,377  
 ; PRIOR FILING DATE: 1997-04-04  
 ; PRIOR APPLICATION NUMBER: 09/420,056  
 ; PRIOR FILING DATE: 1999-10-18  
 ; PRIOR APPLICATION NUMBER: 09/717,828  
 ; PRIOR FILING DATE: 2000-11-20  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 4



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; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-4

Query Match      100.0%; Score 17; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
    |||||
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 6
US-10-359-935-27
; Sequence 27, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; Fung, Junli
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-359-935-27

Query Match      88.2%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCAGCAGCTGACA 17
    |||||
Db 9 GGGCAGCAGCTGACA 23
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```
RESULT 7
US-60-427-808-681796/c
; Sequence 681796, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 681796
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-681796

Query Match      84.7%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGGGCCAGCAGCTGACA 17
    |||||
Db 24 CGGGCCAGCAGCTGACA 9

RESULT 8
US-09-536-058D-52/c
; Sequence 52, Application US/09536058D
; GENERAL INFORMATION:
; APPLICANT: BEGER, CARMELA
; APPLICANT: BARBER, JACK
; APPLICANT: WONG-STAAI, FLOSSIE
; TITLE OF INVENTION: BRCA-1 REGULATORS AND METHODS OF USE
; FILE REFERENCE: 039316/0601
; CURRENT APPLICATION NUMBER: US/09/536,058D
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-058D-52

Query Match      82.4%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
    |||||
Db 23 CGGGCCAGCAGCTG 10

RESULT 9
US-60-427-808-148950
; Sequence 148950, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 148950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
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US-60-427-808-148950

Query Match 82.4%; Score 14; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14  
DB 10 CGGGCCAGCAGCTG 23

RESULT 10

US-09-749-2808-6883/c  
; Sequence 6883, Application US/097492808  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard A.  
; TITLE OF INVENTION: Nucleic Acids Containing Single  
; FILE REFERENCE: 47416  
; CURRENT APPLICATION NUMBER: US/09/749,2808  
; CURRENT FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: 60/173,419  
; NUMBER OF SEQ ID NOS: 10038  
; SOFTWARE: Curagen Patent Formatter Version 0.9  
; SEQ ID NO 6883  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: (26)...(0)  
; OTHER INFORMATION: single nucleotide polymorphism  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)...(26)  
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Accession number cg43987514  
US-09-749-2808-6883

Query Match 81.2%; Score 13.8; DB 5; Length 50;  
Best Local Similarity 88.2%; Pred. No. 6.5e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
DB 36 CGGGCCAGCAGCGCCA 20

RESULT 11

US-10-303-778-7843/c  
; Sequence 7843, Application US/10303778  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL  
; FILE REFERENCE: 47416  
; CURRENT APPLICATION NUMBER: US/10/303,778  
; CURRENT FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 17608  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7843  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-303-778-7843

Query Match 78.8%; Score 13.4; DB 9; Length 22;  
Best Local Similarity 93.3%; Pred. No. 9.7e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGCTGAC 16  
DB 21 GGGACAGCAGCTGAC 7

RESULT 12

US-60-427-808-12244/c  
; Sequence 12244, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 12244  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-12244

Query Match 78.8%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 9.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGCAGCAGCTGACA 17  
DB 20 GGGCAGCAGCTGTCA 6

RESULT 13

US-60-427-808-16616  
; Sequence 16616, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 16616  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-16616

Query Match 78.8%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 9.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGCTGAC 16  
DB 4 GGGCCAGCAGCTCAC 18

RESULT 14

US-60-427-808-153744  
; Sequence 153744, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 153744  
; LENGTH: 25  
; TYPE: DNA

; ORGANISM: Mus musculus  
US-60-427-808-153744

Query Match 78.8%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 9.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17  
|||||  
DB 8 GGCCAGCAGCAGACA 22

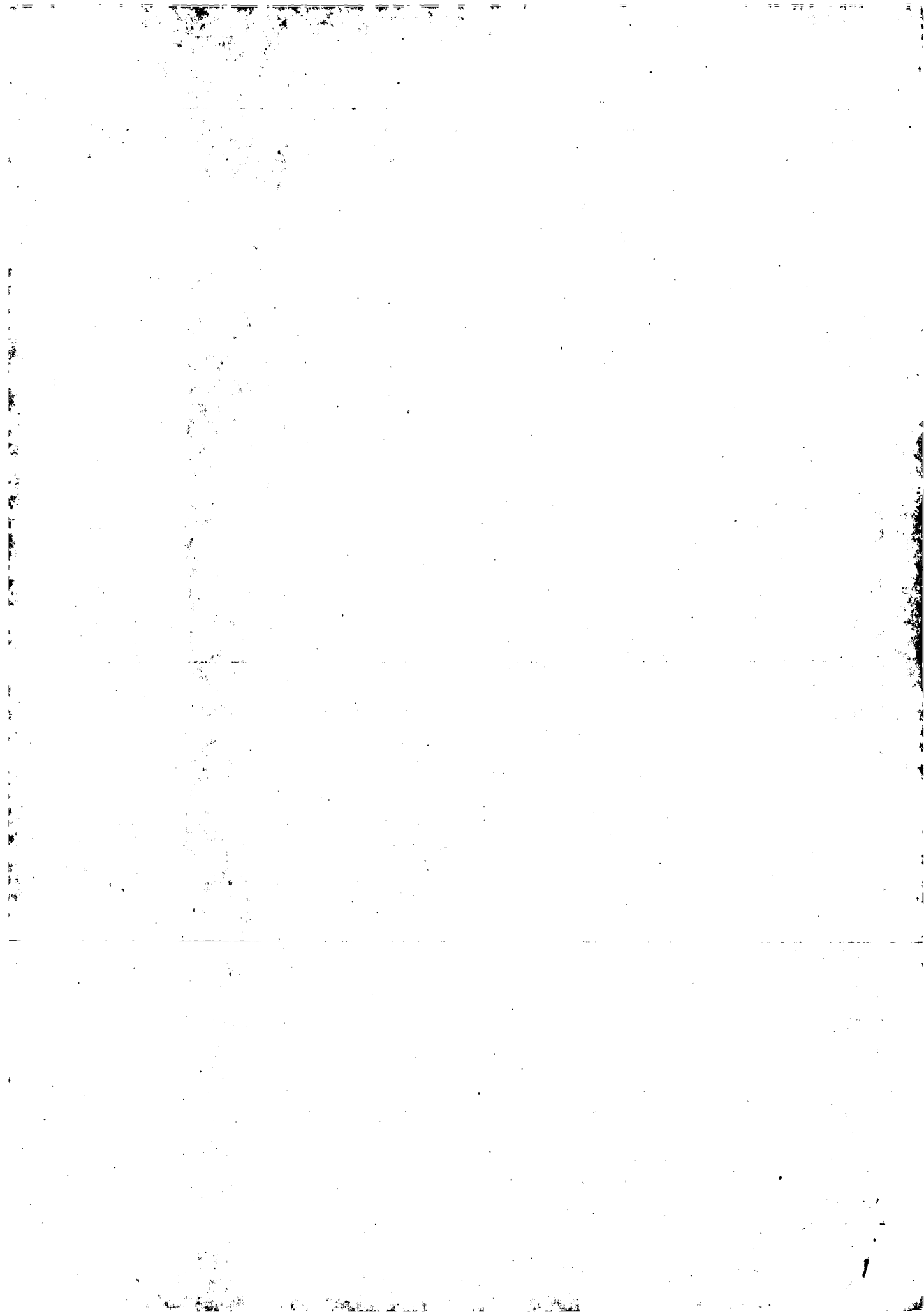
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US-60-427-808-834500/c  
; Sequence 834500, Application US/60427808  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528  
; CURRENT APPLICATION NUMBER: US/60/427,808  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 834500  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-60-427-808-834500

Query Match 78.8%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 9.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCCAGCAGCTGAC 16  
|||||  
DB 22 GGCCAGCAGCTGAC 8

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Job time : 407.411 secs



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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1442.49 Seconds  
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Title: US-08-770-564A-14

Perfect score: 17  
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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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36: /cgn2\_6/ptodata/2/pna/US08 COMB.seq.\*  
37: /cgn2\_6/ptodata/2/pna/US08 COMB.seq.\*  
38: /cgn2\_6/ptodata/2/pna/US08 COMB.seq.\*  
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40: /cgn2\_6/ptodata/2/pna/US08 COMB.seq.\*  
41: /cgn2\_6/ptodata/2/pna/US08 COMB.seq.\*  
42: /cgn2\_6/ptodata/2/pna/US08 COMB.seq.\*  
43: /cgn2\_6/ptodata/2/pna/US08 COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	1	PCT-US97-23619-14
2	17	100.0	17	11	US-08-770-564A-14
3	17	100.0	25	23	US-09-601-267-20
4	17	100.0	30	9	US-08-510-736-4
5	17	100.0	30	28	US-09-717-828A-4
6	17	100.0	30	28	US-09-717-828B-4
7	17	100.0	30	28	US-09-717-829A-4
8	15	88.2	25	8	US-08-472-802A-27
9	15	88.2	25	8	US-08-472-802B-27
10	15	88.2	25	9	US-08-482-115A-26
11	15	88.2	25	9	US-08-521-634-44
12	15	88.2	25	14	US-09-057-351-27
13	14.4	84.7	25	17	US-09-396-196F-47051
14	14.4	84.7	25	17	US-09-396-196G-47051
15	14	82.4	24	20	US-09-536-058C-52
16	14	82.4	24	20	US-09-536-058C-52
17	14	82.4	42	13	US-08-973-589-12
18	13.8	81.2	25	36	US-09-956-584-40691
19	13.8	81.2	25	67	US-60-234-017-62949
20	13.4	78.8	25	17	US-09-396-196F-33812
21	13.4	78.8	25	17	US-09-396-196F-107046
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 20, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 27, Appl
					Sequence 27, Appl
					Sequence 26, Appl
					Sequence 44, Appl
					Sequence 27, Appl
					Sequence 47051, A
					Sequence 52, Appl
					Sequence 52, Appl
					Sequence 12, Appl
					Sequence 40691, A
					Sequence 62949, A
					Sequence 33812, A
					Sequence 107046,

C 22 13.4 78.8 25 17 US-09-396-196G-33812  
C 23 13.4 78.8 25 17 US-09-396-196G-107046  
C 24 13.4 78.8 26 1 PCT-US01-21880-18  
C 25 13.4 78.8 26 31 US-09-815-171A-18  
C 26 13.4 78.8 42 15 US-09-103-636-2542  
C 27 13 76.5 14 15 US-09-164-961-2894  
C 28 13 76.5 24 9 US-08-521-634-11  
C 29 13 76.5 25 17 US-09-396-196F-64639  
C 30 13 76.5 25 17 US-09-396-196G-64639  
C 31 13 76.5 47 1 PCT-US02-35943-58545  
C 32 13 76.5 47 42 US-10-227-565-58545  
C 33 13 76.5 49 17 US-09-397-424-3647  
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C 35 12.8 75.3 18 17 US-09-341-700A-294  
C 36 12.8 75.3 22 18 US-09-490-700-14  
C 37 12.8 75.3 25 36 US-09-956-584-66914  
C 38 12.8 75.3 25 36 US-09-956-604-40137  
C 39 12.8 75.3 25 36 US-09-956-604-40139  
C 40 12.8 75.3 25 36 US-09-956-604-40141  
C 41 12.8 75.3 25 36 US-09-956-604-40152  
C 42 12.8 75.3 25 36 US-09-956-604-40153  
C 43 12.8 75.3 25 36 US-09-956-604-40155  
C 44 12.8 75.3 25 36 US-09-956-604-40156  
C 45 12.8 75.3 25 36 US-09-956-604-40157

ALIGNMENTS

RESULT 1  
PCT-US97-23619-14  
; Sequence 14, Application PC/TUS9723619  
; GENERAL INFORMATION:  
; APPLICANT:   
; APPLICANT:   
; APPLICANT:   
; APPLICANT:   
; APPLICANT:   
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
; TITLE OF INVENTION: RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/23619  
; FILING DATE: Not yet assigned  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/770,564  
; FILING DATE: 20-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/770,565  
; FILING DATE: 20-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 15389-27PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0300  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:

Sequence 33812, A  
Sequence 107046, A  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 2542, Ap  
Sequence 2894, Ap  
Sequence 11, Appl  
Sequence 64639, A  
Sequence 64639, A  
Sequence 58545, A  
Sequence 58545, A  
Sequence 3647, Ap  
Sequence 3647, Ap  
Sequence 294, Appl  
Sequence 66914, A  
Sequence 40137, A  
Sequence 40139, A  
Sequence 40141, A  
Sequence 40152, A  
Sequence 40153, A  
Sequence 40155, A  
Sequence 40156, A  
Sequence 40157, A

; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..17  
; OTHER INFORMATION: /note="polynucleotide RP2"  
PCT-US97-23619-14  
Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGGCCAGCAGCTGACA 17  
Db 1 CGGGCCAGCAGCTGACA 17  
RESULT 2  
US-08-770-564A-14  
; Sequence 14, Application US/08770564A  
; GENERAL INFORMATION:  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ron  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
; TITLE OF INVENTION: Against the RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,564A  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002200US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-564A-14  
Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGGCCAGCAGCTGACA 17  
Db 1 CGGGCCAGCAGCTGACA 17  
RESULT 3  
US-09-601-267-20

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; Sequence 20, Application US/09601267
; GENERAL INFORMATION:
; APPLICANT: William Nicol KEITH
; TITLE OF INVENTION: Promoter Regions of the Mouse and Human Telomerase RNA Component
; FILE REFERENCE: 9013.18
; CURRENT APPLICATION NUMBER: US/09/601,267
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/GB99/00308
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: GB 9801902.9
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-601-267-20

Query Match      100.0%; Score 17; DB 23; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTGACA 17
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DB      7 CGGGCCAGCAGCTGACA 23

RESULT 4
US-08-510-736-4
; Sequence 4, Application US/08510736
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Methods for Purifying Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,736
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 015389-001100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-510-736-4
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Query Match      100.0%; Score 17; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTGACA 17
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DB      4 CGGGCCAGCAGCTGACA 20

RESULT 5
US-09-717-828A-4
; Sequence 4, Application US/09717828A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Purified Telomerase
; FILE REFERENCE: PurifiedTelomerase01base
; CURRENT APPLICATION NUMBER: US/09/717,828A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 (edited)
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828A-4

Query Match      100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTGACA 17
        |||||
DB      4 CGGGCCAGCAGCTGACA 20

RESULT 6
US-09-717-828B-4
; Sequence 4, Application US/09717828B
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase01base
; CURRENT APPLICATION NUMBER: US/09/717,828B
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO 4
; LENGTH: 30
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828B-4
Query Match 100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 7
US-09-717-829A-4
; Sequence 4, Application US/09717829A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Alain P
; APPLICANT: Priznan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: Purified telomerase oligobase
; CURRENT APPLICATION NUMBER: US/09/717,829A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO 4
; TYPE: DNA
; LENGTH: 30
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-829A-4
Query Match 100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 8
US-08-472-802A-27
; Sequence 27, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

```

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; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-27
Query Match 88.2%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
Db 9 GGCCAGCAGCTGACA 23

RESULT 9
US-08-472-802B-27
; Sequence 27, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123

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;; FILING DATE: 27-OCT-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223  
;; REFERENCE/DOCKET NUMBER: 15389-000820  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 27:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-472-802B-27

Query Match 88.2%; Score 15; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17  
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DB 9 GGCCAGCAGCTGACA 23

RESULT 10  
US-08-482-115A-26  
;; Sequence 26, Application US/08482115A  
;; GENERAL INFORMATION:  
;; APPLICANT: VILLEPONTEAU, Bryant  
;; APPLICANT: FENG, Junli  
;; APPLICANT: FUNK, Walter  
;; APPLICANT: ANDREWS, William H.  
;; TITLE OF INVENTION: HUMAN TELOMERASE  
;; NUMBER OF SEQUENCES: 34  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, 8th Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: US  
;; ZIP: 94111  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/482,115A  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION NUMBER: US 08/330,123  
;; FILING DATE: 27-OCT-1994  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-482-115A-26

;; FILING DATE: 27-OCT-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223  
;; REFERENCE/DOCKET NUMBER: 15389-000830  
;; TELEPHONE: (415) 326-2400  
;; TELEFAX: (415) 326-2422  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-482-115A-26

Query Match 88.2%; Score 15; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGCCAGCAGCTGACA 17  
|||  
DB 9 GGCCAGCAGCTGACA 23

RESULT 11  
US-08-521-634-44  
;; Sequence 44, Application US/08521634  
;; GENERAL INFORMATION:  
;; APPLICANT: Villeponteau, Bryant  
;; APPLICANT: FENG, Junli  
;; APPLICANT: FUNK, Walter  
;; APPLICANT: ANDREWS, William  
;; TITLE OF INVENTION: Mammalian Telomerase  
;; NUMBER OF SEQUENCES: 66  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew  
;; STREET: One Market Plaza, Steuart Tower, Suite 2000  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94105  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/521,634  
;; FILING DATE: 31-AUG-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/482,115  
;; FILING DATE: 7-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/472,802  
;; FILING DATE: 7-JUN-1995  
;; APPLICATION NUMBER: US 08/330,123  
;; FILING DATE: 27-OCT-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/272,102  
;; FILING DATE: 7-JUL-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Dunn, Tracy J.  
;; REGISTRATION NUMBER: 34,587  
;; REFERENCE/DOCKET NUMBER: 15389-000850  
;; TELEPHONE: 415-326-2400  
;; TELEFAX: 415-326-2422  
;; INFORMATION FOR SEQ ID NO: 44:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (primer)  
;; ANTI-SENSE: YES  
US-08-521-634-44

Query Match 88.2%; Score 15; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17  
|||  
DB 9 GGCCAGCAGCTGACA 23

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RESULT 12
US-09-057-351-27
; Sequence 27, Application US/09057351
; GENERAL INFORMATION:
; APPLICANT: Valleponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorello, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-27

Query Match      88.2%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  GGCCAGCAGCTGACA 17
DB      9  GGCCAGCAGCTGACA 23

RESULT 13
US-09-396-196F-47051/c
; Sequence 47051, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15

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; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47051
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-47051

Query Match      84.7%; Score 14.4; DB 17; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  GGCCAGCAGCTGACA 17
DB      24 GGCCAGCAGCTCACA 9

RESULT 14
US-09-396-196G-47051/c
; Sequence 47051, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47051
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-47051

Query Match      84.7%; Score 14.4; DB 17; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  GGCCAGCAGCTGACA 17
DB      24 GGCCAGCAGCTCACA 9

RESULT 15
US-09-536-058-52/c
; Sequence 52, Application US/09536058
; GENERAL INFORMATION:
; APPLICANT: Beger, Carmela
; APPLICANT: Barber, Jack
; APPLICANT: Wong-Staal, Flossie
; TITLE OF INVENTION: BRCA-1 Regulators and Methods of Use
; FILE REFERENCE: P-IU 3842
; CURRENT APPLICATION NUMBER: US/09/536,058
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-536-058-52

Query Match      82.4%; Score 14; DB 20; Length 24;

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Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCAGCAGCTG 14  
Db 23 CGGGCCAGCAGCTG 10

Search completed: June 25, 2003, 06:20:30  
Job time : 1444.11 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 51.6773 Seconds  
(without alignments)  
482.732 Million cell updates/sec

Title: US-08-770-564A-14  
Perfect score: 17  
Sequence: 1 CGGCGCAGCAGTGACA 17

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	88.2	25	10	US-09-057-351-27
2	13.4	78.8	26	10	US-09-815-171A-18
3	12.4	72.9	24	9	US-10-027-961A-1
4	12.4	72.9	24	9	US-10-175-268-1
5	12.4	72.9	24	10	US-09-803-552-1
6	12.4	72.9	24	10	US-09-803-347-1
7	12.4	72.9	24	10	US-09-931-700-13
8	12.4	72.9	24	10	US-09-803-549-1
9	12.4	72.9	24	10	US-09-803-402-1
10	12.4	72.9	24	10	US-09-968-445-1
11	12.4	72.9	50	9	US-09-943-722-9
12	12.2	71.8	25	9	US-10-098-263B-37688
13	12.2	71.8	25	9	US-10-098-263B-38944
14	12	70.6	23	9	US-10-320-230-30
15	12	70.6	23	10	US-09-817-387-18
16	12	70.6	25	9	US-10-215-112-2064
17	12	70.6	31	9	US-09-912-263-184
18	12	70.6	38	9	US-09-930-423-2661
19	12	70.6	38	9	US-09-930-423-2713

20	12	70.6	48	9	US-09-848-754A-7985	Sequence 7985, Ap
21	12	70.6	48	9	US-09-848-754A-8229	Sequence 8229, Ap
22	12	70.6	50	9	US-09-943-722-5	Sequence 5, Appli
23	11.8	69.4	19	9	US-10-044-692-168	Sequence 168, App
24	11.8	69.4	19	9	US-10-044-539-168	Sequence 168, App
25	11.8	69.4	20	9	US-09-915-814-148	Sequence 148, App
26	11.8	69.4	21	9	US-10-044-692-275	Sequence 275, App
27	11.8	69.4	21	9	US-10-044-539-275	Sequence 275, App
28	11.8	69.4	24	9	US-09-940-185-704	Sequence 704, App
29	11.8	69.4	25	9	US-09-940-185-4670	Sequence 4670, Ap
30	11.8	69.4	30	9	US-09-957-483-39	Sequence 39, Appl
31	11.8	69.4	34	9	US-09-957-483-13	Sequence 13, Appl
32	11.8	69.4	38	9	US-09-930-423-3161	Sequence 3161, Ap
33	11.8	69.4	50	9	US-09-920-394-6	Sequence 6, Appli
34	11.4	67.1	19	10	US-09-942-374-4	Sequence 4, Appli
35	11.4	67.1	25	9	US-10-215-112-1826	Sequence 1826, Ap
36	11.4	67.1	25	9	US-10-215-112-12785	Sequence 12785, A
37	11.4	67.1	31	9	US-09-961-077-417	Sequence 417, App
38	11.4	67.1	31	9	US-09-912-263-75	Sequence 75, Appl
39	11.4	67.1	31	9	US-09-999-220B-82	Sequence 82, Appl
40	11.4	67.1	31	9	US-09-999-220B-89	Sequence 89, Appl
41	11.4	67.1	31	9	US-09-999-220B-101	Sequence 101, App
42	11.4	67.1	39	9	US-10-087-993-17	Sequence 17, Appl
43	11.4	67.1	39	10	US-09-905-999-9	Sequence 9, Appli
44	11.4	67.1	45	9	US-09-925-922-8	Sequence 8, Appli
45	11.4	67.1	48	10	US-09-822-698A-62	Sequence 62, Appl

## ALIGNMENTS

RESULT 1  
US-09-057-351-27  
; Sequence 27, Application US/09057351  
; Patent No. US20010034439A1  
; GENERAL INFORMATION:  
; APPLICANT: Villegonteau, Bryant  
; APPLICANT: Funk, Junli  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,351  
; FILING DATE: 08-APR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,802  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-000821US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200

```
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-27

Query Match      88.2%; Score 15; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  GCCCAGCAGCTGACA 17
Db      9  GCCCAGCAGCTGACA 23

RESULT 2
US-09-815-171A-18/c
; Sequence 18, Application US/09815171A
; Patent No. US20020064780A1
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Zichi, Dominic
; APPLICANT: Jenison, Robert D
; APPLICANT: Schneider, Daniel J
; TITLE OF INVENTION: Method and Apparatus for the Automated Generation of
; FILE REFERENCE: SML.03
; CURRENT APPLICATION NUMBER: US/09/815,171A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/616,284
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/356,233
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/232,946
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 08/792,075
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: 09/143,190
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 08/469,609
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 18
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-815-171A-18

Query Match      78.8%; Score 13.4; DB 10; Length 26;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  GCCCAGCAGCTGACA 17
Db      25  GCCCAGCAGCTCACA 11

RESULT 3
US-10-027-961A-1/c
; Sequence 1, Application US/10027961A
; Publication No. US20030032789A1
```

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; GENERAL INFORMATION:
; APPLICANT: O'NEILL, GARY P.
; APPLICANT: MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; FILE REFERENCE: CYCLOOXYGENASE-2
; CURRENT APPLICATION NUMBER: US/10/027,961A
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/599,781
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 08/930,589
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: PCT/CA94/00501
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 08/084,033
; PRIOR FILING DATE: 1993-09-27
; PRIOR APPLICATION NUMBER: 08/064,271
; PRIOR FILING DATE: 1993-05-06
; PRIOR APPLICATION NUMBER: 07/994,760
; PRIOR FILING DATE: 1992-12-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Human
US-10-027-961A-1

Query Match      72.9%; Score 12.4; DB 9; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CGGGCCAGCAGCTG 14
Db      18  CGGGCCAGGAGCTG 5

RESULT 4
US-10-175-268-1/c
; Sequence 1, Application US/10175268
; Publication No. US20030032827A1
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/175,268
; FILING DATE: 19-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,610
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/077,300
; FILING DATE: 15-JUNE-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-175-268-1

Query Match 72.9%; Score 12.4; DB 9; Length 24;  
Best Local Similarity 92.9%; Pred. No. 5e+03; 1; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14  
|||||  
DB 18 CGGGCCAGCAGCTG 5

RESULT 5  
US-09-803-552-1/c  
; Sequence 1, Application US/09803552  
; Patent No. US20010031882A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles N. Serhan  
; TITLE OF INVENTION: Lipoxin Compounds  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/803,552  
; FILING DATE: 09-Mar-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/803,552  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/712,610  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: BWI-112CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-803-552-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;  
Best Local Similarity 92.9%; Pred. No. 5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14  
|||||  
DB 18 CGGGCCAGCAGCTG 5

## RESULT 6

US-09-803-347-1/c  
; Sequence 1, Application US/09803347  
; Patent No. US20020010351A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles N. Serhan  
; TITLE OF INVENTION: Lipoxin Compounds  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/803,347  
; FILING DATE: 12-Mar-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/803,347  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/712,610  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: BWI-112CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-803-347-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;  
Best Local Similarity 92.9%; Pred. No. 5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14  
|||||  
DB 18 CGGGCCAGCAGCTG 5

## RESULT 7

US-09-931-700-13  
; Sequence 13, Application US/09931700  
; Patent No. US20020055615A1  
; GENERAL INFORMATION:  
; APPLICANT: CUTTITTA, FRANK  
; APPLICANT: MARTINEZ, ALFREDO  
; APPLICANT: MILLER, MAE JEAN  
; APPLICANT: UNSWORTH, EDWARD J.  
; APPLICANT: HOOK, WILLIAM  
; APPLICANT: WALSH, THOMAS  
; APPLICANT: GREY, KAREN  
; APPLICANT: MACRI, CHARLES  
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the  
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and  
; TITLE OF INVENTION: Physiology  
; FILE REFERENCE: 2026-4202US4

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; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid,
; OTHER INFORMATION: AM-R antisense probe (nucleotides 788-811)
US-09-931-700-13

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCCAGCAGCTGACA 17
DB 10 GCCAGCAGATGACA 23

RESULT 8
US-09-803-549-1/c
; Sequence 1, Application US/09803549
; Patent No. US2002082435A1
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/803,549
; FILING DATE: 09-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/803,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/712,610
; FILING DATE: <Unknown>
; FILING DATE: 15-JUNE-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-803-549-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
DB 18 CGGGCCAGGAGCTG 5

RESULT 10
US-09-968-445-1/c
; Sequence 1, Application US/09968445
; Patent No. US20020111505A1

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; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-803-549-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
DB 18 CGGGCCAGGAGCTG 5

RESULT 9
US-09-803-402-1/c
; Sequence 1, Application US/09803402
; Patent No. US20020091279A1
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/803,402
; FILING DATE: 09-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,610
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/077,300
; FILING DATE: 15-JUNE-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-803-402-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
DB 18 CGGGCCAGGAGCTG 5

RESULT 10
US-09-968-445-1/c
; Sequence 1, Application US/09968445
; Patent No. US20020111505A1

```



GENERAL INFORMATION:  
APPLICANT: Charles N. Serhan  
TITLE OF INVENTION: Lipoxin Compounds  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/968,445  
FILING DATE: 01-Oct-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/260,030  
FILING DATE: 15-JUNE-1994  
APPLICATION NUMBER: 08/077,300  
FILING DATE: 15-JUNE-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: BWI-112CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-968-445-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;  
Best Local Similarity 92.9%; Pred. No. 5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14  
Db 18 CGGGCCAGCAGCTG 5

RESULT 11  
US-09-943-722-9  
Sequence 9, Application US/09943722  
Publication No. US20020192660A1  
GENERAL INFORMATION:  
APPLICANT:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
COMPUTER: FLOPPY DISK  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/943,722  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/850,049  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/050,478  
FILING DATE: 26-OCT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02908  
FILING DATE: 29-MAR-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/858,747  
FILING DATE: 27-MAR-1992  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2026-4006US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
US-09-943-722-9

Query Match 72.9%; Score 12.4; DB 9; Length 50;  
Best Local Similarity 92.9%; Pred. No. 4.8e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGAGCAGCTGACA 17  
Db 33 GCGAGCAGCTGACA 46

RESULT 12  
US-10-098-263B-37688/c  
Sequence 37688, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Mittman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 37688  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-37688

Query Match 71.8%; Score 12.2; DB 9; Length 25;  
Best Local Similarity 82.4%; Pred. No. 6.3e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
Db 21 CGGTCCAGCAGCTGACA 5

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RESULT 13
US-10-098-263B-38944/c
; Sequence 38944, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 38944
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-38944
Query Match 71.8%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGGCCGACGCTGACA 17
Db 23 CGGCCATGAGTGACA 7

RESULT 14
US-10-320-230-30
; Sequence 30, Application US/10320230
; Publication No. US20030110529A1
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElver, John A.
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; FILE REFERENCE: 0926D
; CURRENT APPLICATION NUMBER: US/10/320,230
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/398,858
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)...(23)
US-10-320-230-30
Query Match 70.6%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCAGCAGCTGA 15
Db 9 GCCAGCAGCTGA 20

RESULT 15
US-09-817-387-18
; Sequence 18, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotides, linkages between positions 1
; OTHER INFORMATION: to 12 are phosphorothioates, linkages between
; OTHER INFORMATION: positions 12 to 20 are phosphodiester
; OTHER INFORMATION: positions 13 to 23 carry 2'-OCH3 modified ribosyl
; OTHER INFORMATION: residues
; OTHER INFORMATION: linkages between positions 20 to 23 are
; OTHER INFORMATION: phosphorothioates
US-09-817-387-18
Query Match 70.6%; Score 12; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCACGACGCTG 14
Db 1 GGCACGACGCTG 12

Search completed: June 25, 2003, 22:25:10
Job time : 52.6773 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 25.8048 Seconds  
(without alignments)  
202.036 Million cell updates/sec

Title: US-08-770-564A-14  
Perfect score: 17 CCGGCCAGCAGCTGACA 17  
Sequence: 1

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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3: /cgn2\_6/prodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/2/ina/PCUS COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	2	US-08-770-565-14
2	17	100.0	30	2	US-08-833-377-5
3	15	88.2	25	1	US-08-482-115B-26
4	15	88.2	25	2	US-08-472-802C-27
5	12.4	72.9	24	1	US-08-064-271-1
6	12.4	72.9	24	3	US-08-712-610-1
7	12.4	72.9	24	3	US-08-930-589A-1
8	12.4	72.9	24	4	US-09-309-423-1
9	12.4	72.9	24	4	US-09-011-922A-13
10	12.4	72.9	24	4	US-09-599-781-1
11	12.4	72.9	27	3	US-08-832-399-3
12	12.4	72.9	27	4	US-09-372-498-3
13	12.4	72.9	30	3	US-08-513-974B-136
14	12.4	72.9	48	1	US-07-720-222-41
15	12.4	72.9	48	1	US-08-066-961-2
16	12.4	72.9	50	2	US-08-850-049-9
17	12.4	72.9	50	2	US-08-050-478-9
18	12.4	72.9	50	4	US-07-858-747B-9
19	12.4	72.9	50	4	US-09-414-117-9
20	12.4	72.9	50	4	US-09-678-437-9
21	12.2	71.8	29	1	US-08-082-843-1
22	12	70.6	18	4	US-08-584-040-8292
23	12	70.6	18	4	US-08-584-040-8293
24	12	70.6	50	2	US-08-850-049-5
25	12	70.6	50	2	US-08-050-478-5
26	12	70.6	50	4	US-07-858-747B-5
27	12	70.6	50	4	US-09-414-117-5

28	12	70.6	50	4	US-09-678-437-5	Sequence 5, Appli
29	11.8	69.4	19	4	US-08-974-549A-401	Sequence 401, App
30	11.8	69.4	20	4	US-08-687-421-329	Sequence 329, App
31	11.8	69.4	21	4	US-08-974-549A-508	Sequence 508, App
32	11.8	69.4	30	1	US-07-602-608-19	Sequence 19, Appl
33	11.8	69.4	30	1	US-08-261-578-19	Sequence 19, Appl
34	11.8	69.4	30	4	US-08-974-549A-723	Sequence 723, Appl
35	11.8	69.4	34	4	US-09-560-367A-13	Sequence 13, Appl
36	11.8	69.4	36	2	US-08-925-708-4	Sequence 4, Appli
37	11.8	69.4	36	2	US-08-925-708-5	Sequence 5, Appli
38	11.8	69.4	40	1	US-08-087-772A-10	Sequence 10, Appl
39	11.8	69.4	49	1	US-08-530-492-89	Sequence 89, Appl
40	11.8	69.4	49	4	US-08-906-517-89	Sequence 89, Appl
41	11.4	67.1	24	1	US-08-072-063-3	Sequence 3, Appli
42	11.4	67.1	24	1	US-08-064-693-3	Sequence 3, Appli
43	11.4	67.1	24	4	US-08-885-366-3	Sequence 3, Appli
44	11.4	67.1	24	5	PCT-US93-04754-3	Sequence 3, Appli
45	11.4	67.1	27	3	US-08-513-974B-87	Sequence 87, Appl

## ALIGNMENTS

RESULT 1  
US-08-770-565-14  
; Sequence 14, Application US/08770565  
; Patent No. 5846723  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; TITLE OF INVENTION: Telomerase  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-00230005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-565-14

Query Match 100.0%; Score 17; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCGGCCAGCAGCTGACA 17

Db 1 CGGCCAGCAGCTGACA 17

RESULT 2

US-08-833-377-5  
; Sequence 5, Application US/08833377  
; Patent No. 5968506  
; GENERAL INFORMATION:  
; APPLICANT: Weinrich, Scott L.  
; APPLICANT: Atkinson III, Edward M.  
; APPLICANT: Lichtsteiner, Serge P.  
; APPLICANT: Vasserot, Alain P.  
; APPLICANT: Pruzan, Ronald A.  
; APPLICANT: Kealey, James T.  
; TITLE OF INVENTION: Purified Telomerase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/833,377  
; FILING DATE: 04-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: US 08/510,736  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-001110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0300  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 1  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "N = 5' biotinylated guanosine"  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..30  
; OTHER INFORMATION: /note= "Oligo 13"  
US-08-833-377-5  
Query Match 100.0%; Score 17; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGCCAGCAGCTGACA 17  
Db 4 CGGCCAGCAGCTGACA 20  
RESULT 3  
US-08-482-115B-26  
; Sequence 26, Application US/08482115B

; Patent No. 5776579  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Assays for the RNA Component of Human  
; TITLE OF INVENTION: Telomerase  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/482,115B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-000830US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-482-115B-26  
Query Match 88.2%; Score 15; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGCAGCAGCTGACA 17  
Db 9 GGCAGCAGCTGACA 23  
RESULT 4  
US-08-472-802C-27  
; Sequence 27, Application US/08472802C  
; Patent No. 5958680  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,802C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000820  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-472-802C-27

Query Match 88.2%; Score 15; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17  
DB 9 GGCCAGCAGCTGACA 23

RESULT 5  
US-08-064-271-1/c  
Sequence 1, Application US/08064271  
Patent No. 5543297  
GENERAL INFORMATION:  
APPLICANT: Kennedy, Brian P.  
APPLICANT: Cromlish, Wanda A.  
APPLICANT: Mancini, Joseph A.  
APPLICANT: O'Neil, Gary  
APPLICANT: Vickers, Philip J.  
APPLICANT: Wong, Elizabeth  
TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 CDNA AND  
ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: 126 Lincoln Avenue  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 in, 1.4Kb  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: System 7  
SOFTWARE: Microsoft Word 5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/064,271  
FILING DATE: 19930506  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Panzer, Curtis C.  
REGISTRATION NUMBER: 33,752

REFERENCE/DOCKET NUMBER: 189061A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)594-3199  
TELEFAX: (908)594-4720  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-064-271-1

Query Match 72.9%; Score 12.4; DB 1; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14  
DB 18 CGGGCCAGCAGCTG 5

RESULT 6  
US-08-712-610-1/c  
Sequence 1, Application US/08712610  
Patent No. 6048897  
GENERAL INFORMATION:  
APPLICANT: Charles N. Serhan  
TITLE OF INVENTION: Lipoxin Compounds  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/712,610  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/260,030  
FILING DATE: 15-JUNE-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,300  
FILING DATE: 15-JUNE-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: BWI-112CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
ANTI-SENSE: NO  
US-08-712-610-1

Query Match 72.9%; Score 12.4; DB 3; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14

Db 18 CGGGCCAGGAGCTG 5

RESULT 7  
US-08-930-589A-1/c  
; Sequence 1, Application US/08930589A  
; Patent No. 6107087  
; GENERAL INFORMATION:  
; APPLICANT: MERCK FROSST CANADA & CO.  
; APPLICANT: O'NEILL, GARY P.  
; APPLICANT: MANCINI, JOSEPH A.  
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN  
; TITLE OF INVENTION: CYCLOOXYGENASE-2  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,589A  
; FILING DATE: 28-JUN-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coppola, Joseph A.  
; REGISTRATION NUMBER: 38,413  
; REFERENCE/DOCKET NUMBER: 19029PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-6734  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-930-589A-1

Query Match 72.9%; Score 12.4; DB 3; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGGAGCTG 14  
Db 18 CGGGCCAGGAGCTG 5

RESULT 8  
US-09-309-423-1/c  
; Sequence 1, Application US/09309423  
; Patent No. 6316648  
; GENERAL INFORMATION:  
; APPLICANT: Charles N. Serhan  
; TITLE OF INVENTION: Lipoxin Compounds  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts

COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/309,423  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/260,030  
FILING DATE: 15-JUNE-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,300  
FILING DATE: 15-JUNE-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: BWI-112CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
ANTI-SENSE: NO  
US-09-309-423-1

Query Match 72.9%; Score 12.4; DB 4; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGGAGCTG 14  
Db 18 CGGGCCAGGAGCTG 5

RESULT 9  
US-09-011-922A-13  
; Sequence 13, Application US/09011922A  
; Patent No. 6320022  
; GENERAL INFORMATION:  
; APPLICANT: Cuttitta, Frank; Martinez,  
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward  
; APPLICANT: J. Hook; William; Walsh, Thomas; Grey,  
; APPLICANT: Karen; Macri; Charles  
; TITLE OF INVENTION: Functional Role of  
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related  
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and  
; TITLE OF INVENTION: Physiology  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: MS WORD 97  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/011,922A  
; FILING DATE: 17-Feb-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/60/002,514

;; FILING DATE: 18-Aug-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/60/002,936  
;; FILING DATE: 30-Aug-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/60/013,172  
;; FILING DATE: 12-Mar-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US96/13286  
;; FILING DATE: 16-Aug-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Leslie A. Serunian  
;; REGISTRATION NUMBER: 35,353  
;; REFERENCE/DOCKET NUMBER: 2026-4202US3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 758-4800  
;; TELEFAX: (212) 751-6849  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 24 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: oligonucleotide  
;; HYPOTHETICAL: No  
;; ANTI-SENSE: Yes  
;; FEATURE:  
;; NAME/KEY: AM-R(788-811)  
;; OTHER INFORMATION: AM-R antisense probe  
US-09-011-922A-13

Query Match 72.9%; Score 12.4; DB 4; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCCAGCAGCTGACA 17  
Db 10 GCCAGCAGATGACA 23

RESULT 10  
US-09-599-781-1/C  
; Sequence 1, Application US/09599781  
; Patent No. 6362327  
; GENERAL INFORMATION:  
; APPLICANT: MERCK PROST CANADA & CO.  
; O'NEILL, GARY P.  
; MANCINI, JOSEPH A.  
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN  
; CYCLOOXYGENASE-2  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/599,781  
; FILING DATE: 21-Jun-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/084,033  
; FILING DATE: 27-Sep-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coppola, Joseph A  
; REGISTRATION NUMBER: 38,413

;; REFERENCE/DOCKET NUMBER: 19029PC  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 732-594-6734  
;; TELEFAX: 732-594-4720  
;; TELEX: <unknown>  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 24 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-599-781-1

Query Match 72.9%; Score 12.4; DB 4; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGGCCAGCAGCTG 14  
Db 18 CGGGCCAGGAGCTG 5

RESULT 11  
US-08-832-399-3  
; Sequence 3, Application US/08832399  
; Patent No. 6008050  
; GENERAL INFORMATION:  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Shabon, Usman  
; TITLE OF INVENTION: NOVEL HUMAN NEUROTENSIN RECEPTOR TYPE 2  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY:  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/832,399  
; FILING DATE: 02-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: King, William T  
; REGISTRATION NUMBER: 30,954  
; REFERENCE/DOCKET NUMBER: GH50020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5515  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-832-399-3

Query Match 72.9%; Score 12.4; DB 3; Length 27;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      4 GCCAGCAGCTGACA 17
      6 GCCAGCAGATGACA 19

RESULT 12
US-09-372-498-3
; Sequence 3, Application US/09372498
; Patent No. 6166182
; GENERAL INFORMATION:
; APPLICANT: Derek J. Bergsma
; APPLICANT: Usman Shabon
; TITLE OF INVENTION: NOVEL HUMAN NEUROTENSIN RECEPTOR TYPE 2
; FILE REFERENCE: GH-50020-1
; CURRENT APPLICATION NUMBER: US/09/372,498
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: 08/832,399
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-372-498-3

Query Match      72.9%; Score 12.4; DB 4; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCCAGCAGCTGACA 17
      6 GCCAGCAGATGACA 19

RESULT 13
US-08-513-974B-136/c
; Sequence 136, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA: JP 7-007177
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA: JP 6-326611
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA: JP 6-270017
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA: JP 6-236357
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA: JP 6-236356
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA: JP 6-189274
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA: JP 6-189273
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA: JP 6-189272
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-136

Query Match      72.9%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCCAGCAGCTGACA 17
      6 GCCAGCAGATGACA 3

RESULT 14
US-07-720-222-41
; Sequence 41, Application US/07720222
; Patent No. 5190873
; GENERAL INFORMATION:
; APPLICANT: Lernhardt, Waldemar
; APPLICANT: Bourdon, Mario
; APPLICANT: Youderian, Phil
; TITLE OF INVENTION: HYBRID PROTEINS CONTAINING BINDING SITES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birmingham & Pitting
; STREET: 11230 Sorrento Valley Road, Suite 200
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/720,222  
;; FILING DATE: 19910621  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bingham, Douglas A.  
;; REGISTRATION NUMBER: 32,457  
;; REFERENCE/DOCKET NUMBER: CIB0012P  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-587-3533  
;; INFORMATION FOR SEQ ID NO: 41:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 48 base pairs  
;; TYPE: NUCLEIC ACID  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-07-720-222-41

Query Match 72.9%; Score 12.4; DB 1; Length 48;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

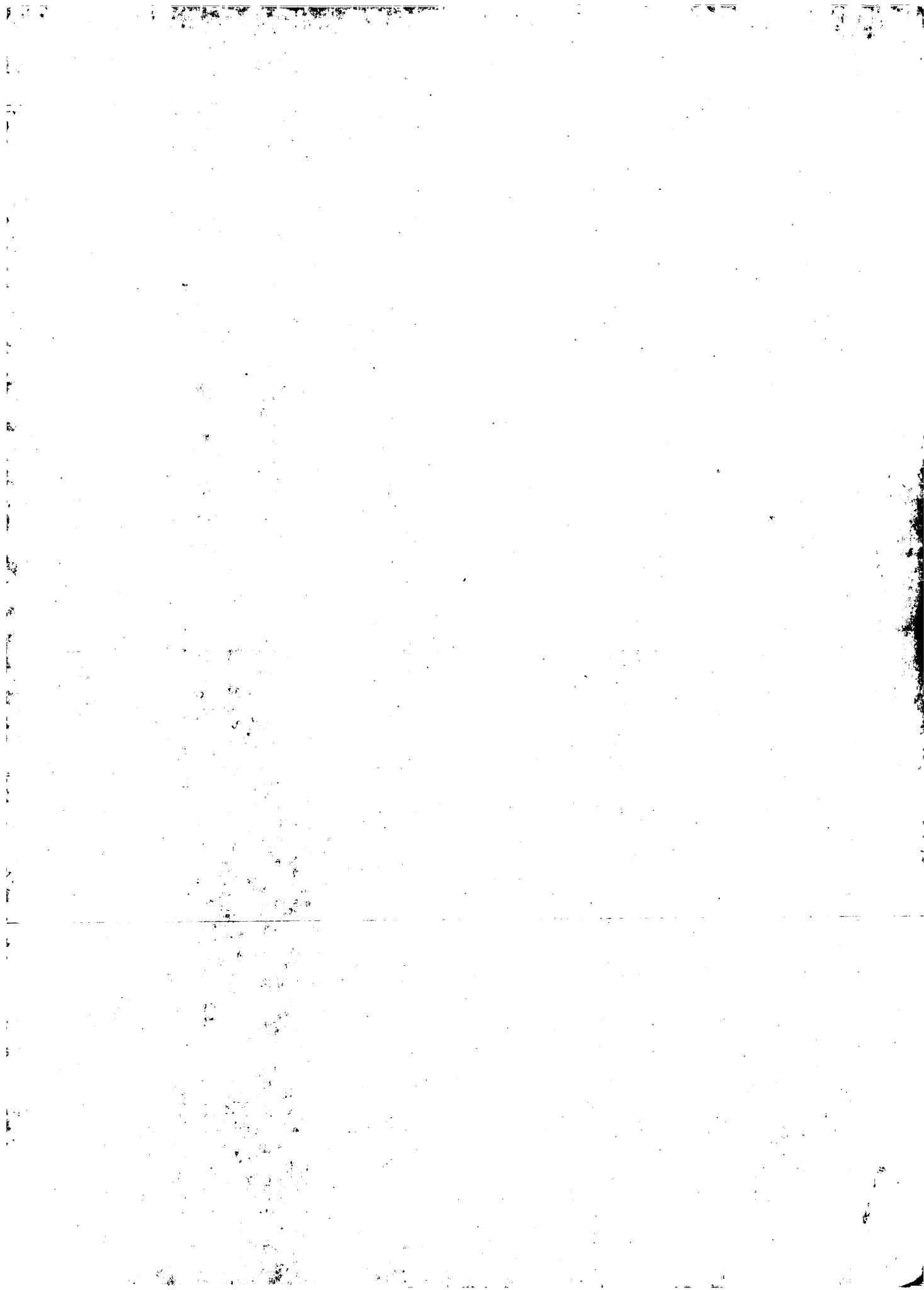
QY 2 GGGCCAGCAGCTGA 15  
| | | | | | | | | | | | | | |  
DB 6 GAGCCAGCAGCTGA 19

RESULT 15  
US-08-066-961-2/c  
;; Sequence 2, Application US/08066961  
;; Patent No. 5432271  
;; GENERAL INFORMATION:  
;; APPLICANT: Barns, Susan M.  
;; APPLICANT: Halbert, Donald N.  
;; APPLICANT: Lane, David J.  
;; TITLE OF INVENTION: Nucleic Acid Probes for the Detection of  
;; TITLE OF INVENTION: Neisseria Gonorrhoeae  
;; NUMBER OF SEQUENCES: 45  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Amoco Corporation  
;; STREET: 55 Shuman Blvd., Suite 600  
;; CITY: Naperville  
;; STATE: IL  
;; COUNTRY: USA  
;; ZIP: 60563  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/066,961  
;; FILING DATE: 19930525  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/775,210  
;; FILING DATE: 10-NOV-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/356,155  
;; FILING DATE: 24-MAY-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Giesser, Joanne M.  
;; REGISTRATION NUMBER: 32,838  
;; REFERENCE/DOCKET NUMBER: 5825-02  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (708) 717-2443  
;; TELEFAX: (708) 717-2430  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 48 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-066-961-2

Query Match 72.9%; Score 12.4; DB 1; Length 48;  
Best Local Similarity 92.9%; Pred. No. 1.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CGGGCCAGCAGCTG 14  
| | | | | | | | | | | | | | |  
DB 25 CGTGCAGCAGCTG 12

Search completed: June 25, 2003, 00:24:42  
Job time : 25.8048 secs



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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 876.482 Seconds  
(without alignments)  
314.123 Million cell updates/sec

Title: US-08-770-564A-14

Perfect score: 17  
Sequence: 1 CGGGCCAGCAGTGACA 17

Scoring table: OLIGO\_NUC  
Gapop\_60.0, Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estml:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	76.5	46	14	H51364
C 2	13	76.5	49	9	A1159805
C 3	12	70.6	38	17	AZ815373
C 4	12	70.6	40	9	A1570731
C 5	12	70.6	49	9	AA914273
C 6	12	70.6	50	9	AU103700

C 7	64.7	30	13	BI463777
C 8	64.7	37	9	A1181597
C 9	64.7	41	12	BG718339
10	64.7	41	13	BI465330
C 11	64.7	46	9	AA871967
C 12	64.7	46	9	AA542511
C 13	64.7	49	9	AA213878
C 14	64.7	50	9	AU107010
C 15	64.7	50	9	AU107011
C 16	64.7	50	9	AU107012
C 17	64.7	50	9	AU107015
C 18	64.7	50	9	AU107015
C 19	58.8	22	17	AZ797063
C 20	58.8	29	17	AZ636336
C 21	58.8	33	17	AZ344584
C 22	58.8	34	17	AZ581060
C 23	58.8	35	17	AZ645669
C 24	58.8	35	17	AZ291H03Q
C 25	58.8	38	17	AZ311715
C 26	58.8	39	9	AU007553
C 27	58.8	39	9	AU010017
C 28	58.8	40	14	H29926
C 29	58.8	40	17	AZ576156
C 30	58.8	42	17	AZ760286
C 31	58.8	43	9	AA209184
C 32	58.8	45	14	T69111
C 33	58.8	46	9	AA932841
C 34	58.8	46	9	AI284114
C 35	58.8	46	13	BI523407
C 36	58.8	46	13	BI523407
C 37	58.8	46	17	AZ776000
C 38	58.8	49	9	AA237940
C 39	58.8	49	17	AQ073133
C 40	58.8	50	9	AU102703
C 41	58.8	50	9	AU103464
C 42	58.8	50	9	AU107013
C 43	58.8	50	9	AU107184
C 44	58.8	50	9	AU107185
C 45	58.8	50	9	AU107189

#### ALIGNMENTS

RESULT 1  
H51364  
LOCUS  
DEFINITION  
H51364 46 bp mRNA linear EST 18-SEP-1995  
IMAGE:179484 5' similar to SP:ACON\_PIG P16276 ACONITATE HYDRATASE  
PRECURSOR ; mRNA sequence.  
ACCESSION H51364  
VERSION H51364.1 GI:991205  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marr, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
Insert Size: 701  
High quality sequence starts: 1  
High quality sequence stops: 1

Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Insert Length: 701 Std Error: 0.00  
 Seq primer: M13RP1  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 46  
 /organism="Homo sapiens"  
 /db\_xref="GDB:3841680"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:179484"  
 /clone\_lib="Soares adult brain N2b5HB55Y"  
 /sex="Male"  
 /dev\_stage="55-year old"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: brain; Vector: pTV73D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 TGTTACCAATCTGAAGTGGCGGCGGCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pTV73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 53. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. The adult brain RNA was  
 provided by Dr. Donald H. Gilden. Tissue was acquired  
 17-18 hours after death which occurred in consequence of a  
 ruptured aortic aneurysm. RNA was prepared from a pool of  
 tissues representing the following areas of the brain:  
 frontal, parietal, temporal and occipital cortex from the  
 left and right hemispheres, subcortical white matter,  
 basal ganglia, thalamus, cerebellum, midbrain, pons and  
 medulla." 8 a 12 c 12 g 13 t 1 others

BASE COUNT 8 a 12 c 12 g 13 t 1 others  
 ORIGIN  
 Query Match 76.5%; Score 13; DB 14; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCCCAGCAGCTGA 15  
 |||||  
 Db 1 GCCCAGCAGCTGA 13

RESULT 2  
 A1159805/c 49 bp mRNA linear EST 28-OCT-1998  
 LOCUS  
 DEFINITION  
 qc73c05.x1 Soares placenta 8to9weeks 2NBHP8to9M Homo sapiens cDNA  
 clone IMAGE:1715240 3', similar to TR-Q15726 Q15726 MALIGNANT  
 MELANOMA METASTASIS-SUPPRESSOR. ;, mRNA sequence.

ACCESSION A1159805.1 GI:3693164  
 VERSION EST  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 49)  
 REFERENCE  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Insert Length: 545 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 49  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1715240"  
 /clone\_lib="Soares placenta 8to9weeks 2NBHP8to9M"  
 /dev\_stage="two placentae; One from 8 weeks and another  
 from 9 weeks post conception"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: placenta; Vector: pTV73D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 TGTTACCAATCTGAAGTGGCGGCGGCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pTV73 vector  
 (Pharmacia). Library constructed by Bento Soares and  
 M. Fatima Bonaldo." 5 a 16 c 22 g 6 t

BASE COUNT 5 a 16 c 22 g 6 t  
 ORIGIN  
 Query Match 76.5%; Score 13; DB 9; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGCCAGCAGCT 13  
 |||||  
 Db 45 CGGCGCCAGCAGCT 33

RESULT 3  
 A2815373/c 38 bp DNA linear GSS 20-FEB-2001  
 LOCUS  
 DEFINITION  
 2M0083M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0083M06 R, DNA sequence.

ACCESSION A2815373  
 VERSION A2815373.1 GI:12985281  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 38)  
 REFERENCE  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112 USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0683 row: M, column: 06  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 38.  
 Location/Qualifiers  
 1. 38  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0083M06"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

FEATURES  
 source

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 13 c 12 g 6 t

Query Match 70.6%; Score 12; DB 17; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0;

OY 1 CGGGCCAGCAGC 12  
|||||  
Db 24 CGGGCCAGCAGC 13

RESULT 4  
AI570731/c  
LOCUS  
DEFINITION  
tr66c01.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:223264 3',  
similar to TR:Q14678 O14678 PEROXISOMAL MEMBRANE PROTEIN 69. ;,  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
AI570731  
AI570731.1 GI:4534105  
EST.  
human.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
1 (bases 1 to 40)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
COMMENT  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov

Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 2315 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=NO.

FEATURES  
source  
1. .40  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:223264"  
/clone\_lib="NCI CGAP Pan1"  
/issue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:

BASE COUNT 6 a 15 c 10 g 9 t

Query Match 70.6%; Score 12; DB 9; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0;

OY 3 GGCCAGCAGCTG 14  
|||||  
Db 13 GGCCAGCAGCTG 2

RESULT 5  
AA914273  
LOCUS  
DEFINITION  
v99a03.r1 Soares mammary\_gland NDMMG Mus musculus cDNA clone  
IMAGE:1314316 5' similar to TR:P97369 P97369 NEUTROPHIL CYTOSOLIC  
FACTOR 4 ;, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
AA914273  
AA914273.1 GI:3053665  
EST.

ORGANISM  
house mouse.  
Mus musculus

REFERENCE  
AUTHORS  
1 (bases 1 to 49)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE  
JOURNAL  
COMMENT  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:684612

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .49  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_image="IMAGE:1314316"  
/clone\_lib="Soares\_mammary\_gland\_NDMMG"  
/sex="male"  
/issue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer [5'  
TGTTCACCATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTT  
T 3'] ; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M. Fatima  
Bonaldo."

BASE COUNT 10 a 15 c 16 g 8 t

FEATURES  
source  
1. .49  
Location/Qualifiers

Query Match 70.6%; Score 12; DB 9; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCCAGCAGCTG 14  
 |||||  
 Db 8 GCGCCAGCAGCTG 19

RESULT 6  
 AUI03700/c  
 LOCUS AUI03700 Sugano Homo sapiens cDNA library EST 30-AUG-2001  
 DEFINITION CAS01030, mRNA sequence.  
 ACCESSION AUI03700  
 VERSION AUI03700.1 GI:13553221  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 50)  
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata  
 , H., Ota, T., Isogai, T., Tanaka, T., Mochishita, S., Okubo, K., Sakaki  
 , Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 MEDLINE 21270072  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuk@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
 , S. Construction and characterization of a full length-enriched and  
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
 Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CAS01030"  
 /clone\_lib="Sugano Homo sapiens cDNA library"  
 /note="Differential display comparison of untreated and  
 dimethylfumarate treated U937 cells"  
 8 a 14 c 15 g 13 t

BASE COUNT  
 ORIGIN

Query Match 70.6%; Score 12; DB 9; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCAGCAGC 12  
 |||||  
 Db 21 CGGCCAGCAGC 10

RESULT 7  
 BI463777/c  
 LOCUS BI463777 30 bp mRNA linear EST 21-AUG-2001  
 DEFINITION 603203487F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:5269437 5',  
 mRNA sequence.  
 ACCESSION BI463777  
 VERSION BI463777.1 GI:15254433  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 30)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: rsb@nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: IMAGE1679 row: m column: 22  
 High quality sequence stop: 30.  
 Location/Qualifiers  
 1..30  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5269437"  
 /clone\_lib="NIH\_MGC\_97"  
 /lab\_host="DH10B"  
 /note="Organ: testis; Vector: pBluescriptR (modified  
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcggg  
 ); Oligo-dr primed using primer 5'-TTTTTTTTTTTTVN-3',  
 size-selected for average insert size 2.2 kb and  
 normalized to Rot 5. This is a primary library enriched  
 for full-length clones and constructed using the  
 Cap-trapper method (Carninci, in preparation). Library  
 constructed by M. Brownstein (NIH/NHGRI, National  
 Institutes of Health). Note: this is a NIH\_MGC Library."  
 1 a 11 c 12 g 6 t

BASE COUNT  
 ORIGIN

Query Match 64.7%; Score 11; DB 13; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+04; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGGCCAGCAGC 12  
 |||||  
 Db 27 CGGCCAGCAGC 17

RESULT 8  
 AUI181597/c  
 LOCUS AUI181597 37 bp mRNA linear EST 08-OCT-1998  
 DEFINITION uc63dl1.r1 Soares\_mammary\_gland NBMGC Mus musculus cDNA clone  
 IMAGE:1430325 5' similar to SW:CIB\_HUMAN Q99828 SNK INTERACTING  
 PROTEIN 2-28 ;, mRNA sequence.  
 ACCESSION AUI181597  
 VERSION AUI181597.1 GI:3732235  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 37)  
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.  
 TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MG1:914393  
 Trace considered overall poor quality  
 POSSIBLE reversed clone: similarity on wrong strand

FEATURES	source
Seq primer: -28ml3 rev2 ET from Amerham	
High quality sequence stop: 1.	
Location/Qualifiers	
1. .37	
/organism="Mus musculus"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="IMAGE:1430325"	
/clone_lib="Soares_mammary_gland_NbMMG"	
/sex="male"	
/tissue type="mammary gland"	
/dev stage="4 weeks"	
/lab_host="DH10B"	
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia	
RI; with a modified polylinker; Site 1: Not I; Site 2: Eco	
RI; left strand cDNA was primed with a Not I - oligo(dT)	
primer [5'	
TGTTACCATCTGAGTGGGCGCGCGAATGTTTGTGTGTGTGTGTGTGTGT	
T 3'; double-stranded cDNA was ligated to Eco RI	
adaptors (Pharmacia), digested with Not I and cloned into	
the Not I and Eco RI sites of the modified pT7T3 vector.	
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library	
constructed and normalized by Bento Soares and M. Patricia	
Bonaldo."	
BASE COUNT	7 a 10 c 13 g 7 t
ORIGIN	
Query Match	64.7%; Score 11; DB 9; Length 37;
Best Local Similarity	100.0%; Pred. No. 4.6e+04;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Db	28 GGCCAGCAGCT 18
RESULT 9	
LOCUS	602696344F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828451 5',
DEFINITION	mRNA sequence.
ACCESSION	EG718339
VERSION	EG718339.1 GI:13997526
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	NIH-MGC http://imgc.ncbi.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
Contact: Robert Strausberg, Ph.D.	
Email: cgapbs-r@mail.nih.gov	
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.	
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki	
Toshiyuki and Piero Carninci (RIKEN)	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be	
found through the I.M.A.G.E. Consortium/LLNL at:	
http://image.llnl.gov	
Plate: LLAM10746 row: g column: 12	
High quality sequence stop: 41.	
Location/Qualifiers	
1. .41	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:4828451"	
/clone_lib="NIH_MGC_97"	
/lab_host="DH10B"	
/note="Organ: testis; Vector: pBluescriptR (modified	
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgcg	
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgcg	
BASE COUNT	7 a 10 c 13 g 7 t
ORIGIN	
Query Match	64.7%; Score 11; DB 9; Length 37;
Best Local Similarity	100.0%; Pred. No. 4.6e+04;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 GGCCAGCAGCT 13
Db	28 GGCCAGCAGCT 18
RESULT 9	
LOCUS	602696344F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828451 5',
DEFINITION	mRNA sequence.
ACCESSION	EG718339
VERSION	EG718339.1 GI:13997526
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	NIH-MGC http://imgc.ncbi.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
Contact: Robert Strausberg, Ph.D.	
Email: cgapbs-r@mail.nih.gov	
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.	
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki	
Toshiyuki and Piero Carninci (RIKEN)	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be	
found through the I.M.A.G.E. Consortium/LLNL at:	
http://image.llnl.gov	
Plate: LLAM10746 row: g column: 12	
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Location/Qualifiers	
1. .41	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
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/clone_lib="NIH_MGC_97"	
/lab_host="DH10B"	
/note="Organ: testis; Vector: pBluescriptR (modified	
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BASE COUNT	7 a 10 c 13 g 7 t
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Query Match	64.7%; Score 11; DB 13; Length 41;
Best Local Similarity	100.0%; Pred. No. 4.6e+04;
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Qy	2 GGCCAGCAGC 12
Db	14 GGCCAGCAGC 24
BASE COUNT	7 a 12 c 20 g 2 t
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Best Local Similarity	100.0%; Pred. No. 4.6e+04;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2 GGCCAGCAGC 12
Db	14 GGCCAGCAGC 24
BASE COUNT	7 a 12 c 20 g 2 t
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Best Local Similarity	100.0%; Pred. No. 4.6e+04;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2 GGCCAGCAGC 12
Db	14 GGCCAGCAGC 24
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Query Match	64.7%; Score 11; DB 13; Length 41;
Best Local Similarity	100.0%; Pred. No. 4.6e+04;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2 GGCCAGCAGC 12
Db	14 GGCCAGCAGC 24
BASE COUNT	7 a 12 c 20 g 2 t
ORIGIN	
Query Match	64.7%; Score 11; DB 13; Length 41;
Best Local Similarity	100.0%; Pred. No. 4.6e+04;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2 GGCCAGCAGC 12







Oy 3 GCCCAGCAGCT 13  
Db 41 GCCCAGCAGCT 31

Search completed: June 23, 2003, 10:10:37  
Job time : 878.636 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 746.239 Seconds  
(without alignments)  
158.668 Million cell updates/sec

Title: US-08-770-564A-14  
Perfect score: 17  
Sequence: 1 CGGCGCAGCAGCTGACA 17

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents\_NA\_New.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17	100.0	19	1	PCT-US03-04088-16
2	17	100.0	19	1	PCT-US03-04088-280
3	17	100.0	22	1	PCT-US02-33146-10
4	17	100.0	30	10	US-10-330-872-4
5	17	100.0	30	10	US-10-330-872A-4
6	15	88.2	25	9	US-10-359-935-27
7	14	82.4	24	6	US-09-536-058D-52
8	14	82.4	25	12	US-60-427-808-148950
9	13	76.5	15	10	US-10-287-787-16506
10	13	76.5	15	10	US-10-287-787-18526
11	13	76.5	16	9	US-10-310-188-5556
12	13	76.5	17	9	US-10-303-778-7849
13	13	76.5	17	9	US-10-310-188-14135
14	13	76.5	17	9	US-10-310-188-57644
15	13	76.5	17	10	US-10-299-054A-1993
16	13	76.5	17	10	US-10-299-054A-1994
17	13	76.5	18	9	US-10-310-188-39627
18	13	76.5	18	10	US-10-287-787-23414
19	13	76.5	18	10	US-10-287-787-23415
20	13	76.5	24	10	US-10-287-787-12803

21	13	76.5	25	12	US-60-427-808-467694	Sequence 467694,
22	13	76.5	25	12	US-60-427-836-391360	Sequence 391360,
23	13	76.5	25	12	US-60-427-836-421414	Sequence 421414,
24	13	76.5	25	12	US-60-427-836-455025	Sequence 455025,
25	13	76.5	39	10	US-10-287-787-12804	Sequence 12804, A
26	12	70.6	15	10	US-10-367-892-15273	Sequence 15273, A
C 27	12	70.6	18	10	US-10-287-949A-3950	Sequence 3950, Ap
C 28	12	70.6	18	10	US-10-287-949A-3951	Sequence 3951, Ap
C 29	12	70.6	19	1	PCT-US03-04250-62	Sequence 62, Appl
C 30	12	70.6	19	1	PCT-US03-04250-320	Sequence 320, Appl
C 31	12	70.6	20	9	US-10-303-778-16537	Sequence 16537, A
C 32	12	70.6	21	1	PCT-US03-04250-556	Sequence 556, App
C 33	12	70.6	21	1	PCT-US03-04250-557	Sequence 557, App
C 34	12	70.6	21	1	PCT-US03-04250-558	Sequence 558, App
C 35	12	70.6	21	1	PCT-US03-04250-559	Sequence 559, App
C 36	12	70.6	21	1	PCT-US03-04250-560	Sequence 560, App
C 37	12	70.6	21	1	PCT-US03-04250-561	Sequence 561, App
C 38	12	70.6	21	1	PCT-US03-04250-562	Sequence 562, App
C 39	12	70.6	21	1	PCT-US03-04250-563	Sequence 563, App
C 40	12	70.6	21	1	PCT-US03-04250-564	Sequence 564, App
C 41	12	70.6	21	1	PCT-US03-04250-565	Sequence 565, App
C 42	12	70.6	21	1	PCT-US03-04250-566	Sequence 566, App
C 43	12	70.6	23	6	US-09-398-858-30	Sequence 30, Appl
C 44	12	70.6	23	9	US-10-320-230-30	Sequence 30, Appl
C 45	12	70.6	23	9	US-10-348-110-30	Sequence 30, Appl

## ALIGNMENTS

## RESULT 1

PCT-US03-04088-16/c  
; Sequence 16, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
; OTHER INFORMATION: region  
PCT-US03-04088-16

Query Match 100.0%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
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 Db 18 CGGGCCAGCAGCTGACA 2

RESULT 2  
 PCT-US03-04088-280  
 ; Sequence 280, Application PC/TUS0304088  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McSwiggan, James  
 ; APPLICANT: Belgelman, Leonid  
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
 ; FILE REFERENCE: 02-708-A (400/080)  
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088  
 ; CURRENT FILING DATE: 2003-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/396,600  
 ; PRIOR FILING DATE: 2002-07-17  
 ; PRIOR APPLICATION NUMBER: US 60/358,580  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: US 60/363,124  
 ; PRIOR FILING DATE: 2002-03-11  
 ; PRIOR APPLICATION NUMBER: US 60/386,782  
 ; PRIOR FILING DATE: 2002-06-06  
 ; PRIOR APPLICATION NUMBER: US 60/406,784  
 ; PRIOR FILING DATE: 2002-08-29  
 ; PRIOR APPLICATION NUMBER: US 60/408,378  
 ; PRIOR FILING DATE: 2002-09-05  
 ; PRIOR APPLICATION NUMBER: US 60/409,293  
 ; PRIOR FILING DATE: 2002-09-09  
 ; PRIOR APPLICATION NUMBER: US 60/440,129  
 ; PRIOR FILING DATE: 2003-01-15  
 ; NUMBER OF SEQ ID NOS: 626  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 280  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense  
 ; OTHER INFORMATION: region  
 PCT-US03-04088-280

Query Match 100.0%; Score 17; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 28;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
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 Db 2 CGGGCCAGCAGCUGACA 18

RESULT 3  
 PCT-US02-33146-10  
 ; Sequence 10, Application PC/TUS0233146  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Rochester Medical Center  
 ; APPLICANT: Rowley, Peter  
 ; TITLE OF INVENTION: Telomerase Interference  
 ; FILE REFERENCE: FP-71506-2/RFT/SRN  
 ; CURRENT APPLICATION NUMBER: PCT/US02/33146  
 ; CURRENT FILING DATE: 2002-12-05  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 22  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US02-33146-10

Query Match 100.0%; Score 17; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 28;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGGGCCAGCAGCTGACA 17  
 |||||  
 Db 5 CGGGCCAGCAGCTGACA 21

RESULT 4  
 US-10-330-872-4  
 ; Sequence 4, Application US/10330872  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Weinrich, Scott  
 ; APPLICANT: Atkinson III, Edward  
 ; APPLICANT: Lichtsteiner, Serge  
 ; APPLICANT: Vasserot, Alain  
 ; APPLICANT: Pruzan, Ronald  
 ; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and  
 ; TITLE OF INVENTION: Inhibitors  
 ; FILE REFERENCE: 011/006C  
 ; CURRENT APPLICATION NUMBER: US/10/330,872  
 ; CURRENT FILING DATE: 2002-12-24  
 ; PRIOR APPLICATION NUMBER: 08/510,736  
 ; PRIOR FILING DATE: 1995-08-04  
 ; PRIOR APPLICATION NUMBER: 08/833,377  
 ; PRIOR FILING DATE: 1997-04-04  
 ; PRIOR APPLICATION NUMBER: 09/420,056  
 ; PRIOR FILING DATE: 1999-10-18  
 ; PRIOR APPLICATION NUMBER: 09/717,828  
 ; PRIOR FILING DATE: 2000-11-20  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 30  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-330-872-4

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 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
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 Db 4 CGGGCCAGCAGCTGACA 20

RESULT 5  
 US-10-330-872A-4  
 ; Sequence 4, Application US/10330872A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Weinrich, Scott  
 ; APPLICANT: Atkinson III, Edward  
 ; APPLICANT: Lichtsteiner, Serge  
 ; APPLICANT: Vasserot, Alain  
 ; APPLICANT: Pruzan, Ronald  
 ; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and  
 ; TITLE OF INVENTION: Inhibitors  
 ; FILE REFERENCE: 011/006C  
 ; CURRENT APPLICATION NUMBER: US/10/330,872A  
 ; CURRENT FILING DATE: 2002-12-24  
 ; PRIOR APPLICATION NUMBER: 08/510,736  
 ; PRIOR FILING DATE: 1995-08-04  
 ; PRIOR APPLICATION NUMBER: 08/833,377  
 ; PRIOR FILING DATE: 1997-04-04  
 ; PRIOR APPLICATION NUMBER: 09/420,056  
 ; PRIOR FILING DATE: 1999-10-18  
 ; PRIOR APPLICATION NUMBER: 09/717,828  
 ; PRIOR FILING DATE: 2000-11-20  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4

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; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-4

Query Match      100.0%; Score 17; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
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Db 4 CGGGCCAGCAGCTGACA 20

RESULT 6
US-10-359-935-27
; Sequence 27, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; Fung, Junli
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-359-935-27

Query Match      88.2%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCAGCAGCTGACA 17
   |||||
Db 9 GGGCAGCAGCTGACA 23

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RESULT 7
US-09-536-058D-52/c
; Sequence 52, Application US/09536058D
; GENERAL INFORMATION:
; APPLICANT: BEGER, CARMELA
; APPLICANT: BARBER, JACK
; APPLICANT: WONG-STAAAL, FLOSSIE
; TITLE OF INVENTION: BRCA-1 REGULATORS AND METHODS OF USE
; FILE REFERENCE: 039316/0601
; CURRENT APPLICATION NUMBER: US/09/536,058D
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-058D-52

Query Match      82.4%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
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Db 23 CGGGCCAGCAGCTG 10

RESULT 8
US-60-427-808-148950
; Sequence 148950, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 148950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-148950

Query Match      82.4%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
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Db 10 CGGGCCAGCAGCTG 23

RESULT 9
US-10-287-787-16506/c
; Sequence 16506, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 16506
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.

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; FEATURE: (2498987) ... (2498911)
; LOCATION: (2498987) ... (2498911)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 18293
US-10-287-787-16506

Query Match 76.5%; Score 13; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGCTG 14
Db 14 GGGCCAGCAGCTG 2

RESULT 10
US-10-287-787-18526/c
; Sequence 18526, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7849
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-7849

Query Match 76.5%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCCAGCAGCTGA 15
Db 1 GGGCCAGCAGCTGA 13

RESULT 13
US-10-310-188-14135
; Sequence 14135, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14135
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-14135

Query Match 76.5%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCCAGCAGCTGA 15
Db 1 GGGCCAGCAGCTGA 13

RESULT 14
US-10-310-188-57644
; Sequence 57644, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57644
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-57644

Query Match 76.5%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCCAGCAGCTGA 15
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RESULT 15
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; Sequence 57644, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57644
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-57644

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QY 2 GGGCCAGCAGCTG 14
Db 16 GGGCCAGCAGCTG 4

RESULT 12
US-10-303-778-7849
; Sequence 7849, Application US/10303778
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Db 1 CGGGCCAGCAGCT 13

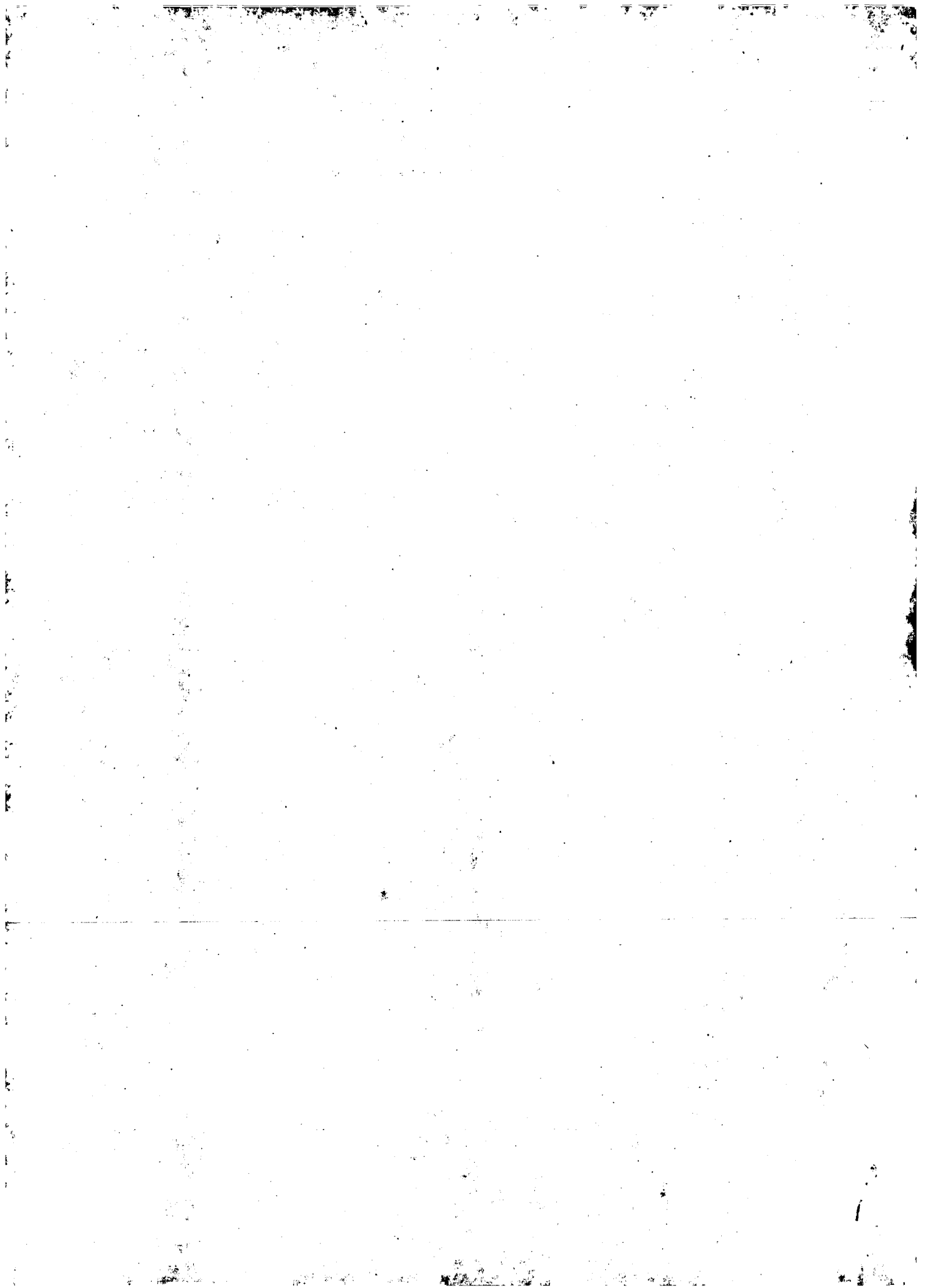
RESULT 15

US-10-299-054A-1993/c  
; Sequence 1993, Application US/10299054A  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/299,054A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 11910  
; SOFTWARE: Proprietary  
; SEQ ID NO 1993  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis complete genome.  
; FEATURE:  
; LOCATION: (766683)...(766700)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 2403  
US-10-299-054A-1993

Query Match 76.5%; Score 13; DB 10; Length 17;  
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QY 2 GGGCCAGCAGCTG 14  
Db 13 GGGCCAGCAGCTG 1

Search completed: June 23, 2003, 19:12:14  
Job time : 746.239 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1425.83 Seconds  
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Title: US-08-770-564A-14  
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Searched: 24791104 seqs, 12571243825 residues

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	17	100.0	30	9	US-08-510-736-4
5	17	100.0	30	28	US-09-717-828A-4
6	17	100.0	30	28	US-09-717-828B-4
7	17	100.0	30	28	US-09-717-829A-4
8	15	88.2	25	8	US-08-472-802A-27
9	15	88.2	25	8	US-08-472-802B-27
10	15	88.2	25	9	US-08-482-115A-26
11	15	88.2	25	9	US-08-521-634-44
12	15	88.2	25	14	US-09-057-351-27
C 13	14	82.4	24	20	US-09-536-058-52
C 14	14	82.4	24	20	US-09-536-058C-52
C 15	14	82.4	42	13	US-08-973-589-12
C 16	13	76.5	14	15	US-09-164-961-2894
C 17	13	76.5	24	9	US-08-521-634-11
C 18	13	76.5	25	17	US-09-396-196F-64639
C 19	13	76.5	25	17	US-09-396-196F-107046
C 20	13	76.5	25	17	US-09-396-196G-64639
C 21	13	76.5	25	17	US-09-396-196G-107046

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; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..17
; OTHER INFORMATION: /note= "polynucleotide RP2"
PCT-US97-23619-14

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

QY 1 CGGGCCAGCAGCTGACA 17
DB 1 CGGGCCAGCAGCTGACA 17

RESULT 2
US-08-770-564A-14
; Sequence 14, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzar, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-Dec-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-14

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

QY 1 CGGGCCAGCAGCTGACA 17
DB 1 CGGGCCAGCAGCTGACA 17

RESULT 3
US-09-601-267-20

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; Sequence 20, Application US/09601267
; GENERAL INFORMATION:
; APPLICANT: William Nicol KEITH
; TITLE OF INVENTION: Promoter Regions of the Mouse and Human Telomerase RNA Component
; FILE REFERENCE: 9013.18
; CURRENT APPLICATION NUMBER: US/09/601,267
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/GB99/00308
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: GB 9801902.9
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-601-267-20

Query Match      100.0%; Score 17; DB 23; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 7 CGGGCCAGCAGCTGACA 23

RESULT 4
US-08-510-736-4
; Sequence 4, Application US/08510736
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Methods for Purifying Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,736
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 015389-001100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-510-736-4
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Query Match      100.0%; Score 17; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 5
US-09-717-828A-4
; Sequence 4, Application US/09717828A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Purified Telomerase
; FILE REFERENCE: PurifiedTelomerase01base
; CURRENT APPLICATION NUMBER: US/09/717,828A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1 (edited)
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828A-4

Query Match      100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 6
US-09-717-828B-4
; Sequence 4, Application US/09717828B
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase01base
; CURRENT APPLICATION NUMBER: US/09/717,828B
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1 edited
; SEQ ID NO 4
; LENGTH: 30
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-829B-4
Query Match 100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 7
US-09-717-829A-4
; Sequence 4, Application US/09717829A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Allain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,829A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO: 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-829A-4
Query Match 100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 8
US-08-472-802A-27
; Sequence 27, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

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; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-27
Query Match 88.2%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
Db 9 GGCCAGCAGCTGACA 23

RESULT 9
US-08-472-802B-27
; Sequence 27, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123

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;; FILING DATE: 27-OCT-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223  
;; REFERENCE/DOCKET NUMBER: 15389-000820  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 27:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-472-802B-27

Query Match 88.2%; Score 15; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17  
|||  
DB 9 GGCCAGCAGCTGACA 23

RESULT 10  
US-08-482-115A-26  
;; Sequence 26, Application US/08482115A  
;; GENERAL INFORMATION:  
;; APPLICANT: VILLEPONTEAU, Bryant  
;; APPLICANT: FENG, Junli  
;; APPLICANT: FUNK, Walter  
;; APPLICANT: ANDREWS, William H.  
;; TITLE OF INVENTION: HUMAN TELOMERASE  
;; NUMBER OF SEQUENCES: 34  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, 8th Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: US  
;; ZIP: 94111  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION NUMBER: US 08/482,115A  
;; APPLICATION NUMBER: US 08/330,123  
;; FILING DATE: 27-OCT-1994  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-482-115A-26

;; FILING DATE: 27-OCT-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223  
;; REFERENCE/DOCKET NUMBER: 15389-000830  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 326-2400  
;; TELEFAX: (415) 326-2422  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-482-115A-26

Query Match 88.2%; Score 15; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17  
|||  
DB 9 GGCCAGCAGCTGACA 23

RESULT 11  
US-08-521-634-44  
;; Sequence 44, Application US/08521634  
;; GENERAL INFORMATION:  
;; APPLICANT: VILLEPONTEAU, Bryant  
;; APPLICANT: FENG, Junli  
;; APPLICANT: FUNK, Walter  
;; APPLICANT: ANDREWS, William  
;; TITLE OF INVENTION: Mammalian Telomerase  
;; NUMBER OF SEQUENCES: 66  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew  
;; STREET: One Market Plaza, Steuart Tower, Suite 2000  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94105  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/521,634  
;; FILING DATE: 31-AUG-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/482,115  
;; FILING DATE: 7-JUN-1995  
;; PRIOR APPLICATION NUMBER: US 08/330,123  
;; APPLICATION NUMBER: US 08/472,802  
;; FILING DATE: 7-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/330,123  
;; FILING DATE: 27-OCT-1994  
;; INFORMATION FOR SEQ ID NO: 44:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (primer)  
;; ANTI-SENSE: YES  
US-08-521-634-44

;; FILING DATE: 7-JUL-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Dunn, Tracy J.  
;; REGISTRATION NUMBER: 34,587  
;; REFERENCE/DOCKET NUMBER: 15389-000850  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-326-2400  
;; TELEFAX: 415-326-2422  
;; INFORMATION FOR SEQ ID NO: 44:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 25 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (primer)  
;; ANTI-SENSE: YES  
US-08-521-634-44

Query Match 88.2%; Score 15; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17  
|||  
DB 9 GGCCAGCAGCTGACA 23

```
RESULT 12
US-09-057-351-27
; Sequence 27, Application US/09057351
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-27

Query Match      88.2%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  GCCCAGCAGCTGACA 17
DB      9  GCCCAGCAGCTGACA 23

RESULT 13
US-09-536-058-52/c
; Sequence 52, Application US/09536058
; GENERAL INFORMATION:
; APPLICANT: Beger, Carmela
; APPLICANT: Wong-Staal, Flossie
; TITLE OF INVENTION: BRCA-1 Regulators and Methods of Use
; FILE REFERENCE: P-IU 3842
; CURRENT APPLICATION NUMBER: US/09/536,058
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 231
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-536-058-52

Query Match      82.4%; Score 14; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGGGCCAGCAGCTG 14
DB      23 CGGGCCAGCAGCTG 10

RESULT 14
US-09-536-058C-52/c
; Sequence 52, Application US/09536058C
; GENERAL INFORMATION:
; APPLICANT: Beger, Carmela
; APPLICANT: Barber, Jack
; APPLICANT: Wong-Staal, Flossie
; TITLE OF INVENTION: BRCA-1 REGULATORS AND METHODS OF USE
; FILE REFERENCE: 039316/0601
; CURRENT APPLICATION NUMBER: US/09/536,058C
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-058C-52

Query Match      82.4%; Score 14; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGGGCCAGCAGCTG 14
DB      23 CGGGCCAGCAGCTG 10

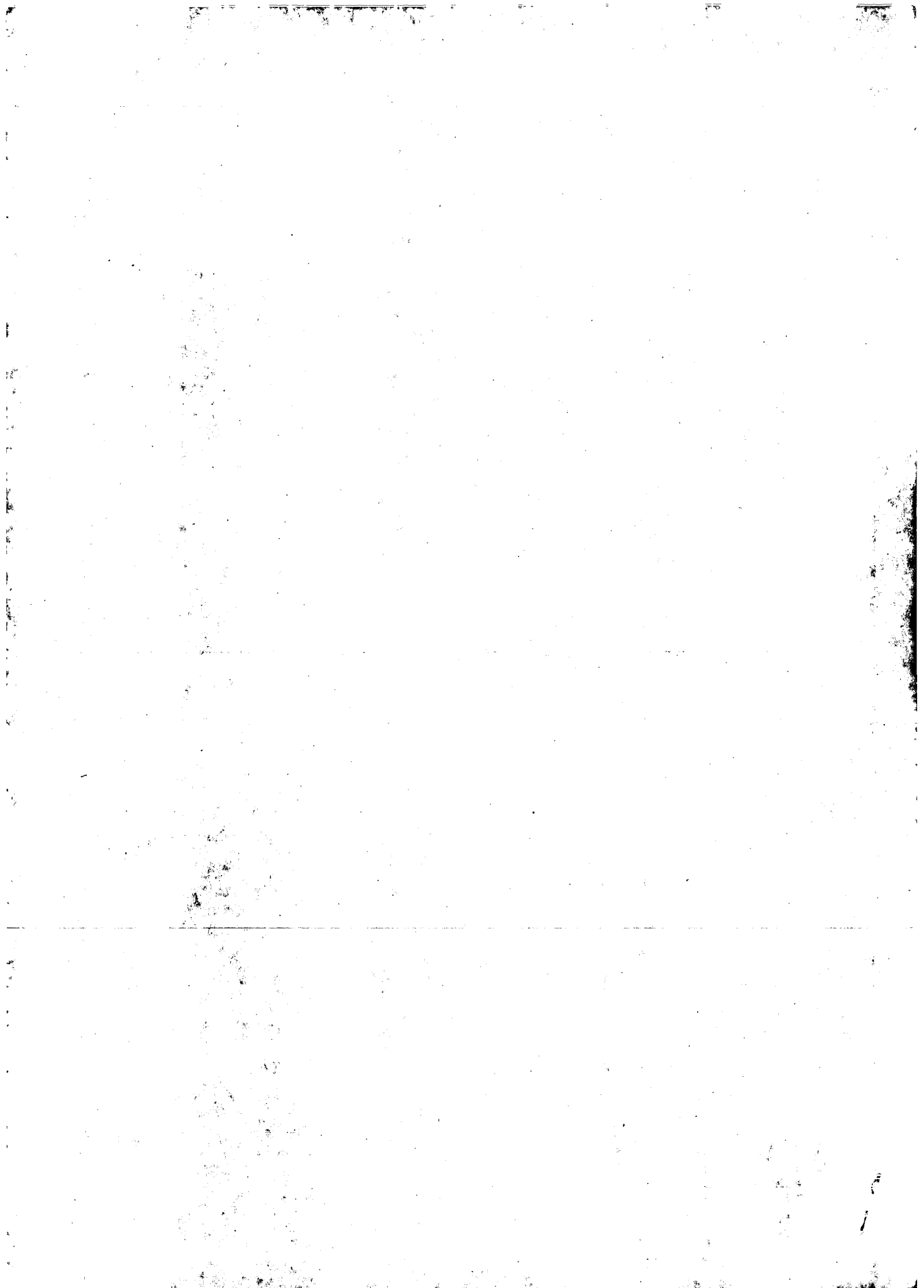
RESULT 15
US-08-973-589-12/c
; Sequence 12, Application US/08973589
; GENERAL INFORMATION:
; APPLICANT: Greider, Carol
; APPLICANT: Pruzan, Ronald
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: ESSENTIAL OLIGONUCLEOTIDES OF VERTEBRATE
; FILE REFERENCE: CSHL95-02A
; CURRENT APPLICATION NUMBER: US/08/973,589
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US96/09517
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/478,352
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
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US-08-973-589-12

Query Match 82.4%; Score 14; DB 13; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14  
 |||||  
 Db 39 CGGGCCAGCAGCTG 26

Search completed: June 23, 2003, 16:08:25  
 Job time : 1426.91 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 136.61 Seconds  
(without alignments)  
182.610 Million cell updates/sec

Title: US-08-770-564A-14

Perfect score: 17  
Sequence: 1 CGGGCAGCAGCTGACA 17

Scoring table:  
OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/prodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
10: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
12: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	88.2	25	10	US-09-057-351-27
2	12	70.6	23	9	US-10-320-230-30
3	12	70.6	23	10	US-09-817-387-18
4	12	70.6	25	9	US-10-215-112-2064
5	12	70.6	38	9	US-09-930-423-2661
6	12	70.6	38	9	US-09-330-423-2713
7	12	70.6	48	9	US-09-848-754A-7985
8	12	70.6	48	9	US-09-848-754A-8229
9	12	70.6	50	9	US-09-943-722-5
10	12	70.6	50	9	US-09-943-722-9
11	11	64.7	19	10	US-09-879-792-9
12	11	64.7	19	10	US-09-942-374-4
13	11	64.7	20	9	US-10-181-846-121
14	11	64.7	21	9	US-09-949-427-318
15	11	64.7	25	9	US-10-098-263B-32486
16	11	64.7	26	10	US-09-815-171A-18
17	11	64.7	28	9	US-09-872-712-9
18	11	64.7	30	9	US-09-972-656-120
19	11	64.7	31	9	US-09-961-077-417

Sequence 21, Appl  
Sequence 1733, Ap  
Sequence 1783, Ap  
Sequence 1733, Ap  
Sequence 1783, Ap  
Sequence 2007, Ap  
Sequence 2355, Ap  
Sequence 2444, Ap  
Sequence 2667, Ap  
Sequence 4597, Ap  
Sequence 2554, Ap  
Sequence 17, Appl  
Sequence 18, Appl  
Sequence 17, Appl  
Sequence 18, Appl  
Sequence 8533, Ap  
Sequence 1442, Ap  
Sequence 1442, Ap  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 3966, Ap  
Sequence 3967, Ap  
Sequence 1409, Ap  
Sequence 1410, Ap

20 11 64.7 36 9 US-10-244-715-21  
21 11 64.7 36 10 US-09-504-231A-1733  
22 11 64.7 36 10 US-09-504-231A-1783  
23 11 64.7 36 10 US-09-274-553D-1733  
24 11 64.7 36 10 US-09-274-553D-1783  
25 11 64.7 38 9 US-09-730-289B-2007  
26 11 64.7 38 9 US-09-730-289B-2355  
27 11 64.7 38 9 US-09-730-289B-2444  
28 11 64.7 38 9 US-09-730-289B-2667  
29 11 64.7 38 9 US-09-780-533A-4597  
30 11 64.7 38 9 US-09-877-478-2554  
31 11 64.7 39 9 US-09-423-800-17  
32 11 64.7 39 9 US-09-423-800-18  
33 11 64.7 39 9 US-10-182-018-17  
34 11 64.7 39 9 US-10-182-018-18  
35 11 64.7 48 9 US-09-848-754A-8468  
36 11 64.7 48 9 US-09-848-754A-8533  
37 10 58.8 14 10 US-09-504-231A-1442  
38 10 58.8 14 10 US-09-274-553D-1442  
39 10 58.8 15 9 US-10-104-611-26  
40 10 58.8 15 9 US-10-112-547-26  
41 10 58.8 15 9 US-10-112-547-26  
42 10 58.8 17 9 US-09-818-875-3966  
43 10 58.8 17 9 US-09-818-875-3967  
44 10 58.8 17 9 US-09-877-478-1409  
45 10 58.8 17 9 US-09-877-478-1410

#### ALIGNMENTS

RESULT 1  
US-09-057-351-27  
; Sequence 27, Application US/09057351  
; Patent No. US2001003439A1  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,351  
; FILING DATE: 08-APR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,802  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-000821US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200

```
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-27

Query Match      88.2%; Score 15; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCACGACGCTGACA 17
DB 9 GGCACGACGCTGACA 23

RESULT 2
US-10-320-230-30
; Sequence 30, Application US/10320230
; Publication No. US20030110529A1
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McSilver, John A.
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: 0926D
; CURRENT APPLICATION NUMBER: US/10/320,230
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/398,858
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)...(23)
US-10-320-230-30

Query Match      70.6%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACGACGCTCA 15
DB 9 GCCACGACGCTCA 20

RESULT 3
US-09-817-387-18
; Sequence 18, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 18
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotides, linkages between positions 1
; OTHER INFORMATION: to 12 are phosphorothioates, linkages between
; OTHER INFORMATION: positions 12 to 20 are phosphodiester
; OTHER INFORMATION: positions 13 to 23 carry 2'-OCH3 modified ribosyl
; OTHER INFORMATION: residues
; OTHER INFORMATION: linkages between positions 20 to 23 are
; OTHER INFORMATION: phosphorothioates
US-09-817-387-18

Query Match      70.6%; Score 12; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCACGACGCTG 14
DB 1 GGCACGACGCTG 12

RESULT 4
US-10-215-112-2064
; Sequence 2064, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2064
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2064

Query Match      70.6%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCACGACGCT 13
DB 4 GGCACGACGCT 15

RESULT 5
US-09-930-423-2661
; Sequence 2661, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00,918-A,400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2661
; LENGTH: 38
; TYPE: RNA
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ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 NAME/KEY: misc.Feature  
 LOCATION: (31)..(31)  
 OTHER INFORMATION: n stands for inosine  
 US-09-930-423-2661

Query Match 70.6%; Score 12; DB 9; Length 38;  
 Best Local Similarity 91.7%; Pred. No. 9.1e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGCAGCTGA 15  
 |||||:|  
 DB 1 GCCAGCAGCTGA 12

RESULT 6

US-09-930-423-2713  
 Sequence 2713, Application US/09930423  
 Publication No. US20030092003A1  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: Blatt, Larry  
 APPLICANT: McSwiggen, Jim  
 TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
 FILE REFERENCE: MBH00-918-A 400/027  
 CURRENT APPLICATION NUMBER: US/09/930,423  
 CURRENT FILING DATE: 2001-08-15  
 NUMBER OF SEQ ID NOS: 4553  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 2713  
 LENGTH: 38  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 NAME/KEY: misc.Feature  
 LOCATION: (31)..(31)  
 OTHER INFORMATION: n stands for inosine  
 US-09-930-423-2713

Query Match 70.6%; Score 12; DB 9; Length 38;  
 Best Local Similarity 91.7%; Pred. No. 9.1e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGCAGCTGA 15  
 |||||:|  
 DB 1 GCCAGCAGCTGA 12

RESULT 7

US-09-848-754A-7985  
 Sequence 7985, Application US/09848754A  
 Publication No. US20030073207A1  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors  
 FILE REFERENCE: MBH00-958-I (400/018)  
 CURRENT APPLICATION NUMBER: US/09/848,754A  
 CURRENT FILING DATE: 2001-05-03  
 NUMBER OF SEQ ID NOS: 9645  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 7985  
 LENGTH: 48  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 US-09-848-754A-7985

Query Match 70.6%; Score 12; DB 9; Length 48;

Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGC 12  
 |||||:|  
 DB 37 CGGGCCAGCAGC 48

RESULT 8

US-09-848-754A-8229  
 Sequence 8229, Application US/09848754A  
 Publication No. US20030073207A1  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors  
 FILE REFERENCE: MBH00-958-I (400/018)  
 CURRENT APPLICATION NUMBER: US/09/848,754A  
 CURRENT FILING DATE: 2001-05-03  
 NUMBER OF SEQ ID NOS: 9645  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 8229  
 LENGTH: 48  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 US-09-848-754A-8229

Query Match 70.6%; Score 12; DB 9; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGC 12  
 |||||:|  
 DB 37 CGGGCCAGCAGC 48

RESULT 9

US-09-943-722-5  
 Sequence 5, Application US/09943722  
 Publication No. US20020192860A1  
 GENERAL INFORMATION:  
 APPLICANT:  
 APPLICANT:  
 TITLE OF INVENTION: METHOD OF ELIMINATING INHIBITORY/INSTABILITY REGIONS OF mRNA  
 NUMBER OF SEQUENCES: 130  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: MORGAN & FINNEGAN  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/943,722  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/850,049  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/050,478  
 FILING DATE: 26-OCT-1994  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:

us-08-770-564a-14.oligo.rnpb

Fri Jun 27 07:41:33 2003

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APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-09-943-722-5

Query Match      70.6%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CAGCAGCTGACA 17
Db      35 CAGCAGCTGACA 46

RESULT 10
US-09-943-722-5
Sequence 9, Application US/09943722
Publication No. US20020192660A1
GENERAL INFORMATION:
APPLICANT: MORGAN & FINNEGAN
TITLE OF INVENTION: METHOD OF ELIMINATING
INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESS: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,722
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,049
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA: PCT/US93/02908
APPLICATION NUMBER:
FILING DATE: 29-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION:

APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-09-943-722-9

Query Match      70.6%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CAGCAGCTGACA 17
Db      35 CAGCAGCTGACA 46

RESULT 11
US-09-879-792-9
Sequence 9, Application US/09879792
Patent No. US20020061850A1
GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human Transmembrane Serine
PROTEASE
FILE REFERENCE: 02973.00035
CURRENT APPLICATION NUMBER: US/09/879,792
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/211,224
PRIOR FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 60/283,353
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/283,648
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-09-879-792-9

Query Match      64.7%; Score 11; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GCCAGCAGCTG 14
Db      3 GCCAGCAGCTG 13

RESULT 12
US-09-942-374-4
Sequence 4, Application US/09942374
Patent No. US20020137063A1
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Glimeno, Ruth
APPLICANT: White, David
TITLE OF INVENTION: Receptor Family Member and Uses Therefor
FILE REFERENCE: WPI2000-368P1R
CURRENT APPLICATION NUMBER: US/09/942,374

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; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/228,409
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: murine 57242 primer sequence
US-09-942-374-4

Query Match      64.7%; Score 11; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CAGCAGCTGAC 16
        |||||
Db       3 CAGCAGCTGAC 13

RESULT 13
US-10-181-846-121
; Sequence 121, Application US/10181846
; Publication No. US20030083297A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RISP-0363
; CURRENT APPLICATION NUMBER: US/10/181,846
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US01/01416
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/490,692
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 121
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-846-121

Query Match      64.7%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GCCAGCAGCTG 14
        |||||
Db       2 GCCAGCAGCTG 12

RESULT 14
US-09-949-427-318/c
; Sequence 318, Application US/09949427
; Publication No. US20030054418A1
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lusia, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
; FILE REFERENCE: 02810.0014.NFUS02
; CURRENT APPLICATION NUMBER: US/09/949,427
; CURRENT FILING DATE: 2001-09-07

; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 318
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-427-318

Query Match      64.7%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

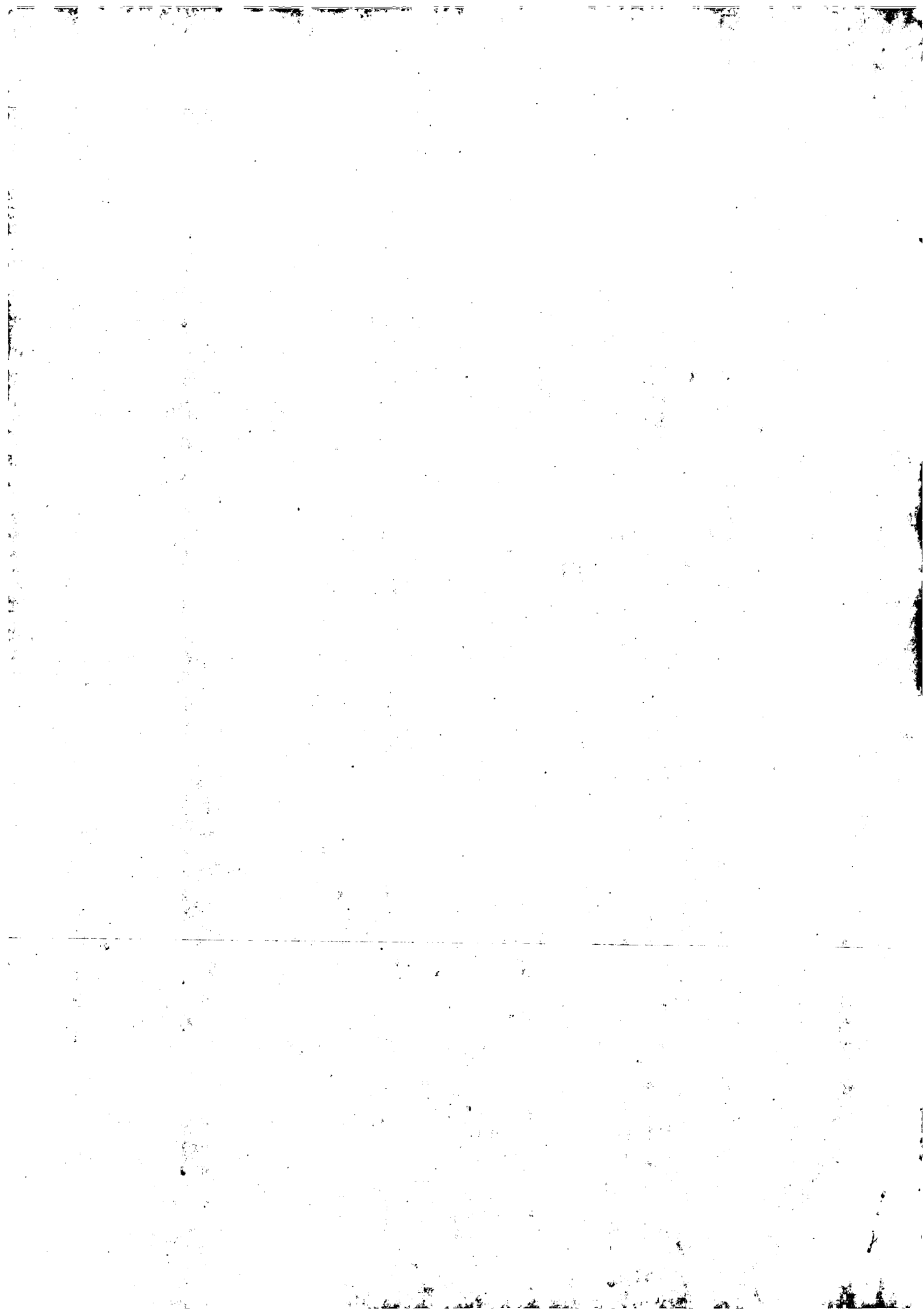
QY      4 GCCAGCAGCTG 14
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Db       16 GCCAGCAGCTG 6

RESULT 15
US-10-098-263B-32486/c
; Sequence 32486, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 32486
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-32486

Query Match      64.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 AGCAGCTGACA 17
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Db       19 AGCAGCTGACA 9

Search completed: June 23, 2003, 20:01:35
Job time : 137.61 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 26.6175 Seconds  
(without alignments)  
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Title: US-08-770-564A-14

Perfect score: 17  
Sequence: 1 CGGGCCAGCAGCTGACA 17

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database : Issued Patents NA:  
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6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	2	US-08-770-565-14
2	17	100.0	30	2	US-08-833-377-5
3	15	88.2	25	1	US-08-482-115B-26
4	15	88.2	25	2	US-08-472-802C-27
5	12	70.6	18	4	US-08-584-040-8292
6	12	70.6	18	4	US-08-584-040-8293
7	12	70.6	48	1	US-07-720-222-41
8	12	70.6	50	2	US-08-850-049-5
9	12	70.6	50	2	US-08-850-049-9
10	12	70.6	50	2	US-08-050-478-5
11	12	70.6	50	2	US-08-050-478-9
12	12	70.6	50	4	US-07-858-747B-5
13	12	70.6	50	4	US-07-858-747B-9
14	12	70.6	50	4	US-09-414-117-5
15	12	70.6	50	4	US-09-414-117-9
16	12	70.6	50	4	US-09-678-437-5
17	12	70.6	50	4	US-09-678-437-9
18	11	64.7	14	3	US-08-998-099-368
19	11	64.7	17	1	US-08-257-784A-8
20	11	64.7	17	2	US-08-489-066A-12
21	11	64.7	17	3	US-08-489-072A-12
22	11	64.7	17	4	US-08-489-071A-12
23	11	64.7	17	4	US-08-584-040-7226
24	11	64.7	20	2	US-08-837-201C-19
25	11	64.7	20	4	US-09-490-692-121
26	11	64.7	22	4	US-09-364-416-19
27	11	64.7	22	1	US-08-482-115B-32

28	11	64.7	22	2	US-08-472-802C-37	Sequence 37, Appl
c 29	11	64.7	27	2	US-08-793-229-23	Sequence 23, Appl
c 30	11	64.7	27	3	US-09-285-957-23	Sequence 23, Appl
31	11	64.7	27	4	US-08-584-040-5244	Sequence 5244, Ap
32	11	64.7	31	4	US-08-679-645-417	Sequence 417, App
c 33	11	64.7	32	4	US-09-813-781-124	Sequence 124, App
34	11	64.7	33	3	US-08-816-346-52	Sequence 52, Appl
35	11	64.7	33	3	US-09-335-411-52	Sequence 52, Appl
36	11	64.7	36	2	US-08-292-620A-1158	Sequence 1158, Ap
c 37	11	64.7	36	2	US-08-925-708-4	Sequence 4, Appli
38	11	64.7	36	2	US-08-925-708-5	Sequence 5, Appli
39	11	64.7	36	3	US-09-071-845-1158	Sequence 1158, Ap
c 40	11	64.7	37	1	US-08-330-638D-9	Sequence 9, Appli
c 41	11	64.7	37	2	US-08-906-746A-9	Sequence 9, Appli
c 42	11	64.7	46	5	PCT-US91-02954-9	Sequence 2, Appli
c 43	11	64.7	48	1	US-08-066-961-2	Sequence 2, Appli
c 44	11	64.7	49	1	US-08-530-492-89	Sequence 89, Appl
c 45	11	64.7	49	4	US-08-906-517-89	Sequence 89, Appl

## ALIGNMENTS

RESULT 1  
US-08-770-565-14  
; Sequence 14, Application US/08770565  
; Patent No. 5846723  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; TITLE OF INVENTION: Telomerase  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002300US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-565-14

Query Match 100.0%; Score 17; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0;  
QY 1 CGGGCCAGCAGCTGACA 17

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Db      1 CGGGCCAGCAGCTGACA 17
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RESULT 2
US-08-833-377-5      Application US/08833377
; Sequence 5, Application US/08833377
; Patent No. 5968506
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; APPLICANT: Kealey, James T.
; TITLE OF INVENTION: Purified Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,377
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,736
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = 5' biotinylated guanosine"
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..30
; OTHER INFORMATION: /note= "Oligo 13"
; US-08-833-377-5
Query Match      100.0%; Score 17; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGGGCCAGCAGCTGACA 17
Db      4 CGGGCCAGCAGCTGACA 20
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RESULT 3
US-08-482-115B-26
; Sequence 26, Application US/08482115B
; Patent No. 5776579
; GENERAL INFORMATION:
; APPLICANT: Villegonteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00083003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-482-115B-26
Query Match      88.2%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 CGCCAGCAGCTGACA 17
Db      9 CGCCAGCAGCTGACA 23
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RESULT 4
US-08-472-802C-27
; Sequence 27, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villegonteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,802C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000820  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-472-802C-27

Query Match 88.2%; Score 15; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCACAGCTGCA 17  
DB 9 GGCACAGCTGACA 23

RESULT 5  
US-08-584-040-8292/C  
Sequence 8292, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 8292:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-8292

Query Match 70.6%; Score 12; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCAGCAGCTGAC 16  
DB 15 CCAGCAGCTGAC 4

RESULT 6  
US-08-584-040-8293/C  
Sequence 8293, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 8293:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-8293

Query Match 70.6%; Score 12; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCGAGCAGCTGAC 16  
DB 12 CCGAGCAGCTGAC 1

RESULT 7  
US-07-720-222-41  
Sequence 41, Application US/07720222  
Patent No. 5190873  
GENERAL INFORMATION:  
APPLICANT: Lernhardt, Waldemar  
APPLICANT: Bourdon, Mario  
APPLICANT: Youderlian, Phil  
TITLE OF INVENTION: HYBRID PROTEINS CONTAINING BINDING SITES  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Bingham & Fitting  
STREET: 11230 Sorrento Valley Road, Suite 200  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/720,222  
FILING DATE: 19910621  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bingham, Douglas A.  
REGISTRATION NUMBER: 32,457  
REFERENCE/DOCKET NUMBER: CIB0012P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-587-3533  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-720-222-41

Query Match 70.6%; Score 12; DB 1; Length 48;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGCAGCTGA 15  
DB 8 GCCAGCAGCTGA 19

RESULT 8  
US-08-850-049-5  
Sequence 5, Application US/08850049  
Patent No. 5965726

GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: METHOD OF ELIMINATING  
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,049  
FILING DATE: 02-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/050,478  
FILING DATE: 26-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02908  
FILING DATE: 29-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/858,747  
FILING DATE: 27-MAR-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRIS, MARY J.  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2026-4006US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)751-6849  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
US-08-850-049-5

Query Match 70.6%; Score 12; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17  
DB 35 CAGCAGCTGACA 46

RESULT 9  
US-08-850-049-9  
Sequence 9, Application US/08850049  
Patent No. 5965726  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: METHOD OF ELIMINATING  
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE

CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,049  
FILING DATE: 02-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/050,478  
FILING DATE: 26-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02908  
FILING DATE: 29-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/858,747  
FILING DATE: 27-MAR-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2026-4006US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
US-08-850-049-9

Query Match 70.6%; Score 12; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17  
|||||  
Db 35 CAGCAGCTGACA 46

RESULT 10  
US-08-050-478-5  
Sequence 5, Application US/08050478  
Patent No. 5972596  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: METHOD OF ELIMINATING  
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,478  
FILING DATE: 26-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02908  
FILING DATE: 29-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/858,747  
FILING DATE: 27-MAR-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2026-4006US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
US-08-050-478-5

Query Match 70.6%; Score 12; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17  
|||||  
Db 35 CAGCAGCTGACA 46

RESULT 11  
US-08-050-478-9  
Sequence 9, Application US/08050478  
Patent No. 5972596  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: METHOD OF ELIMINATING  
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,478  
FILING DATE: 26-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02908  
FILING DATE: 29-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/858,747  
FILING DATE: 27-MAR-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398

Fri Jun 27 07:41:32 2003

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Page 6

REFERENCE/DOCKET NUMBER: 2026-4006US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
US-08-050-478-9

Query Match 70.6%; Score 12; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CAGCAGCTGACA 17  
DB 35 CAGCAGCTGACA 46

RESULT 12  
US-07-858-747B-5  
Sequence 5, Application US/07858747B  
Patent No. 617466  
GENERAL INFORMATION:  
APPLICANT: PAVLAKIS, GEORGE N.; FELBER, BARBARA  
APPLICANT: K.  
TITLE OF INVENTION: METHOD OF ELIMINATING  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/858,747B  
FILING DATE: 19920327  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MARY J. MORRY  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2026-4006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)751-6849  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: RNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: HIV-1  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:

CELL LINE:  
ORGANELLE:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
CODING SEQUENCE SPANNING NT  
OTHER INFORMATION: 654-703 OF THE REVISED NT SEQUENCE OF THE HIV-1  
OTHER INFORMATION: MOLECULAR CLONE PHX82  
US-07-858-747B-5

Query Match 70.6%; Score 12; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CAGCAGCTGACA 17  
DB 35 CAGCAGCTGACA 46

RESULT 13  
US-07-858-747B-9  
Sequence 9, Application US/07858747B  
Patent No. 617466  
GENERAL INFORMATION:  
APPLICANT: PAVLAKIS, GEORGE N.; FELBER, BARBARA  
APPLICANT: K.  
TITLE OF INVENTION: METHOD OF ELIMINATING  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/858,747B  
FILING DATE: 19920327  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MARY J. MORRY  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2026-4006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)751-6849  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE: OTHER  
HYPOTHETICAL: YES  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: OLIGONUCLEOTIDE M4  
US-07-858-747B-9

Query Match 70.6%; Score 12; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CAGCAGCTGACA 17  
Db 35 CAGCAGCTGACA 46

RESULT 14  
US-09-414-117-5  
; Sequence 5, Application US/09414117  
; Patent No. 6291664  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: METHOD OF ELIMINATING  
; INHIBITORY/INSTABILITY REGIONS OF mRNA  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/414,117  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/850,049  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: PCT/US93/02908  
; APPLICATION NUMBER: 2026-4006US1  
; FILING DATE: 29-MAR-1993  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/858,747  
; FILING DATE: 27-MAR-1992  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORRIS, MARY J.  
; REGISTRATION NUMBER: 34,398  
; REFERENCE/DOCKET NUMBER: 2026-4006US1  
; TELEPHONE: (212)758-4800  
; TELEFAX: (212)751-6849  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; US-09-414-117-5

Query Match 70.6%; Score 12; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CAGCAGCTGACA 17  
Db 35 CAGCAGCTGACA 46

RESULT 15  
US-09-414-117-9  
; Sequence 9, Application US/09414117

; Patent No. 6291664  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: METHOD OF ELIMINATING  
; INHIBITORY/INSTABILITY REGIONS OF mRNA  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/414,117  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/850,049  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: PCT/US93/02908  
; APPLICATION NUMBER: 2026-4006US1  
; FILING DATE: 29-MAR-1993  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/858,747  
; FILING DATE: 27-MAR-1992  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORRIS, MARY J.  
; REGISTRATION NUMBER: 34,398  
; REFERENCE/DOCKET NUMBER: 2026-4006US1  
; TELEPHONE: (212)758-4800  
; TELEFAX: (212)751-6849  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; US-09-414-117-9

Query Match 70.6%; Score 12; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CAGCAGCTGACA 17  
Db 35 CAGCAGCTGACA 46

Search completed: June 23, 2003, 10:17:10  
Job time : 27.6175 secs





XX New polynucleotide(s) anti-sense to human telomerase - used for  
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,  
 PT contraception, immuno-suppression or treating infection  
 PS  
 PS Claim 11; Page 65; 80pp; English.

XX Sequences shown in AAV1169 to AAV1181 represent antisense  
 CC oligonucleotides to the RNA component of human telomerase (hTR). These  
 CC antisense oligonucleotides specifically hybridize to a nucleotide  
 CC sequence within an accessible region of the hTR, but that does not  
 CC hybridize to a sequence within the template region of hTR. These  
 CC oligonucleotides may specifically be used for detection of an RNA  
 CC component of human telomerase in a sample. This is useful for diagnosing  
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),  
 CC and providing prognosis for a cancer patient. The inhibitory  
 CC oligonucleotides can inhibit the telomerase activity level in a cell by  
 CC interfering with transcription of the RNA component, decreasing the  
 CC half-life of the telomerase RNA component transcript, inhibiting assembly  
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the  
 CC polymerase activity of telomerase. These antisense oligonucleotides can  
 CC be used for inhibiting telomerase activity in both cultured cells and in  
 CC cells in vivo. They can be used in therapeutics for treating or  
 CC preventing cancer, for contraception or sterilization, for  
 CC immunosuppression, and for selectively down-regulating specific branches  
 CC of the immune system, e.g. a specific subset of T-cells, in  
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,  
 CC parasites or fungi.  
 CC  
 SQ Sequence 17 BP; 4 A; 6 C; 6 G; 1 T; 0 other;

Query Match 100.0%; Score 17; DB 19; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
 |||||  
 DB 1 CGGGCCAGCAGCTGACA 17

RESULT 2  
 AA207280  
 ID AA207280 standard; DNA; 25 BP.

XX AA207280;  
 AC  
 DT 22-OCT-1999 (first entry)

XX Human telomerase RNA gene (hTR) specific primer TRC3R.

XX Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;  
 KW gene therapy; thymidine kinase gene; anticancer therapy; human;  
 KW PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO938964-A2.

XX 05-AUG-1999.

XX 29-JAN-1999; 99WO-GB00308.

XX 29-JAN-1998; 98GB-0001902.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

PA Keith WN;

PI

XX WPI; 1999-479183/40.

XX Mouse and human telomerase RNA gene promoters, useful for tumor

PT specific gene therapy

XX Disclosure; Fig 6; 10pp; English.

PS The invention relates to promoter regions from mouse and human  
 XX telomerase RNA (TR) component genes. The TR gene promoter can be linked  
 CC to a heterologous gene, especially a gene encoding a cytotoxin, for  
 CC therapy of cancer, especially neoplasias. The telomerase is necessary for  
 CC the unrestricted proliferative capacity of many human cancers. Mutation  
 CC or dysregulation of the telomerase repression pathway may cause  
 CC substances, identified in the methods, can be used to block transcription  
 CC from the TR gene promoter through interaction of the 5' regulatory  
 CC sequences. These substances, e.g. antisense oligonucleotides,  
 CC transcription factors, peptide nucleic acids and factors that disrupt  
 CC signal transduction, are useful for cancer therapy. In particular, gene  
 CC therapy vectors (especially pGR2-codAmp) comprising the promoter and a  
 CC viral thymidine kinase gene can be used to convert or treated. Direct  
 CC gene therapy, so that neoplasia can be controlled or treated. Direct  
 CC down-regulation of telomerase RNA gene through manipulation of  
 CC transcription factors may be effective anticancer therapy and the cloning  
 CC of the TR gene promoter allows the analysis of therapeutic molecules  
 CC which modulate TR promoter activity. Sequences AA20723-80 represents  
 CC PCR primers for amplifying human TR gene (hTR) promoter sequence.  
 CC  
 SQ Sequence 25 BP; 6 A; 7 C; 9 G; 3 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17  
 |||||  
 DB 7 CGGGCCAGCAGCTGACA 23

RESULT 3  
 AAV63648  
 ID AAV63648 standard; DNA; 30 BP.

XX AAV63648;

DT 15-FEB-1999 (first entry)

XX Antisense oligonucleotide 13 for human telomerase RNA component.

XX Human; telomerase RNA component; anticancer therapy; purification;  
 KW assay; vaccine; cancer; antisense oligonucleotide; ss.

XX Synthetic.

OS Homo sapiens.

XX Key

FT modified\_base 1 Location/Qualifiers

FT /tag= "a

FT /note= "biotinylated"

XX WO9845450-A1.

XX 15-OCT-1998.

XX 04-APR-1997; 97WO-US06012.

XX 04-APR-1997; 97WO-US06012.

XX (GERO-) GERON CORP.

PA

XX Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA;

PI Vassero AP, Weinrich SL;

XX WPI; 1998-59485/50.

XX Purification of telomerase on affinity material - useful for, e.g.

XX diagnosis and treatment of cancer

PT



XX Disclosure; Page 24; 76pp; English.  
 PS The present sequence represents an antisense oligonucleotide.  
 XX CC directed against the human telomerase RNA component gene sequences.  
 CC The oligonucleotide can be used as an affinity agent in the methods of  
 CC the invention, which are used to purify human telomerase. The methods  
 CC involve the use of several sequential steps, including the use of two  
 CC matrices that bind molecules bearing negative charges, a matrix that  
 CC binds molecules bearing positive charges, an affinity purification step  
 CC and a size separation. Telomerase is a particular target of anticancer  
 CC therapies, and is useful in assays for characterizing (pre)cancerous  
 CC cells. Telomerase can also be used to screen for specific modulators,  
 CC for biochemical analysis of its activity, and in preparation of  
 CC antibodies. Fragments of telomerase, or nucleic acid encoding them,  
 CC are used in vaccines, and for treating over expression of telomerase,  
 CC particularly in cancer.  
 XX SQ Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 other;  
 Query Match 100.0%; Score 17; DB 19; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGGGCCAGCAGCTGACA 17  
 Db 4 CGGGCCAGCAGCTGACA 20  
 RESULT 4  
 ID AA223630 standard; DNA; 30 BP.  
 XX AA223630;  
 AC 07-JUN-2000 (first entry)  
 XX  
 DT Human clone 28-1, telomerase oligonucleotide oligo-13.  
 XX  
 DE Telomerase; human; immune response; cancer; vaccine; treatment;  
 KW disease; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /note= "5'-biotinylated guanosine"  
 FT  
 PN US5968506-A.  
 XX  
 PD 19-OCT-1999.  
 XX  
 PF 04-APR-1997; 97US-0833377.  
 XX  
 PR 04-AUG-1995; 95US-0510736.  
 XX  
 PA (GERO-) GERON CORP.  
 XX  
 PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;  
 PI Vasserot AP;  
 PI  
 DR WPI; 1999-590379/50.  
 XX  
 XX Compositions comprising human telomerase, useful for treating diseases  
 PT associated with overexpression of telomerase e.g. cancer -  
 XX  
 XX Disclosure; Column 45-46; 34pp; English.  
 XX  
 CC This invention describes a novel composition comprising human telomerase  
 CC having at least 2000-fold (preferably at least 60000-fold) increased  
 CC relative purity compared with crude extract of cells from

CC adenovirus-transformed kidney cell line. The composition is useful for  
 CC eliciting an immune response in animals and may therefore be used as a  
 CC vaccine for treating diseases associated with the overexpression of  
 CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used  
 CC in the isolation of human clone 28-1 which contains a fragment of the  
 CC human telomerase described in the method of the invention.  
 XX SQ Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 other;  
 Query Match 100.0%; Score 17; DB 20; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGGGCCAGCAGCTGACA 17  
 Db 4 CGGGCCAGCAGCTGACA 20  
 RESULT 5  
 ID AA509475 standard; DNA; 30 BP.  
 XX AA509475;  
 AC 24-OCT-2001 (first entry)  
 XX  
 DT Antisense oligonucleotide for human telomerase, Oligo 13.  
 XX  
 DE Human; Telomerase; vaccine; antibody; cancer; E2H;  
 KW nucleolin; antisense oligonucleotide; Oligo 13; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= G  
 FT /note= "G is biotinylated"  
 FT  
 PN US6261556-B1.  
 XX  
 PD 17-JUL-2001.  
 XX  
 PF 18-OCT-1999; 99US-0420056.  
 XX  
 PR 04-APR-1997; 97US-0833377.  
 XX  
 PR 04-AUG-1995; 95US-0510736.  
 XX  
 PA (GERO-) GERON CORP.  
 XX  
 PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA;  
 PI Kealey JT;  
 PI  
 DR WPI; 2001-450477/48.  
 XX  
 XX Purified human telomerase, useful for inducing immune response in  
 PT animals, comprises several thousand folds increased purity compared  
 PT with cytoplasmic crude cell preparations -  
 XX  
 XX Disclosure; Column 18; 29pp; English.  
 XX  
 CC The sequence represents a biotinylated antisense oligonucleotide  
 CC used in the purification of human telomerase. The invention  
 CC relates to a purified human telomerase core enzyme protein comprising  
 CC 2000-fold increased purity compared with a crude extract of cells from  
 CC adenovirus-transformed kidney cell line (293 cells) and when associated  
 CC with telomerase RNA component has DNA polymerase activity and a molecular  
 CC weight of 200-2000 kDa. The purified telomerase is useful  
 CC for inducing a humoral or cell-mediated immune response in an animal.  
 CC Purified telomerase or immunogenic fragments are useful as vaccines for  
 CC treating diseases associated with over-expression of telomerase, such as  
 CC cancer and for producing antibodies that recognize telomerase, which are  
 CC useful as affinity agents in isolating the proteins and for detecting the

CC presence of proteins in a sample, such as cell or tissue. Identification  
CC of telomerase aids in diagnosis of cancer or pre-cancerous states.  
CC Telomerase and/or telomerase associated proteins are also useful for  
CC screening compounds to identify agents that alter the association of  
CC telomerase-associated proteins, such as nucleolin or E2F2 with  
CC telomerase.  
XX  
SQ Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 other;

Query Match 100.0%; Score 17; DB 22; Length 30;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGGCCAGCAGCTGACA 17  
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 6  
AAT10302  
ID AAT10302 standard; DNA; 25 BP.

XX AAT10302;

DT 10-SEP-1996 (first entry)

DE RNA component of human telomerase antisense TRC3 5' RACE primer.

KW RNA component: human; telomerase; antisense; 5' RACE; primer;  
KW recombinant production; synthesis; mutant detection; mammalian;  
KW identification; modulating agent; neoplastic condition; mammalian;  
KW transcriptional regulatory sequence; gene therapy; disease; ss.  
XX  
OS Synthetic.  
XX  
PN WO9601835-A1.

DE 06-JUL-1995; 95WO-US08530.

XX 07-JUN-1995; 95US-0482115.  
XX 07-JUL-1994; 94US-0272102.  
XX 27-OCT-1994; 94US-0330123.  
XX 07-JUN-1995; 95US-0472802.

PA (GERO-) GERON CORP.

XX Andrews WH, Feng J, Funk W, Villaponteau B,  
XX WPI; 1996-097581/10.

XX RNA component of mammalian telomerase, esp. human - useful in  
XX identifying e.g. candidate telomerase-modulating agents  
XX  
XX Example 10; Page 82; 11pp; English.

XX The present sequence, an antisense primer for the RNA component  
XX of human telomerase (RCHT), was used in a 5' RACE procedure. The  
XX RCHT can be used in the recombinant prodn. of an active telomerase  
XX mol., capable of adding sequences to chromosomal DNA telomeres, and  
XX in the synthesis of mutant sequences for the detection of mutant  
XX mammalian telomerase RNA component polynucleotides. The RCHT may  
XX also be used in the identification of telomerase modulating agents,  
XX and in the detection of telomerase related, or neoplastic  
XX conditions in a patient. Polynucleotides of at least 25  
XX consecutive nucleotides identical, or complementary to the RCHT  
XX sequence linked to heterologous transcriptional regulatory  
XX sequences, can be used for the gene therapy of human diseases.  
XX  
SQ Sequence 25 BP; 8 A; 8 C; 6 G; 3 T; 0 other;

Query Match 88.2%; Score 15; DB 17; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GGCCAGCAGCTGACA 17  
Db 9 GGCCAGCAGCTGACA 23

RESULT 7  
AAS56779/c  
ID AAS56779 standard; DNA; 24 BP.

XX AAS56779;

DT 16-JAN-2002 (first entry)

DE BRCA-1 promoter region PCR primer #1.

KW Human; BRCA-1 regulator; ribozyme; BR1; RNA target recognition; probe;  
KW cytosolic; RNA cleavage; tumour suppressor; PCR primer; CHR2; Afe; BR2;  
KW inhibitor dominant negative 4; breast basic conserved protein 1; BRCL1;  
KW BR3; ID4; cancer; proliferative disorder; tumour proliferation; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200170982-A2.

DE 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09559.

PR 23-MAR-2000; 2000US-0536058.

PA (TMU-) TMUSOL INC.  
PA (BERG/) BEGER C.

XX Begger C, Barber J, Wong-staal F,  
XX WPI; 2001-611503/70.

XX Novel polypeptides that are the regulators of BRCA-1, useful for  
XX creating cancer and diagnosing the presence of neoplastic cells in  
XX biological sample.  
XX  
XX Example 2; Page 52; 97pp; English.

XX Sequences AAS56779-AAS56968 represent DNA encoding BRCA-1 regulators,  
XX ribozyme target recognition RNA sequences, DNA fragments encoding the RNA  
XX and primers used in the methods of the invention. Hybridisation of the  
XX ribozymes to their targets results in cleavage of the RNA target. The  
XX ribozymes can be used to cleave regulators of the tumour suppressor  
XX BRCA-1, resulting in upregulation or downregulation of BRCA-1 in a cell.  
XX The mRNA targets include those encoding the BRCA-1 regulator BR1,  
XX inhibitor dominant negative 4 (ID4), breast basic conserved protein 1  
XX (BBCL1), CHR2, Afe, BR2 and BR3. Regulation of BRCA-1 is useful for  
XX treating and diagnosing cancer and other proliferative disorders. The  
XX severity of an incidence of cancer can be lessened by regulating tumour  
XX proliferation through modulation of BRCA-1 expression. The sequences of  
XX the invention are useful in the development of anti-cancer drugs.  
XX  
SQ Sequence 24 BP; 2 A; 8 C; 7 G; 7 T; 0 other;

Query Match 82.4%; Score 14; DB 22; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGGCCAGCAGCTG 14  
Db 23 CGGGCCAGCAGCTG 10

RESULT 8

AA58806/c  
 ID AAT58806 standard; DNA; 42 BP.  
 XX  
 AC AAT58806;  
 XX  
 DT 20-NOV-1997 (first entry)  
 XX  
 DE Human telomerase template PCR primer hTR170.  
 XX  
 KW Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;  
 KW protozoa; tumour; antibody; polymerase chain reaction; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9640868-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US09517.  
 XX  
 PR 07-JUN-1995; 95US-0478352.  
 XX  
 XX (COLD-) COLD SPRING HARBOR LAB.  
 PA  
 XX Autexier C, Greider C;  
 PI  
 XX WPI; 1997-099928/09.  
 XX  
 XX DNA encoding essential RNA components of human telomerase - also  
 PT truncated or recombinant telomerase, useful for diagnosis and  
 PT treatment of cancer and infection by eukaryotic parasites  
 XX  
 XX Example 4; Page 30; 48pp; English.  
 PS  
 XX The present sequence represents PCR primer hTR170 used for amplifying  
 CC the human telomerase (hTR) template. The RNA and DNA can be used in  
 CC hybridisation assays to detect or quantify telomerase activity in cells,  
 CC tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites  
 CC (yeast and protozoa) or tumours. It is also useful as primers for  
 CC amplification assays. The truncated or recombinant vertebrate telomerase  
 CC is used therapeutically to increase telomerase activity (also as  
 CC reagents in the screening assay) while the RNA or other inhibitors such  
 CC as antisense molecules, are used to reduce such activity. Typical  
 CC applications are initiation/restoration of activity to cause senescence  
 CC or to prevent immortalisation of cells in tumours or parasites. The DNA  
 CC is also used to produce recombinant telomerase, which can then be used  
 CC conventionally to raise antibodies for diagnostic detection of  
 CC telomerase. Detecting telomerase allows early diagnosis of tumour or  
 CC infection, before clinical signs manifest. Telomerase inhibitors  
 CC directed against e.g. Trypanosoma should cause fewer side effects than  
 CC drugs currently used to treat such infections. The DNA encodes those  
 CC parts of hTR RNA essential for activity but are significantly shorter  
 CC than the endogenous RNA component.  
 XX  
 SQ Sequence 42 BP; 8 A; 10 C; 12 G; 12 T; 0 other;  
 Query Match 82.4%; Score 14; DB 18; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGGGCCAGCAGCTG 14  
 Db 39 CGGGCCAGCAGCTG 26  
 |||||  
 RESULT 9  
 AAV93815/c  
 ID AAV93815 standard; RNA; 14 BP.  
 XX  
 AC AAV93815;  
 XX  
 XX 18-FEB-1999 (first entry)  
 DT  
 XX

DE Human B-raf target sequence nucleotide position 2205.  
 XX  
 KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalyst; modulation; expression; Raf gene;  
 KW delivery; screening; identification; synthesis; deprotection;  
 KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;  
 KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9850530-A2.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US09249.  
 XX  
 PR 19-DEC-1997; 97US-0068212.  
 PR 09-MAY-1997; 97US-0046059.  
 PR 09-JUN-1997; 97US-0049002.  
 PR 03-JUL-1997; 97US-0051718.  
 PR 22-AUG-1997; 97US-0056808.  
 PR 02-OCT-1997; 97US-0061321.  
 PR 02-OCT-1997; 97US-0061324.  
 PR 05-NOV-1997; 97US-0064866.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;  
 PI Karpeisky A, Kisch K, Matulic-Adamic J, McSwigen JA;  
 PI Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;  
 XX  
 XX WPI; 1999-009494/01.  
 DR  
 XX Identifying new catalytic nucleic acid that modulates selected  
 PT processes - especially ribozymes that cleave Raf RNA for treating  
 PT cancer, restenosis, and also new ribozymes and modified nucleoside  
 PT triphosphates used as antiviral agents and synthons  
 XX  
 PS Claim 179; Page 175; 259pp; English.  
 XX  
 XX A method has been developed for the identification of a nucleic acid  
 CC capable of modulating a process in a biological system. The method  
 CC comprises: (a) introducing into the system a random library of nucleic  
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
 CC in systems where modulation has occurred and/or determining the sequence  
 CC of at least part of the SBDs in such systems. Nucleic acid molecules  
 CC with endonuclease activity and catalytic activity, from the present  
 CC invention, are used to modulate gene expression in plant and mammalian  
 CC cells and to cleave target nucleic acid, particularly for treating  
 CC systemic diseases caused by specific RNA, e.g. cancer, inflammation,  
 CC psoriasis, non-hepatic ascites and infection. They may also be used to  
 CC detect genetic drift and mutations in diseased cells and to determine  
 CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate  
 CC expression of the Raf gene, are used to treat cancer, restenosis,  
 CC psoriasis or rheumatoid arthritis, or generally any condition associated  
 CC with the level of c-raf. Introduction of sugar/phosphate modifications  
 CC increases stability against nuclease and activity. AAV90922 to AAV93877  
 CC represent NACs that can be used in the method, specifically for  
 CC modulating the expression of a Raf gene.  
 XX  
 SQ Sequence 14 BP; 1 A; 5 C; 6 G; 2 U; 0 other;  
 Query Match 76.5%; Score 13; DB 20; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGGGCCAGCAGCT 13  
 Db 14 CGGGCCAGCAGCT 2  
 |||||  
 RESULT 10

AAZ65597  
 ID AAZ65597 standard; DNA; 17 BP.  
 XX  
 AC AAZ65597;  
 XX  
 DT 30-MAR-2000 (first entry)  
 XX  
 DE Immunosuppressant inhibitor oligonucleotide flt-rm-2115.  
 XX  
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGSE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; ss;  
 KW atherosclerosis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO963975-A2.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 10-JUN-1999; 99WO-EP04013.  
 XX  
 PR 10-JUN-1998; 98EP-0110709.  
 XX  
 PR 25-JUL-1998; 98EP-0113974.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;  
 XX  
 DR WPI; 2000-097470/08.  
 XX  
 PT Composition containing immune stimulant and inhibitor of agent that  
 PT adversely affects the immune response, for treating cancers and  
 PT infections.  
 XX  
 PS Claim 10; Figure 1; 30pp; English.  
 XX  
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which  
 CC is used in the invention. The invention relates to a composition which  
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
 CC transforming growth factor TGF-beta, vascular endothelial growth factor  
 CC VEGF, interleukin-10, prostaglandin E2, PGSE2, or their receptors)  
 CC that adversely affects the immune response. The composition also includes  
 CC at least one stimulant that positively affects the immune response. This  
 CC oligonucleotide is an example of an inhibitor that is used in the  
 CC composition. The composition is used as an immunostimulant for the  
 CC treatment of neoplasms and infections, particularly hyperproliferation;  
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as  
 CC anti-inflammatory for treating e.g. asthma, Crohn's disease, ulcerative  
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
 CC syndrome and the formation of atherosclerotic plaque.  
 XX  
 SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 other;  
 Query Match 70.6%; Score 12; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 CCAGCAGCTGAC 16  
 DB 1 CCAGCAGCTGAC 12

AAZ75542;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Mouse flt-1 VEGF receptor hairpin ribozyme substrate #1.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;  
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US17480.  
 XX  
 PR 11-JAN-1996; 96US-0584040.  
 PR 26-OCT-1995; 95US-0005974.  
 XX  
 PA (CHIR-) CHIRON CORP.  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;  
 XX  
 DR WPI; 1997-259017/23.  
 XX  
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or  
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,  
 PT psoriasis, rheumatoid arthritis, etc., in a human patient  
 XX  
 PS Claim 4; Page 184; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient of the  
 CC preferably human having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can  
 CC be treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention.  
 XX  
 SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 U; 0 other;  
 Query Match 70.6%; Score 12; DB 18; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 CCAGCAGCTGAC 16  
 DB 15 CCAGCAGCTGAC 4

RESULT 12  
 AAX75543/C  
 ID AAX75543 standard; RNA; 18 BP.  
 XX  
 AC AAX75543;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Mouse flt-1 VEGF receptor hairpin ribozyme substrate #2.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;  
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW

KW foetal liver kinase 1; ss.  
 XX Mus sp.  
 XX WO9715662-A2.  
 XX PD 01-MAY-1997.  
 XX PF 25-OCT-1996; 96WO-US17480.  
 XX PR 11-JAN-1996; 96US-0584040.  
 XX PR 26-OCT-1995; 95US-0005974.  
 XX PA (CHIR ) CHIRON CORP.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;  
 XX WPI; 1997-259017/23.  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or  
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,  
 PT psoriasis, rheumatoid arthritis, etc., in a human patient  
 XX Claim 4; Page 184; 218pp; English.  
 XX The present invention describes nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can  
 CC be treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention.  
 XX  
 XX Sequence 18 BP; 3 A; 6 C; 6 G; 3 U; 0 other;  
 Query Match 70.6%; Score 12; DB 18; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 CCAGCAGCTGAC 16  
 Db 12 CCAGCAGCTGAC 1  
 RESULT 13  
 AAZ38106/c  
 ID AAZ38106 standard; DNA; 21 BP.  
 AC AAZ38106;  
 XX 22-FEB-2000 (first entry)  
 DT Human FKHL7 gene specific reverse primer Fkh10-Rv.  
 DE  
 XX Forkhead transcription factor gene; FKHL7; treatment; glaucoma; human;  
 KW transgenic animal; drug screening; PCR primer; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9953060-A2.  
 PN 21-OCT-1999.  
 XX 14-APR-1999; 99WO-US08148.  
 PF 15-APR-1998; 98US-0081870.  
 XX 22-MAY-1998; 98US-0083352.  
 PR

PA (IOWA ) UNIV IOWA RES FOUND.  
 XX Sheffield VC, Alward WLM, Stone EM, Nishimura D, Patil S;  
 XX WPI; 1999-620429/53.  
 XX New isolated human forkhead transcription factor gene, FKHL7, used to,  
 PT e.g. develop products for the diagnosis -  
 XX Claim 31; Page 87; 99pp; English.  
 XX The invention provides a human forkhead transcription factor gene,  
 CC FKHL7. The FKHL7 protein can be produced by standard recombinant  
 CC methodology. The products can be used for diagnosis, prognosis,  
 CC monitoring, prevention and treatment of glaucoma. They can also be used  
 CC for the production of transgenic animals and drug screening. Sequences  
 CC AAZ38081-110 represent PCR primers specific for the human FKHL7 gene.  
 XX  
 XX Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 other;  
 Query Match 70.6%; Score 12; DB 20; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGGGCCAGCAGC 12  
 Db 12 CGGGCCAGCAGC 1  
 RESULT 14  
 AAZ31700/c  
 ID AAZ31700 standard; DNA; 21 BP.  
 AC AAZ31700;  
 XX 17-JAN-2000 (first entry)  
 DT Human FKHL7 gene PCR primer Fkh10-Rv.  
 DE  
 XX FKHL7; human; forkhead transcription factor gene; diagnosis; therapy;  
 KW congenital heart disease; PCR primer; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9952415-A2.  
 PN 21-OCT-1999.  
 XX 14-APR-1999; 99WO-US08159.  
 PF 15-APR-1998; 98US-0081870.  
 XX 22-MAY-1998; 98US-0083351.  
 PR (IOWA ) UNIV IOWA RES FOUND.  
 PA Sheffield VC, Alward WLM, Stone EM, Nishimura D, Patil S;  
 XX WPI; 1999-620257/53.  
 XX New isolated human forkhead transcription factor gene, FKHL7, used to  
 PT develop products for the diagnosis, prognosis, monitoring, prevention  
 PT or treatment of congenital heart disease -  
 XX Claim 31; Page 85; 98pp; English.  
 XX This sequence represents a PCR primer for DNA encoding the human forkhead  
 CC transcription factor gene, designated FKHL7, of the invention. FKHL7 can  
 CC be used in a novel method for treating or preventing the development of a  
 CC congenital heart disease (CHD) in a subject. The FKHL7 sequences can be  
 CC used for diagnosis, prognosis, monitoring, prevention and treatment of  
 CC CHD. They can also be used for the production of transgenic animals and  
 CC drug screening.

XX Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 other;  
SQ Query Match 70.6%; Score 12; DB 20; Length 21;  
Best Local Similarity 100.0%; Pred. NO. 3.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGGCCAGCAGC 12  
DB 12 CGGGCCAGCAGC 1

RESULT 15  
AAC69270/c  
ID AAC69270 standard; DNA; 22 BP.  
AC AAC69270;  
XX 29-JAN-2001 (first entry)  
DE Human ABC1 gene exon 2 fragment corrected sequence, SEQ ID NO:169.  
XX Human ABC1 cholesterol transporter; chromosome 9q31;  
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
KW cardiovascular disease; coronary artery disease; coronary restenosis;  
KW cerebrovascular disease; peripheral vascular disease;  
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
KW prognosis; prophylaxis; drug screening; transgenic animal; ds.  
XX Homo sapiens.  
XX WO200055318-A2.  
XX 21-SEP-2000.  
XX 15-MAR-2000; 2000WO-IB00532.  
XX 15-MAR-1999; 99US-0124702.  
XX 08-JUN-1999; 99US-0138048.  
XX 17-JUN-1999; 99US-0139600.  
XX 01-SEP-1999; 99US-0151977.  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX (XENO-) XENON BIORESEARCH INC.  
XX Hayden MR, Wilson AR, Pimstone SN;  
XX WPI; 2000-587528/55.  
XX New ABC1 polypeptide is useful for treating diseases associated with  
PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
PT disease and cancer -  
XX Example; Fig 11; 229pp; English.

XX The invention relates to the human ABC1 cholesterol transporter protein  
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
CC proteins, and plays a crucial role in cholesterol transport, particularly  
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
CC located on chromosome 9q31, and mutations in this gene are associated  
CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
CC are distinguishable in that TD is an autosomal recessive disorder, while  
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
CC cholesterol") in the blood correlate with a high risk of cardiovascular  
CC disease, particularly coronary artery disease, but also cerebrovascular  
CC disease, coronary restenosis, and peripheral vascular disease.  
CC Conversely, a high level of HDL has protective effects against  
CC cardiac/vascular disease. The invention provides genetic constructs and

CC transgenic cells and non-human animals comprising human ABC1 nucleic  
CC acids, and methods of gene therapy for the treatment or prevention of  
CC cardiovascular disease comprising the administration of an expression  
CC vector encoding ABC1 or an active fragment thereof. The invention also  
CC encompasses compounds which mimic ABC1 activity, compounds which  
CC stimulate ABC1 expression and methods of screening for such compounds.  
CC It further relates to methods for determining whether a patient has an  
CC increased risk for cardiovascular disease due to polymorphisms in the  
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
CC or prevent cardiovascular disease, especially coronary artery disease,  
CC cerebrovascular disease, coronary restenosis or peripheral vascular  
CC disease. They may also be used in the treatment of diseases associated  
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
CC The invention specifically excludes proteins with the exact amino acid  
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
CC acid with the exact sequence as GenBank Accession No: AJ012376.1.  
CC Sequences C69269-C69282 represent published and corrected versions  
CC of human ABC1 gene exon fragments.

XX Sequence 22 BP; 3 A; 4 C; 9 G; 6 T; 0 other;

Query Match 70.6%; Score 12; DB 21; Length 22;  
Best Local Similarity 100.0%; Pred. NO. 3.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17  
DB 12 CAGCAGCTGACA 1

Search completed: June 23, 2003, 05:43:42  
Job time : 114.28 secs

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OM nucleic - nucleic search, using SW model

Run on: June 24, 2003, 22:19:40 ; Search time 933.379 Seconds  
(Without alignments)  
296.308 Million cell updates/sec

Title: US-08-770-564A-11  
Perfect score: 11  
Sequence: 1 GCTCTAGAAATG 11

Scoring table: IDENTITY NJC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
Maximum DB seq length: 50

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Maximum Match 100%  
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13: /cgn2_6/ptodata/2/pna/US089_COMB.seq.*
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq.*
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq.*
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2	11	100.0	11	1 US-08-770-564A-11	Sequence 11, Appl
3	11	100.0	11	21 US-09-540-119B-11	Sequence 11, Appl
4	11	100.0	11	21 US-09-540-119B-12	Sequence 12, Appl
5	11	100.0	15	1 PCT-US97-23619-10	Sequence 10, Appl
6	11	100.0	15	11 US-08-770-564A-10	Sequence 10, Appl
7	11	100.0	18	13 US-08-974-549-543	Sequence 543, App
8	11	100.0	18	18 US-09-402-181B-543	Sequence 543, App
9	11	100.0	18	18 US-09-402-181B-543	Sequence 543, App
10	11	100.0	18	18 US-09-432-503-543	Sequence 543, App
11	11	100.0	18	29 US-09-721-477-543	Sequence 543, App
12	11	100.0	18	29 US-09-721-506-543	Sequence 543, App
13	11	100.0	19	1 PCT-US97-23619-9	Sequence 9, Appl
14	11	100.0	19	11 US-08-770-564A-9	Sequence 9, Appl
15	11	100.0	21	3 US-07-887-265A-13	Sequence 13, Appl
16	11	100.0	21	6 US-08-244-121-13	Sequence 13, Appl
17	11	100.0	21	37 US-09-997-868-13	Sequence 13, Appl
18	11	100.0	22	30 US-09-765-873A-5	Sequence 5, Appl
19	11	100.0	22	58 US-60-147-719-5	Sequence 5, Appl
20	11	100.0	23	36 US-09-952-522B-9	Sequence 9, Appl
21	11	100.0	23	36 US-09-952-522B-17	Sequence 17, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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22 11 100.0 23 36 US-09-952-522B-31 Sequence 31, Appl
23 11 100.0 24 31 US-09-807-809-5 Sequence 5, Appl
24 11 100.0 24 16 US-10-245-813-2 Sequence 2, Appl
25 11 100.0 25 42 US-09-250-336A-4 Sequence 4, Appl
26 11 100.0 25 35 US-09-642-177-4 Sequence 4, Appl
27 11 100.0 25 36 US-09-956-604-135337 Sequence 135337,
28 11 100.0 25 36 US-09-956-604A-135337 Sequence 135337,
29 11 100.0 25 36 US-09-956-604B-135337 Sequence 135337,
30 11 100.0 25 42 US-10-215-112-6862 Sequence 6862, A
31 11 100.0 25 67 US-60-233-620-66031 Sequence 66031, Ap
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39 11 100.0 26 1 PCT-US99-03302-4 Sequence 4, Appl
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41 11 100.0 26 1 PCT-US98-07533-4 Sequence 4, Appl
42 11 100.0 26 6 US-08-272-102-23 Sequence 23, Appl
43 11 100.0 26 7 US-08-387-524-19 Sequence 19, Appl
44 11 100.0 26 8 US-08-405-496-16 Sequence 16, Appl
45 11 100.0 26 8 US-08-422-711-16 Sequence 16, Appl

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## ALIGNMENTS

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RESULT 1
PCT-US97-23619-11
Sequence 11, Application PC/RUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Scorello, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

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LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: 11
LOCATION: 1..11
OTHER INFORMATION: /note="oligo 21ab2"
PCT-US97-23619-11

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Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTCTGAGATG 11
DB 1 GCTCTGAGATG 11

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RESULT 2
US-08-770-564A-11
Sequence 11, Application US/0870564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinlich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Scorello, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-11

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Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTCTGAGATG 11
DB 1 GCTCTGAGATG 11

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RESULT 3
US-09-540-119B-11

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; Sequence 11, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-11

Query Match      100.0%; Score 11; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATG 11
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Db      1 GCTCTAGATG 11

RESULT 4
US-09-540-119B-12
; Sequence 12, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-12

Query Match      100.0%; Score 11; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATG 11
      |||||
Db      1 GCTCTAGATG 11

RESULT 5
PCT-US97-23619-10
; Sequence 10, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..15
OTHER INFORMATION: /note="oligo 21ab3"
PCT-US97-23619-10

Query Match      100.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATG 11
      |||||
Db      1 GCTCTAGATG 11

RESULT 6
US-08-770-564A-10
; Sequence 10, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
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REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564A-10

Query Match 100.0%; Score 11; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 GCTCTAGATG 11

RESULT 7  
US-08-974-549-543  
Sequence 543, Application US/08974549  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 726  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTR molecule"  
US-08-974-549-543

Query Match 100.0%; Score 11; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTCTAGATG 11  
Db 1 GCTCTAGATG 11

RESULT 8  
US-09-402-181A-543  
Sequence 543, Application US/09402181A  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181A  
FILING DATE: 29-SEP-1997  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017

FILED DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausehus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTRT molecule"  
SEQUENCE DESCRIPTION: SEQ ID NO: 543:  
US-09-402-181A-543  
Query Match 100.0%; Score 11; DB 18; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGATG 11  
Db 1 GCTCTAGATG 11  
RESULT 9  
US-09-402-181B-543  
Sequence 543, Application US/09402181B  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausehus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTRT molecule"  
SEQUENCE DESCRIPTION: SEQ ID NO: 543:  
US-09-402-181B-543  
Query Match 100.0%; Score 11; DB 18; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGATG 11  
Db 1 GCTCTAGATG 11  
RESULT 10  
US-09-432-503-543  
Sequence 543, Application US/09432503  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTERT molecule"  
SEQUENCE DESCRIPTION: SEQ ID NO: 543:  
US-09-432-503-543  
Query Match 100.0%; Score 11; DB 18; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11  
RESULT 11  
US-09-721-477-543  
Sequence 543, Application US/09721477  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morth, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
CORRESPONDENCE ADDRESSES:  
NUMBER OF SEQUENCES: 727  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California

COUNTRY: USA  
ZIP: 94112-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,477  
FILING DATE: 22-Nov-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTERT molecule"  
SEQUENCE DESCRIPTION: SEQ ID NO: 543:  
US-09-721-477-543  
Query Match 100.0%; Score 11; DB 29; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11  
RESULT 12  
US-09-721-506-543  
Sequence 543, Application US/09721506  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morth, Gregg B.  
Harley, Calvin B.  
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/721,506  
FILING DATE: 22-Nov-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note= "antisense hTERT molecule"  
SEQUENCE DESCRIPTION: SEQ ID NO: 543:  
US-09-721-506-543

Query Match 100.0%; Score 11; DB 29; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
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Db 1 GCTCTAGATG 11

RESULT 13  
PCT-US97-23619-9  
; Sequence 9, Application PC/TUS9723619  
; GENERAL INFORMATION:

APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Scirella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..19  
OTHER INFORMATION: /note= "oligo 21ab"  
PCT-US97-23619-9

Query Match 100.0%; Score 11; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
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Db 1 GCTCTAGATG 11

RESULT 14  
US-08-770-564a-9  
; Sequence 9, Application US/08770564A  
; GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ron  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor

Fri Jun 27 07:41:11 2003

us-08-770-564a-11.rnqm

Page 8

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564A-9

Query Match 100.0%; Score 11; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 1 GCTCTAGATG 11

RESULT 15  
US-07-887-265A-13/c  
Sequence 13, Application US/07887265A  
GENERAL INFORMATION:  
APPLICANT: Gorman, Cornelia M.,  
APPLICANT: Mariotti, Dave,  
APPLICANT: Groskreutz, Debyra J  
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/887,265A  
FILING DATE: 19920522  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803631  
FILING DATE: 06-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Carolyn R.  
REGISTRATION NUMBER: 32,324  
REFERENCE/DOCKET NUMBER: 748P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-2614  
TELEFAX: 415/952-9881

TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-887-265A-13

Query Match 100.0%; Score 11; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 11 GCTCTAGATG 1

Search completed: June 25, 2003, 06:20:27  
Job time : 934.994 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 33.4382 Seconds  
(without alignments)  
482.732 Million cell updates/sec

Title: US-08-770-564a-11

Perfect score: 11  
Sequence: 1 GCTCTAGATG 11

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:

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5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	11	100.0	22	10	US-09-765-873A-5
3	11	100.0	23	9	US-09-952-522B-9
4	11	100.0	23	9	US-09-952-522B-17
5	11	100.0	23	9	US-09-952-522B-31
6	11	100.0	25	9	US-10-245-813-2
7	11	100.0	24	9	US-10-215-112-6862
8	11	100.0	26	9	US-10-011-366-16
9	11	100.0	26	9	US-10-118-495-11
10	11	100.0	26	9	US-10-118-495-13
11	11	100.0	26	9	US-09-952-522B-19
12	11	100.0	26	9	US-10-044-692-312
13	11	100.0	26	9	US-10-044-539-312
14	11	100.0	27	10	US-09-057-351-23
15	11	100.0	28	10	US-09-784-508-8
16	11	100.0	28	10	US-09-844-006A-3
17	11	100.0	29	9	US-10-162-223-2
18	11	100.0	34	10	US-09-784-508-10
19	11	100.0	36	9	US-10-166-183-14

C 20	11	100.0	36	9	US-10-127-816-18	Sequence 18, Appl
21	11	100.0	36	10	US-09-784-508-11	Sequence 11, Appl
22	10	90.9	21	8	US-08-913-322-3	Sequence 3, Appl
23	10	90.9	21	10	US-09-767-479-15	Sequence 15, Appl
24	10	90.9	22	9	US-09-981-648-11	Sequence 11, Appl
25	10	90.9	23	9	US-09-989-706-2	Sequence 2, Appl
26	10	90.9	23	9	US-10-071-485-49	Sequence 49, Appl
27	10	90.9	25	9	US-10-098-263B-8894	Sequence 8894, Ap
28	10	90.9	25	9	US-10-098-263B-44593	Sequence 44593, A
29	10	90.9	25	9	US-10-098-263B-44594	Sequence 44594, A
30	10	90.9	25	9	US-10-098-263B-80109	Sequence 80109, A
31	10	90.9	25	9	US-10-098-263B-80110	Sequence 80110, A
32	10	90.9	25	9	US-10-098-263B-104702	Sequence 104702,
33	10	90.9	26	10	US-09-954-695-10	Sequence 30, Appl
34	10	90.9	26	10	US-09-954-695-18	Sequence 34, Appl
35	10	90.9	26	10	US-09-954-695-18	Sequence 38, Appl
36	10	90.9	26	10	US-09-954-695-42	Sequence 42, Appl
37	10	90.9	26	10	US-09-954-695-42	Sequence 40, Appl
38	10	90.9	26	10	US-09-954-586-34	Sequence 34, Appl
39	10	90.9	26	10	US-09-954-586-34	Sequence 38, Appl
40	10	90.9	26	10	US-09-954-586-42	Sequence 42, Appl
41	10	90.9	29	9	US-10-117-846-27	Sequence 27, Appl
42	10	90.9	29	9	US-10-083-590-4	Sequence 4, Appl
43	10	90.9	30	9	US-09-987-021-13	Sequence 13, Appl
44	10	90.9	30	9	US-09-987-021-17	Sequence 17, Appl
45	10	90.9	30	10	US-09-957-485-13	Sequence 13, Appl

## ALIGNMENTS

RESULT 1  
US-09-997-868-13/c  
Sequence 13, Application US/09997868  
Publication No. US20030031654A1  
GENERAL INFORMATION:  
APPLICANT: Gorman, Cornelia M.,  
Groskreutz, Debrya J.  
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/997,868  
FILING DATE: 12-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/887265  
FILING DATE: 22-May-1992  
APPLICATION NUMBER: 07/803631  
FILING DATE: 06-Dec-1992  
APPLICATION NUMBER: PCT/US92/10621  
FILING DATE: 04-Dec-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P0748P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-997-668-13

Query Match 100.0%; Score 11; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 11 GCTCTAGATG 1

RESULT 2  
US-09-765-873A-5  
Sequence 5, Application US/09765873A  
Patent No. US20010053847A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Xiao-Song  
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID  
FILE REFERENCE: BCI009 US CIP  
CURRENT APPLICATION NUMBER: US/09/765,873A  
CURRENT FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: US 09/627,216  
PRIOR FILING DATE: 2000-07-27  
PRIOR APPLICATION NUMBER: US 60/147,719  
PRIOR FILING DATE: 1999-08-06  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Office 97  
SEQ ID NO: 5  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Primer  
US-09-765-873A-5

Query Match 100.0%; Score 11; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 3 GCTCTAGATG 13

RESULT 3  
US-09-952-522B-9  
Sequence 9, Application US/09952522B  
Publication No. US20030082152A1  
GENERAL INFORMATION:  
APPLICANT: Katz, Adam J.  
APPLICANT: Liull, Ramon  
APPLICANT: Futrell, J. William  
APPLICANT: Hedrick, Marc H.  
APPLICANT: Benham, Prosper  
APPLICANT: Lorenz, Hermann Peter  
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
FILE REFERENCE: 30448.77US11  
CURRENT APPLICATION NUMBER: US/09/952,522B  
CURRENT FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: PCT/US00/06232  
PRIOR FILING DATE: 2000-03-10  
PRIOR APPLICATION NUMBER: 60/123,711  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/162,462  
PRIOR FILING DATE: 1999-10-29  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 9  
LENGTH: 23

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: human  
OTHER INFORMATION: osteocalcin forward primer  
US-09-952-522B-9

Query Match 100.0%; Score 11; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 11 GCTCTAGATG 11

RESULT 4  
US-09-952-522B-17  
Sequence 17, Application US/09952522B  
Publication No. US20030082152A1  
GENERAL INFORMATION:  
APPLICANT: Katz, Adam J.  
APPLICANT: Liull, Ramon  
APPLICANT: Futrell, J. William  
APPLICANT: Hedrick, Marc H.  
APPLICANT: Benham, Prosper  
APPLICANT: Lorenz, Hermann Peter  
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
FILE REFERENCE: 30448.77US11  
CURRENT APPLICATION NUMBER: US/09/952,522B  
CURRENT FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: PCT/US00/06232  
PRIOR FILING DATE: 2000-03-10  
PRIOR APPLICATION NUMBER: 60/123,711  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/162,462  
PRIOR FILING DATE: 1999-10-29  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 17  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Osteopontin  
OTHER INFORMATION: forward primer  
US-09-952-522B-17

Query Match 100.0%; Score 11; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 11 GCTCTAGATG 11

RESULT 5  
US-09-952-522B-31  
Sequence 31, Application US/09952522B  
Publication No. US20030082152A1  
GENERAL INFORMATION:  
APPLICANT: Katz, Adam J.  
APPLICANT: Liull, Ramon  
APPLICANT: Futrell, J. William  
APPLICANT: Hedrick, Marc H.  
APPLICANT: Benham, Prosper  
APPLICANT: Lorenz, Hermann Peter  
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
FILE REFERENCE: 30448.77US11  
CURRENT APPLICATION NUMBER: US/09/952,522B



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; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1
; US-09-952-522B-31

Query Match      100.0%; Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
Db      1 GCTCTAGATG 11

RESULT 6
US-10-245-813-2
; Sequence 2, Application US/10245813
; Publication No. US20030060443A1
; GENERAL INFORMATION:
; APPLICANT: Gyun Min Lee
; APPLICANT: No. US20030060443A1Soo Kim
; TITLE OF INVENTION: INHIBITION OF APOPTOSIS BY THE
; TITLE OF INVENTION: EXPRESSION OF ANTISENSE RNA OF CASPASE-2
; FILE REFERENCE: 118.19-US-01
; CURRENT APPLICATION NUMBER: US/10/245,813
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 2001-57353
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: casp3L primer
; US-10-245-813-2

Query Match      100.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
Db      1 GCTCTAGATG 11

RESULT 7
US-10-215-112-6862/c
; Sequence 6862, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 6862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; US-10-215-112-6862

Query Match      100.0%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
Db      15 GCTCTAGATG 5

RESULT 8
US-10-011-366-16
; Sequence 16, Application US/10011366
; Publication No. US20030054493A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Kink, John A.
; TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
; OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
; DISEASE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,366
; FILING DATE: 16-NO. US20030054493A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,310
; FILING DATE: 23-OCT-1997
; APPLICATION NUMBER: US 08/329,154
; FILING DATE: 24-OCT-1994
; APPLICATION NUMBER: US 08/161,907
; FILING DATE: 02-DEC-1993
; APPLICATION NUMBER: US 07/985,321
; FILING DATE: 04-DEC-1992
; APPLICATION NUMBER: US 07/429,791
; FILING DATE: 31-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: OPD-01121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-011-366-16

Query Match      100.0%; Score 11; DB 9; Length 26;
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Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11

RESULT 9  
US-10-118-495-11  
; Sequence 11, Application US/10118495  
; Publication No. US20030074688A1  
; GENERAL INFORMATION:  
; APPLICANT: Benning, Christoph  
; APPLICANT: Riekhof, Wayne  
; APPLICANT: Klug, Rouven  
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids  
; FILE REFERENCE: MSU-06897  
; CURRENT APPLICATION NUMBER: US/10/118,495  
; CURRENT FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: 60/283,812  
; PRIOR FILING DATE: 2001-04-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-118-495-11

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11

RESULT 10  
US-10-118-495-13  
; Sequence 13, Application US/10118495  
; Publication No. US20030074688A1  
; GENERAL INFORMATION:  
; APPLICANT: Benning, Christoph  
; APPLICANT: Riekhof, Wayne  
; APPLICANT: Klug, Rouven  
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids  
; FILE REFERENCE: MSU-06897  
; CURRENT APPLICATION NUMBER: US/10/118,495  
; CURRENT FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: 60/283,812  
; PRIOR FILING DATE: 2001-04-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-118-495-13

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11

RESULT 11  
US-09-952-522B-19  
; Sequence 19, Application US/09952522B  
; Publication No. US20030082152A1  
; GENERAL INFORMATION:  
; APPLICANT: Katz, Adam J.  
; APPLICANT: Liull, Ramon  
; APPLICANT: Futrell, J. William  
; APPLICANT: Hedrick, Marc H.  
; APPLICANT: Benham, Prosper  
; APPLICANT: Lorenz, Hermann Peter  
; APPLICANT: Zhu, Min

; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
; FILE REFERENCE: 30448,77US11  
; CURRENT APPLICATION NUMBER: US/09/952,522B  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: PCT/US00/06232  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 60/123,711  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: 60/162,462  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Bone  
US-09-952-522B-19

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11

RESULT 12  
US-10-044-692-312  
; Sequence 312, Application US/10044692  
; Publication No. US20030096344A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/044,692  
; FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/912,951  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 312:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 312:  
US-10-044-539-312

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
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DB 5 GCTCTAGATG 15

RESULT 13  
US-10-044-539-312  
Sequence 312, Application US/10044539  
Publication No. US20030100093A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: HUMAN TETRAHYDRO CATALYTIC SUBUNIT: DIAGNOSTIC AND  
THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 335  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/044,539  
FILING DATE: 11-Jan-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 312:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 312:  
US-10-044-539-312

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
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DB 5 GCTCTAGATG 15

RESULT 14  
US-09-057-351-23  
Sequence 23, Application US/09057351  
Patent No. US20010034439A1  
GENERAL INFORMATION:  
APPLICANT: Vailleponteau, Bryant  
Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000821US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-057-351-23

Query Match 100.0%; Score 11; DB 10; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
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Db 5 GCTCTAGATG 15

RESULT 15  
US-09-784-508-8  
Sequence 8, Application US/09784508  
Patent No. US20020046417A1  
GENERAL INFORMATION:  
APPLICANT: Martin, Robert R.  
APPLICANT: Mathews, Helena  
APPLICANT: Keller, Karen  
APPLICANT: Kellogg, Jill A.  
APPLICANT: Wagner, Ry  
TITLE OF INVENTION: Development of Resistance to Raspberry  
FILE REFERENCE: 4257-0024.31  
CURRENT APPLICATION NUMBER: US/09/784,508  
CURRENT FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: US 09/737,719  
PRIOR FILING DATE: 2000-12-15  
PRIOR APPLICATION NUMBER: US 60/171,018  
PRIOR FILING DATE: 1999-01-25  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer  
US-09-784-508-8

Query Match 100.0%; Score 11; DB 10; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
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Db 2 GCTCTAGATG 12

Search completed: June 25, 2003, 22:25:08  
Job time : 34.4382 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 16.6972 Seconds  
(without alignments)  
202.036 Million cell updates/sec

Title: US-08-770-564A-11  
Perfect score: 11  
Sequence: 1 GCTCTAGATG 11

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15333831 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/prodata/2/ina/5A\_COMB.seq: \*  
4: /cgn2\_6/prodata/2/ina/5B\_COMB.seq: \*  
5: /cgn2\_6/prodata/2/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/prodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	2	US-08-770-565-11
2	11	100.0	15	2	US-08-770-565-10
3	11	100.0	18	4	US-08-974-549A-543
4	11	100.0	19	2	US-08-770-565-9
5	11	100.0	21	4	US-08-026-143B-13
6	11	100.0	21	5	PCT-US92-10621-13
7	11	100.0	21	5	PCT-US94-02233-13
8	11	100.0	22	4	US-09-627-216A-5
9	11	100.0	22	3	US-08-973-068-46
10	11	100.0	23	1	US-08-330-123A-23
11	11	100.0	26	1	US-08-480-604A-16
12	11	100.0	26	1	US-08-482-115B-23
13	11	100.0	26	2	US-08-660-678A-23
14	11	100.0	26	2	US-08-710-249-26
15	11	100.0	26	2	US-08-485-778-19
16	11	100.0	26	2	US-08-405-496A-16
17	11	100.0	26	2	US-08-472-802C-24
18	11	100.0	26	3	US-08-520-550A-19
19	11	100.0	26	3	US-08-598-443-23
20	11	100.0	26	4	US-08-574-549A-598
21	11	100.0	26	4	US-09-060-523-23
22	11	100.0	26	4	US-08-915-136-16
23	11	100.0	26	4	US-09-220-157A-26
24	11	100.0	26	4	US-09-386-959B-4
25	11	100.0	26	4	US-09-580-517-23
26	11	100.0	26	4	US-09-153-310-4
27	11	100.0	26	4	US-08-957-310-16

28	11	100.0	27	2	US-08-770-565-26	Sequence 26, Appl
29	11	100.0	27	3	US-08-630-172-24	Sequence 24, Appl
30	11	100.0	27	4	US-09-375-419-24	Sequence 24, Appl
31	11	100.0	30	2	US-08-770-565-8	Sequence 8, Appl
32	11	100.0	30	2	US-08-995-927-7	Sequence 7, Appl
33	11	100.0	30	4	US-09-349-627-5	Sequence 5, Appl
34	11	100.0	30	4	US-09-582-096-7	Sequence 7, Appl
35	11	100.0	33	3	US-08-630-172-22	Sequence 22, Appl
36	11	100.0	33	4	US-09-375-419-22	Sequence 22, Appl
37	11	100.0	37	3	US-08-815-190A-3	Sequence 3, Appl
38	11	100.0	39	4	US-09-091-305-3	Sequence 3, Appl
39	11	100.0	40	1	US-08-395-800A-12	Sequence 12, Appl
40	10	90.9	15	2	US-08-624-601-13	Sequence 13, Appl
41	10	90.9	16	4	US-08-687-580B-9	Sequence 9, Appl
42	10	90.9	20	4	US-08-964-722-7	Sequence 7, Appl
43	10	90.9	21	1	US-07-956-700B-114	Sequence 114, App
44	10	90.9	21	1	US-08-476-537-114	Sequence 114, App
45	10	90.9	21	1	US-08-485-607-114	Sequence 114, App

## ALIGNMENTS

RESULT 1  
US-08-770-565-11  
; Sequence 11, Application US/08770565  
; Patent No. 5846723  
GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: PC floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Scorella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-770-565-11  
Query Match 100.0%; Score 11; DB 2; Length 11;  
Best local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGATG 11

|||||  
Db 1 GCTCTAGATG 11

RESULT 2  
US-08-770-565-10  
Sequence 10, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinlich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 01589-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-10  
Query Match 100.0%; Score 11; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GCTCTAGATG 11

RESULT 3  
US-08-974-549A-543  
Sequence 543 Application US/08974549A  
Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTERT molecule"  
US-08-974-549A-543  
Query Match 100.0%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GCTCTAGATG 11

RESULT 4  
US-08-770-565-9  
; Sequence 9, Application US/08770565  
; Patent No. 5846723  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; TITLE OF INVENTION: Telomerase  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002300US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-565-9  
Query Match 100.0%; Score 11; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTTAGATG 11  
|||||  
Db 1 GCTTAGATG 11  
|||||  
RESULT 5  
US-08-026-143B-13/C  
; Sequence 13, Application US/08026143B  
; Patent No. 6348327  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Cornelia M.,  
; Goskreutz, Debya J.  
; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and  
; Polypeptide Synthesis  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/026,143B  
FILING DATE: 01-Mar-1993  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/887265  
FILING DATE: 22-MAY-1992  
APPLICATION NUMBER: 07/803631  
FILING DATE: 06-DEC-1992  
APPLICATION NUMBER: PCT/US92/10621  
FILING DATE: 04-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P0748P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-08-026-143B-13  
Query Match 100.0%; Score 11; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTTAGATG 11  
|||||  
Db 11 GCTTAGATG 1  
|||||  
RESULT 6  
PCT-US92-10621-13/C  
; Sequence 13, Application PC/TUS9210621  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Mariotte, Dave,  
; APPLICANT: Goskreutz, Debya J.  
; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10621  
FILING DATE: 19921204  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/887265  
FILING DATE: 22-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803631  
FILING DATE: 06-DEC-1992  
ATTORNEY/AGENT INFORMATION:

NAME: Adler, Carolyn R.  
REGISTRATION NUMBER: 32,324  
REFERENCE/DOCKET NUMBER: 748P2.PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-2614  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US92-10621-13

Query Match 100.0%; Score 11; DB 5; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11  
Db 11 GCTCTAGATG 1

RESULT 7  
PCT-US94-02233-13/c  
Sequence 13, Application PC/TUS9402233  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02233  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: 748P3PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US94-02233-13

Query Match 100.0%; Score 11; DB 5; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11  
Db 11 GCTCTAGATG 1

RESULT 8  
US-09-627-216A-5  
Sequence 5, Application US/09627216A  
Patent No. 6168837  
GENERAL INFORMATION:  
APPLICANT: Sarsisani, Sima F  
APPLICANT: Tang, Xiao-Song  
APPLICANT: Qi, Wei Wei  
APPLICANT: Vannelli, Todd  
APPLICANT: Gatenby, Anthony  
TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid  
FILE REFERENCE: BC1009 US NA  
CURRENT APPLICATION NUMBER: US/09/627,216A  
CURRENT FILING DATE: 2000-07-27  
PRIOR APPLICATION NUMBER: 60/147,719  
PRIOR FILING DATE: 1999-08-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Microsoft Office 97  
SEQ ID NO: 5  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-627-216A-5

Query Match 100.0%; Score 11; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11  
Db 3 GCTCTAGATG 13

RESULT 9  
US-08-973-068-46  
Sequence 46, Application US/08973068  
Patent No. 6127604  
GENERAL INFORMATION:  
APPLICANT: Dale, James Langham  
APPLICANT: Harding, Robert Maxwell  
APPLICANT: Dugdale, Benjamin  
APPLICANT: Beetham, Peter Ronald  
APPLICANT: Hafner, Gregory John  
APPLICANT: Becker, Douglas Kenneth  
TITLE OF INVENTION: INTERGENIC REGIONS OF BANANA BUNCHY TOP VIRUS  
FILE REFERENCE: 09657/002001  
CURRENT APPLICATION NUMBER: US/08/973,068  
CURRENT FILING DATE: 1998-03-12  
EARLIER APPLICATION NUMBER: PCT/AU96/00335  
EARLIER FILING DATE: 1996-05-31  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PasteSeq for Windows Version 3.0  
SEQ ID NO: 46  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Banana Bunchy Top Virus (BBTV)  
US-08-973-068-46

Query Match 100.0%; Score 11; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11  
Db 1 GCTCTAGATG 11

RESULT 10  
US-08-330-123A-23



Sequence 23, Application US/08330123A  
Patent No. 5583016  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/330,123A  
FILING DATE: 27-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000810  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-330-123A-23

Query Match 100.0%; Score 11; DB 1; Length 26;  
Best local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATG 11  
|||||  
DB 5 GCTCTAGAATG 15

RESULT 11  
US-08-480-604A-16  
Sequence 16, Application US/08480604A  
Patent No. 5736139  
GENERAL INFORMATION:  
APPLICANT: KIRK, JOHN A.  
APPLICANT: THALLEY, BRUCE S.  
APPLICANT: PADHYE, NISHA V.  
APPLICANT: FIRCA, JOSEPH R.  
APPLICANT: STAFORD, DOUGLAS C.  
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND  
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,604A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/422,711  
FILING DATE: 14-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/405,496  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/329,154  
FILING DATE: 25-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,907  
FILING DATE: 02-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/985,321  
FILING DATE: 04-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/429,791  
FILING DATE: 31-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: INGOLIA, DIANE E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: OPND-01763  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-480-604A-16

Query Match 100.0%; Score 11; DB 1; Length 26;  
Best local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATG 11  
|||||  
DB 1 GCTCTAGAATG 11

RESULT 12  
US-08-482-115B-23  
Sequence 23, Application US/08482115B  
Patent No. 5776679  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Assays for the RNA Component of Human  
TITLE OF INVENTION: Telomerase  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,115B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000830US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-482-115B-23

Query Match 100.0%; Score 11; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
Db 5 GCTCTAGATG 15

RESULT 13  
US-08-660-678A-23  
Sequence 23, Application US/08660678A  
Patent No. 5837857  
GENERAL INFORMATION:  
APPLICANT: Valleponneau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,678A  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.

REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000811US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-660-678A-23

Query Match 100.0%; Score 11; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
Db 5 GCTCTAGATG 15

RESULT 14  
US-08-710-249-26  
Sequence 26, Application US/08710249  
Patent No. 5858777  
GENERAL INFORMATION:  
APPLICANT: Valleponneau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Andrews, William H.  
APPLICANT: Adams, Robert R.  
TITLE OF INVENTION: Methods and Reagents for Regulating  
TITLE OF INVENTION: Telomere Length and Telomerase Activity  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,249  
FILING DATE: 13-SEP-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/583,808  
FILING DATE: 05-JAN-1996  
PRIOR APPLICATION NUMBER: US 60/003,492  
FILING DATE: 08-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001220US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-710-249-26

Job time : 17.6972 secs

Query Match 100.0%; Score 11; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
 |||||  
 Db 5 GCTCTAGATG 15

## RESULT 15

US-08-485-778-19  
 ; Sequence 19, Application US/08485778  
 ; Patent No. 5876979  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andrews, William H.  
 ; APPLICANT: Avillion, Ariel Athena  
 ; APPLICANT: Feng, Junli  
 ; APPLICANT: Funk, Walter  
 ; APPLICANT: Greider, Carol  
 ; APPLICANT: Marhuenda, Maria Antonia Biasco  
 ; APPLICANT: Villeponteau, Bryant  
 ; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE  
 ; NUMBER OF SEQUENCES: 45  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 ; STREET: Two Militia Drive  
 ; CITY: Lexington  
 ; STATE: MA  
 ; COUNTRY: US  
 ; ZIP: 02173  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/485,778  
 ; FILING DATE: 07-JE-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/387,524  
 ; FILING DATE: 13-FEB-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/330,123  
 ; FILING DATE: 27-OCT-1994  
 ; PRIOR APPLICATION DATA: US 08/272,102  
 ; FILING DATE: 07-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Granahan, Patricia  
 ; REGISTRATION NUMBER: 32,227  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-861-6240  
 ; TELEFAX: 617-861-9540  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 26 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-485-778-19

Query Match 100.0%; Score 11; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
 |||||  
 Db 5 GCTCTAGATG 15

Search completed: June 25, 2003, 00:24:40



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 567.135 Seconds  
(without alignments)  
314.123 Million cell updates/sec

Title: US-08-770-564A-11  
Perfect score: 11  
Sequence: 1 GCTCTAGAAATG 11

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: gb\_gse:\*  
18: em\_gse\_hum:\*  
19: em\_gse\_inv:\*  
20: em\_gse\_pln:\*  
21: em\_gse\_vrt:\*  
22: em\_gse\_fun:\*  
23: em\_gse\_mam:\*  
24: em\_gse\_mus:\*  
25: em\_gse\_other:\*  
26: em\_gse\_pro:\*  
27: em\_gse\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	10	90.9	19	17	AZ471573
C 2	10	90.9	34	10	AV964763
C 3	10	90.9	49	17	BH791685
C 4	9	81.8	27	17	BH812447
C 5	9	81.8	27	17	BH849811
C 6	9	81.8	27	17	TA349802P

Result No.	Score	Query Match	Length	DB ID	Description
C 7	9	81.8	30	9	AU257604
C 8	9	81.8	31	9	A1032592
C 9	9	81.8	36	17	A2812974
C 10	9	81.8	38	17	A2786040
C 11	9	81.8	40	12	B563012
C 12	9	81.8	41	9	AU258962
C 13	9	81.8	41	17	A2775318
C 14	9	81.8	42	12	B6732142
C 15	9	81.8	42	12	B6613445
C 16	9	81.8	43	17	BH624958
C 17	9	81.8	44	17	BH624958
C 18	9	81.8	46	17	A2812338
C 19	9	81.8	49	10	AM100845
C 20	9	81.8	50	9	AU103413
C 21	9	81.8	50	14	BM889496
C 22	9	81.8	50	17	A2478817
C 23	9	81.8	18	14	BQ790001
C 24	9	81.8	19	17	A2309082
C 25	9	81.8	19	17	A2659092
C 26	9	81.8	24	17	A2325427
C 27	9	81.8	25	9	A1763346
C 28	9	81.8	26	17	A2787926
C 29	9	81.8	26	17	BH791427
C 30	9	81.8	26	17	TA107C03P
C 31	9	81.8	28	9	A1006312
C 32	9	81.8	28	17	BH848015
C 33	9	81.8	28	17	BH848015
C 34	9	81.8	29	17	TA888080
C 35	9	81.8	30	17	A2588091
C 36	9	81.8	31	9	AA858849
C 37	9	81.8	31	14	R68337
C 38	9	81.8	33	17	A2806504
C 39	9	81.8	33	17	BH792618
C 40	9	81.8	34	9	AA921704
C 41	9	81.8	35	17	AA623189
C 42	9	81.8	36	13	B045071
C 43	9	81.8	36	17	A2430239
C 44	9	81.8	37	17	A2787295
C 45	9	81.8	38	14	R82106

#### ALIGNMENTS

RESULT 1  
LOCUS AZ471573 19 bp DNA  
DEFINITION IM0286G13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION AZ471573  
VERSION AZ471573.1 GI:10629698  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rilly,  
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00



BH812447  
 LOCUS BH812447 27 bp DNA linear GSS 02-MAY-2002  
 DEFINITION SALK\_061781 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_061781, DNA sequence.  
 ACCESSION BH812447  
 VERSION BH812447.1 GI:20390902  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 27)  
 Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab,C., Jeake,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
 A Sequence-indexed library of Insertion Mutations in the Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of TDNA.

FEATURES  
 source  
 Location/Qualifiers  
 1..27  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_061781"  
 /note="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT  
 12 a 3 c 5 g 7 t

Query Match 81.8%; Score 9; DB 17; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAT 10  
 |||||  
 18 CTCTAGAT 26

Db 18 CTCTAGAT 26

RESULT 5  
 BH849811 27 bp DNA linear GSS 13-JUN-2002  
 LOCUS SALK\_070310.38.90 x Arabidopsis thaliana TDNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_070310.38.90.x, DNA sequence.  
 ACCESSION BH849811  
 VERSION BH849811.1 GI:21420682  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 27)  
 Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab,C., Jeake,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
 A Sequence-indexed library of Insertion Mutations in the

Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of TDNA.

FEATURES  
 source  
 Location/Qualifiers  
 1..27  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_070310.38.90.x"  
 /note="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT  
 7 a 2 c 8 g 10 t

Query Match 81.8%; Score 9; DB 17; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAT 11  
 |||||  
 8 TCTAGAT 16

Db 8 TCTAGAT 16

RESULT 6  
 TA349B02P 27 bp DNA linear GSS 13-DEC-2000  
 LOCUS T. Brucei sheared genomic DNA clone 349B02, forward sequence.  
 DEFINITION T. Brucei sheared genomic DNA clone 349B02, forward sequence.  
 ACCESSION AL493641  
 VERSION AL493641.1 GI:11869420  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei.  
 ORGANISM Trypanosoma brucei.  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 1 (bases 1 to 27)  
 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
 Direct Submission  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhise@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + l method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds M. Vaudin and B. Barrell, Oxford University Press, 1999).  
 Email: nhise@sanger.ac.uk  
 Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
 Location/Qualifiers  
 1..27  
 /organism="Trypanosoma brucei"

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/strain="TREU927"
/db_xref="taxon:5691"
/clone="349b02"
BASE COUNT      4 a      10 c      8 g      5 t
ORIGIN

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Seq primer: CGTTGTAACGACGGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 36.  
 Location/Qualifiers

Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 38.  
 Location/Qualifiers

## FEATURES

## FEATURES

1..36  
 source

1..38  
 source

/organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0080101"  
 /clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"

/organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0030822"  
 /clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN

BASE COUNT  
 ORIGIN

Query Match 81.8%; Score 9; DB 17; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 81.8%; Score 9; DB 17; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAA 9  
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 Db 3 GCTCTAGAA 11

QY 1 GCTCTAGAA 9  
 |||||  
 Db 12 GCTCTAGAA 4

RESULT 10  
 A2786040 38 bp DNA linear GSS 16-FEB-2001  
 LOCUS A2786040/c  
 DEFINITION 2M0030822R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0030822 R, DNA sequence.

RESULT 11  
 BG563012 40 bp mRNA linear EST 10-APR-2001  
 LOCUS BG563012/c  
 DEFINITION 602581189F1 NIH-MGC\_76 Homo sapiens cDNA clone IMAGE:4708895 5',  
 mRNA sequence.

ACCESSION A2786040  
 VERSION A2786040.1 GI:12923402  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.

ACCESSION BG563012  
 VERSION BG563012  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 38)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 40)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.

AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLES Unpublished (1999)  
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaab@r-mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ULNL at:  
 http://image.llnl.gov

TITLE Plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0030 row: B column: 22

TITLE Plasmid inserts  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaab@r-mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ULNL at:  
 http://image.llnl.gov

High quality sequence stop: 36.  
 Location/Qualifiers

High quality sequence stop: 40.  
 Location/Qualifiers

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 /organism="Homo sapiens"

/db\_xref="taxon:9606"  
 /clone="IMAGE:4708895"  
 /clone\_lib="NIH MGC 76"  
 /lab\_host="DH10B (TI phase-resistant)"  
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:  
 SfiI (ggccgctcggcc); Site 2: SfiI (ggccattatggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.85  
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH MGC library."

BASE COUNT 6 a 8 c 9 g 17 t

Query Match 81.8%; Score 9; DB 12; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAAAT 10  
 |||||  
 Db 9 CTCTAGAAAT 1

RESULT 12 41 bp mRNA linear EST 25-APR-2002  
 AU258962 BED0014206 3', mRNA sequence.  
 LOCUS AU258962  
 DEFINITION

ACCESSION AU258962  
 VERSION AU258962.1 GI:20325030  
 KEYWORDS EST  
 SOURCE house mouse.  
 ORGANISM Mus musculus.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 41)  
 AUTHORS Kato, K. and Matoba, R.  
 TITLE Generation of expressed sequence tags from mouse brain  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kikuya Kato  
 Graduate School of Biological Sciences  
 Nara Institute of Science and Technology  
 8916-5 Takeyama, Ikoma, Nara 630-0101, Japan  
 Tel: 81-743-72-5581  
 Fax: 81-743-72-5589  
 Email: kkatob@is.aist-nara.ac.jp,  
 URL: http://love2.aist-nara.ac.jp/BED/index.html.  
 Location/Qualifiers

FEATURES  
 source 1..41  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="BED0014206"  
 /clone\_lib="3'-directed mouse cDNA library"  
 /cissue\_type="brain"  
 /note="Vector: pDNR-L-easy"

BASE COUNT 14 a 7 c 9 g 10 t 1 others

Query Match 81.8%; Score 9; DB 9; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAAAT 10  
 |||||  
 Db 4 CTCTAGAAAT 12

RESULT 13 41 bp DNA linear GSS 16-FEB-2001  
 AZ775318/c  
 LOCUS 7

DEFINITION 2M0007B12R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC2M0007B12 R, DNA sequence.

ACCESSION A2775318  
 VERSION A2775318.1 GI:12901677  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 41)  
 AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacons, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0007 row: B column: 12  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 41.  
 Location/Qualifiers

FEATURES  
 source 1..41  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC2M0007B12"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /note="Vector: pMD29; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/shares/). The DNA  
 was hydrotynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD29 (gil4732114[gb]/AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 10 a 11 c 11 g 9 t

Query Match 81.8%; Score 9; DB 17; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTAGAA 9  
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 Db 41 GCTTAGAA 33

RESULT 14 42 bp mRNA linear EST 30-MAY-2001  
 BF732142/c  
 LOCUS 8

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DEFINITION EST-NGR-1-20 mouse GR-1+ myeloid progenitor cells cDNA Library Mus
ACCESSION musculus cDNA 3', mRNA sequence.
VERSION BF732142
KEYWORDS BF732142.1 GI:14249762
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 42)
JOURNAL Pattern of gene expression in mouse GR-1+ myeloid progenitor cells
COMMENT Unpublished (2001)
Contact: Wang SM
Hem/Onc
University of Chicago Medical Center
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 773-702-6788
Fax: 773-702-3002
Email: swangl@midway.uchicago.edu
This EST fragment was amplified from mouse GR-1+ myeloid progenitor
cells cDNA library with GLGI technique (Generation of longer cDNA
fragments from SAGE tags for Gene Identification, Proc. Natl. Acad.
Sci. USA 97, 349, 2000), which starts from the 3' end till the last
CATG site of the target cDNA sequence.
Seq primer: M13 Forward.
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            /organism="Mus musculus"
            /strain="C57BL/6"
            /db_xref="taxon:10090"
            /clone_lib="mouse GR-1+ myeloid progenitor cells cDNA
            library"
            /sex="female"
            /tissue_type="bone marrow"
            /cell_type="GR-1+ myeloid progenitor cells"
            /note="cDNA was identified and isolated from Mus musculus
            benzo(a)pyrene-downregulated total RNA pool by
            differential display Polymerase Chain Reaction using
            indicated anchor and arbitrary primer (Hieroglyph mRNA
            Profile Kit 3, Genomix Corporation, Foster City, CA) and
            sequenced directly from PCR products."
BASE COUNT      4 a          7 c          6 g          25 t
ORIGIN
Query Match      81.8%; Score 9; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAA 9
        |||||
        28 GCTCTAGAA 20

Db

RESULT 15
BG613445/c      42 bp      mRNA      linear      EST 18-APR-2001
LOCUS          602641351F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4772341 5',
DEFINITION      mRNA sequence.
ACCESSION      BG613445
VERSION        BG613445
KEYWORDS      BG613445.1 GI:13664816
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE          NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

```

```

Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1642 row: e column: 14
High quality sequence stop: 29.
FEATURES
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="IMAGE:4772341"
            /clone_lib="NIH MGC 61"
            /tissue_type="embryonal carcinoma"
            /lab_host="DH10B (TI phase-resistant)"
            /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
            SfiI (ggcgccctcgcc); Site 2: SfiI (ggccattatggcc);
            Double-stranded cDNA was prepared from cell line RNA. 5'
            and 3' adaptors were used in cloning as follows: 5'
            adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dT(30)BN-3'
            (where B = A, C, or G and N = A, C, G, or T). Average
            insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
            contained inserts by PCR. This library was enriched for
            full-length clones and was constructed by Clontech
            Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
            library."
BASE COUNT      9 a          6 c          11 g          16 t
ORIGIN
Query Match      81.8%; Score 9; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTCTAGAA 10
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        10 CTCTAGAA 2

Db

Search completed: June 23, 2003, 10:10:29
Job time : 569.289 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 / Search time 482.861 Seconds  
(without alignments)  
158.668 Million cell updates/sec

Title: US-08-770-564a-11  
Perfect score: 11  
Sequence: 1 GCTTAGAATG 11

Scoring table: OLIGO NUC  
Gapop 60.0, Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database:

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2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq: \*  
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11: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq: \*  
12: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	18	US-09-721-456-543	Sequence 543, App
2	11	100.0	18	US-10-325-810-543	Sequence 543, App
3	11	100.0	21	PCT-US03-05708-27	Sequence 27, Appl
4	11	100.0	21	PCT-US03-05708-202	Sequence 202, App
5	11	100.0	21	PCT-US03-04088-539	Sequence 539, App
6	11	100.0	21	PCT-US03-04088-543	Sequence 543, App
7	11	100.0	21	PCT-US03-04088-547	Sequence 547, App
8	11	100.0	21	PCT-US03-04088-551	Sequence 551, App
9	11	100.0	21	PCT-US03-04088-555	Sequence 555, App
10	11	100.0	21	PCT-US03-04088-559	Sequence 559, App
11	11	100.0	21	US-10-374-366-27	Sequence 27, Appl
12	11	100.0	21	US-10-374-366-202	Sequence 202, App
13	11	100.0	22	US-10-188-5238-5	Sequence 5, Appl
14	11	100.0	22	US-10-188-5238-5	Sequence 5, Appl
15	11	100.0	23	PCT-US03-04088-520	Sequence 520, App
16	11	100.0	23	PCT-US03-04088-521	Sequence 521, App
17	11	100.0	23	US-10-310-188-36216	Sequence 36216, A
18	11	100.0	24	US-09-807-809A-5	Sequence 5, Appl
19	11	100.0	25	US-09-954-445A-66031	Sequence 66031, A
20	11	100.0	25	US-10-355-577-393144	Sequence 393144, A

21	11	100.0	25	US-10-355-577-396066	Sequence 396066, A
22	11	100.0	25	US-10-355-577-924166	Sequence 924166, A
23	11	100.0	25	US-60-427-808-6866	Sequence 6866, Ap
24	11	100.0	25	US-60-427-808-62369	Sequence 62369, A
25	11	100.0	25	US-60-427-808-104137	Sequence 104137, A
26	11	100.0	25	US-60-427-808-115885	Sequence 115885, A
27	11	100.0	25	US-60-427-808-137579	Sequence 137579, A
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34	11	100.0	25	US-60-427-808-681847	Sequence 681847, A
35	11	100.0	25	US-60-427-808-681848	Sequence 681848, A
36	11	100.0	25	US-60-427-808-887509	Sequence 887509, A
37	11	100.0	25	US-60-427-808-952738	Sequence 952738, A
38	11	100.0	25	US-60-427-836-248462	Sequence 248462, A
39	11	100.0	25	US-60-427-836-248463	Sequence 248463, A
40	11	100.0	25	US-60-427-836-280388	Sequence 280388, A
41	11	100.0	25	US-60-427-836-506901	Sequence 506901, A
42	11	100.0	25	US-60-427-836-612340	Sequence 612340, A
43	11	100.0	25	US-60-427-836-612342	Sequence 612342, A
44	11	100.0	26	PCT-US02-11134-11	Sequence 11, Appl
45	11	100.0	26	PCT-US02-11134-13	Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-09-721-456-543  
Sequence 543, Application US/09721456  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-Nov-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-Nov-1997  
APPLICATION NUMBER: US/08/724,643  
FILING DATE: 01-Oct-1996  
APPLICATION NUMBER: US/08/844,419  
FILING DATE: 18-Apr-1997  
APPLICATION NUMBER: US/08/846,017  
FILING DATE: 25-Apr-1997  
APPLICATION NUMBER: US/08/851,843  
FILING DATE: 06-May-1997  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-May-1997  
APPLICATION NUMBER: US/08/911,312

FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0200  
FILING DATE: 01-OCT-1997  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTdT molecule"  
SEQUENCE DESCRIPTION: SEQ ID NO: 543:  
US-09-721-456-543

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Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAGATG 11  
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DB 1 GCTCTGAGATG 11

RESULT 2  
US-10-325-810-543  
Sequence 543, Application US/10325810  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Hartley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/325,810  
FILING DATE: 20-Dec-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181  
FILING DATE: 29-Sep-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0200  
FILING DATE: 01-OCT-1997  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTdT molecule"  
SEQUENCE DESCRIPTION: SEQ ID NO: 543:  
US-10-325-810-543

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Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAGATG 11  
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DB 1 GCTCTGAGATG 11

RESULT 3  
PCT-US03-05708-27  
Sequence 27, Application PCT/TUS0305708  
GENERAL INFORMATION:  
APPLICANT: E.I. DuPont de Nemours and Company, Inc.  
TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS  
FILE REFERENCE: CL1794 PCT  
CURRENT APPLICATION NUMBER: PCT/US03/05708  
CURRENT FILING DATE: 2003-02-26  
PRIOR APPLICATION NUMBER: 60/360,279  
PRIOR FILING DATE: 2002-02-26  
NUMBER OF SEQ ID NOS: 203  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 27  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer 18-5'  
PCT-US03-05708-27

Query Match 100.0%; Score 11; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 GCTCTGAATG 13

RESULT 4  
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; Sequence 202, Application PC/TUS0305708  
; GENERAL INFORMATION:  
; APPLICANT: E.I. DuPont de Nemours and Company, Inc.  
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS  
; FILE REFERENCE: CL1794 PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/05708  
; PRIOR FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: 60/360,279  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 202  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Rhodospiridium glutinis  
PCT-US03-05708-202

Query Match 100.0%; Score 11; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAATG 11  
|||  
Db 3 GCTCTGAATG 13

RESULT 5  
PCT-US03-04088-539/c  
; Sequence 539, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: MGSwigen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 539  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE: Artificial  
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region  
; NAME/KEY: misc feature  
; LOCATION: (20)..(21)  
; OTHER INFORMATION: n stands for thymidine  
PCT-US03-04088-539

Query Match 100.0%; Score 11; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAATG 11  
|||  
Db 19 GCTCTGAATG 9

RESULT 6  
PCT-US03-04088-543  
; Sequence 543, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: MGSwigen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 543  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE: Artificial  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
; NAME/KEY: misc feature  
; LOCATION: (20)..(21)  
; OTHER INFORMATION: n stands for thymidine  
PCT-US03-04088-543

Query Match 100.0%; Score 11; DB 1; Length 21;  
Best Local Similarity 72.7%; Pred. No. 4.1e+03;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAATG 11  
|||  
Db 1 GCTCTGAATG 11

RESULT 7  
PCT-US03-04088-547/c  
; Sequence 547, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: MGSwigen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600

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1 PRIOR FILING DATE: 2002-07-17
2 PRIOR APPLICATION NUMBER: US 60/358,580
3 PRIOR FILING DATE: 2002-02-20
4 PRIOR APPLICATION NUMBER: US 60/363,124
5 PRIOR FILING DATE: 2002-03-11
6 PRIOR APPLICATION NUMBER: US 60/386,782
7 PRIOR FILING DATE: 2002-06-06
8 PRIOR APPLICATION NUMBER: US 60/406,784
9 PRIOR FILING DATE: 2002-08-29
10 PRIOR APPLICATION NUMBER: US 60/408,378
11 PRIOR FILING DATE: 2002-09-05
12 PRIOR APPLICATION NUMBER: US 60/409,293
13 PRIOR FILING DATE: 2002-09-09
14 PRIOR APPLICATION NUMBER: US 60/440,129
15 PRIOR FILING DATE: 2003-01-15
16 NUMBER OF SEQ ID NOS: 626
17 SOFTWARE: PatencIn version 3.2
18 SEQ ID NO 547
19 LENGTH: 21

```



```

1  TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
2  FILE REFERENCE: 02-708-A (400/080)
3  CURRENT APPLICATION NUMBER: PCT/US03/04088
4  PRIOR FILING DATE: 2003-04-28
5  PRIOR APPLICATION NUMBER: US 60/396,600
6  PRIOR FILING DATE: 2002-07-17
7  PRIOR APPLICATION NUMBER: US 60/358,580
8  PRIOR FILING DATE: 2002-02-20
9  PRIOR APPLICATION NUMBER: US 60/363,124
10 PRIOR FILING DATE: 2002-03-11
11 PRIOR APPLICATION NUMBER: US 60/386,782
12 PRIOR FILING DATE: 2002-06-06
13 PRIOR APPLICATION NUMBER: US 60/406,784
14 PRIOR FILING DATE: 2002-08-29
15 PRIOR APPLICATION NUMBER: US 60/408,378
16 PRIOR FILING DATE: 2002-09-05
17 PRIOR APPLICATION NUMBER: US 60/409,293
18 PRIOR FILING DATE: 2002-09-09
19 PRIOR APPLICATION NUMBER: US 60/440,129
20 PRIOR FILING DATE: 2003-01-15
21 NUMBER OF SEQ ID NOS: 626
22 SOFTWARE: PatentIn version 3.2
23 SEQ ID NO 555
24 LENGTH: 21
25 TYPE: RNA
26 ORGANISM: Artificial
27 FEATURE:
28 OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
29 FEATURE:
30 OTHER INFORMATION: region
31 NAME/KEY: misc_feature
32 LOCATION: (1)..(2)
33 OTHER INFORMATION: 2'-deoxy-2'-fluoro
34 FEATURE:
35 NAME/KEY: misc_feature
36 LOCATION: (1)..(1)
37 OTHER INFORMATION: 5'-3' attached terminal deoxyribose moiety
38 FEATURE:
39 NAME/KEY: misc_feature
40 LOCATION: (3)..(3)
41 OTHER INFORMATION: 2'-deoxy
42 FEATURE:
43 NAME/KEY: misc_feature
44 LOCATION: (4)..(5)
45 OTHER INFORMATION: 2'-deoxy-2'-fluoro
46 FEATURE:
47 NAME/KEY: misc_feature
48 LOCATION: (6)..(6)
49 OTHER INFORMATION: 2'-deoxy
50 FEATURE:
51 NAME/KEY: misc_feature
52 LOCATION: (7)..(9)
53 OTHER INFORMATION: 2'-deoxy-2'-fluoro
54 FEATURE:
55 NAME/KEY: misc_feature
56 LOCATION: (10)..(10)
57 OTHER INFORMATION: 2'-deoxy
58 FEATURE:
59 NAME/KEY: misc_feature
60 LOCATION: (11)..(14)
61 OTHER INFORMATION: 2'-deoxy-2'-fluoro
62 FEATURE:
63 NAME/KEY: misc_feature
64 LOCATION: (15)..(18)
65 OTHER INFORMATION: 2'-deoxy
66 FEATURE:
67 NAME/KEY: misc_feature
68 LOCATION: (19)..(19)
69 OTHER INFORMATION: 2'-deoxy-2'-fluoro
70 FEATURE:
71 NAME/KEY: misc_feature
72 LOCATION: (20)..(21)
73 OTHER INFORMATION: n stands for thymidine

```

```

: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (21)..(21)
: OTHER INFORMATION: 3'-3 attached terminal deoxybasic moiety
PCT-US03-04088-555

Query Match          100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4,1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
      |||||
Db      19 GCTCTAGATG 9

RESULT 10
PCT-US03-04088-555
: Sequence 559, Application PC/TUS0304088
: GENERAL INFORMATION:
: APPLICANT: Ribozyme Pharmaceuticals, Inc.
: APPLICANT: McSwiggen, James
: APPLICANT: Beigelman, Leonid
: TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
: FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
: CURRENT FILING DATE: 2003-04-28
: PRIOR APPLICATION NUMBER: US 60/396,600
: PRIOR FILING DATE: 2002-07-17
: PRIOR APPLICATION NUMBER: US 60/358,580
: PRIOR FILING DATE: 2002-02-20
: PRIOR APPLICATION NUMBER: US 60/363,124
: PRIOR FILING DATE: 2002-03-11
: PRIOR APPLICATION NUMBER: US 60/386,782
: PRIOR FILING DATE: 2002-06-06
: PRIOR APPLICATION NUMBER: US 60/406,784
: PRIOR FILING DATE: 2002-08-29
: PRIOR APPLICATION NUMBER: US 60/408,378
: PRIOR FILING DATE: 2002-09-05
: PRIOR APPLICATION NUMBER: US 60/409,293
: PRIOR FILING DATE: 2002-09-09
: PRIOR APPLICATION NUMBER: US 60/440,129
: PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
: SOFTWARE: PatentIn version 3.2
SEQ ID NO 559
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sRNA
OTHER INFORMATION: antisense region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc feature
LOCATION: (2)..(5)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (6)..(9)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10)..(10)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (11)..(13)
OTHER INFORMATION: 2'-deoxy
FEATURE:

```

```
NAME/KEY: misc_feature
LOCATION: (14)..(14)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(16)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(17)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-internucleotide linkage
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n strands for thymidine
PCT-US03-04088-559
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Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 72.7%; Pred. No. 4.1e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GCTCTAGATG 11
Db 1 GCCTAGATG 11
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RESULT 11
US-10-374-366-27
Sequence 27, Application US/10374366
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
APPLICANT: Milano, Joseph
TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
FILE REFERENCE: CL1794 US NA
CURRENT APPLICATION NUMBER: US/10/374,366
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: 60/360,279
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PatentIn version 3.2
SEQ ID NO 27
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer 18-5'
US-10-374-366-27
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Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GCTCTAGATG 11
Db 3 GCCTAGATG 13
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```
RESULT 12
US-10-374-366-202
Sequence 202, Application US/10374366
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
APPLICANT: Milano, Joseph
TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
FILE REFERENCE: CL1794 US NA
```

```
CURRENT APPLICATION NUMBER: US/10/374,366
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: 60/360,279
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PatentIn version 3.2
SEQ ID NO 202
LENGTH: 21
TYPE: DNA
ORGANISM: Rhodospiridium glutinis
US-10-374-366-202
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Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GCTCTAGATG 11
Db 3 GCCTAGATG 13
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RESULT 13
US-10-188-523B-5
Sequence 5, Application US/10188523B
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009 US DIVCIP
CURRENT APPLICATION NUMBER: US/10/188,523B
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-10-188-523B-5
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Query Match
Best Local Similarity 100.0%; Score 11; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GCTCTAGATG 11
Db 3 GCCTAGATG 13
```

```
RESULT 14
US-10-188-523C-5
Sequence 5, Application US/10188523C
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009-CIP
CURRENT APPLICATION NUMBER: US/10/188,523C
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: primer  
US-10-188-523C-5

Query Match 100.0%; Score 11; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

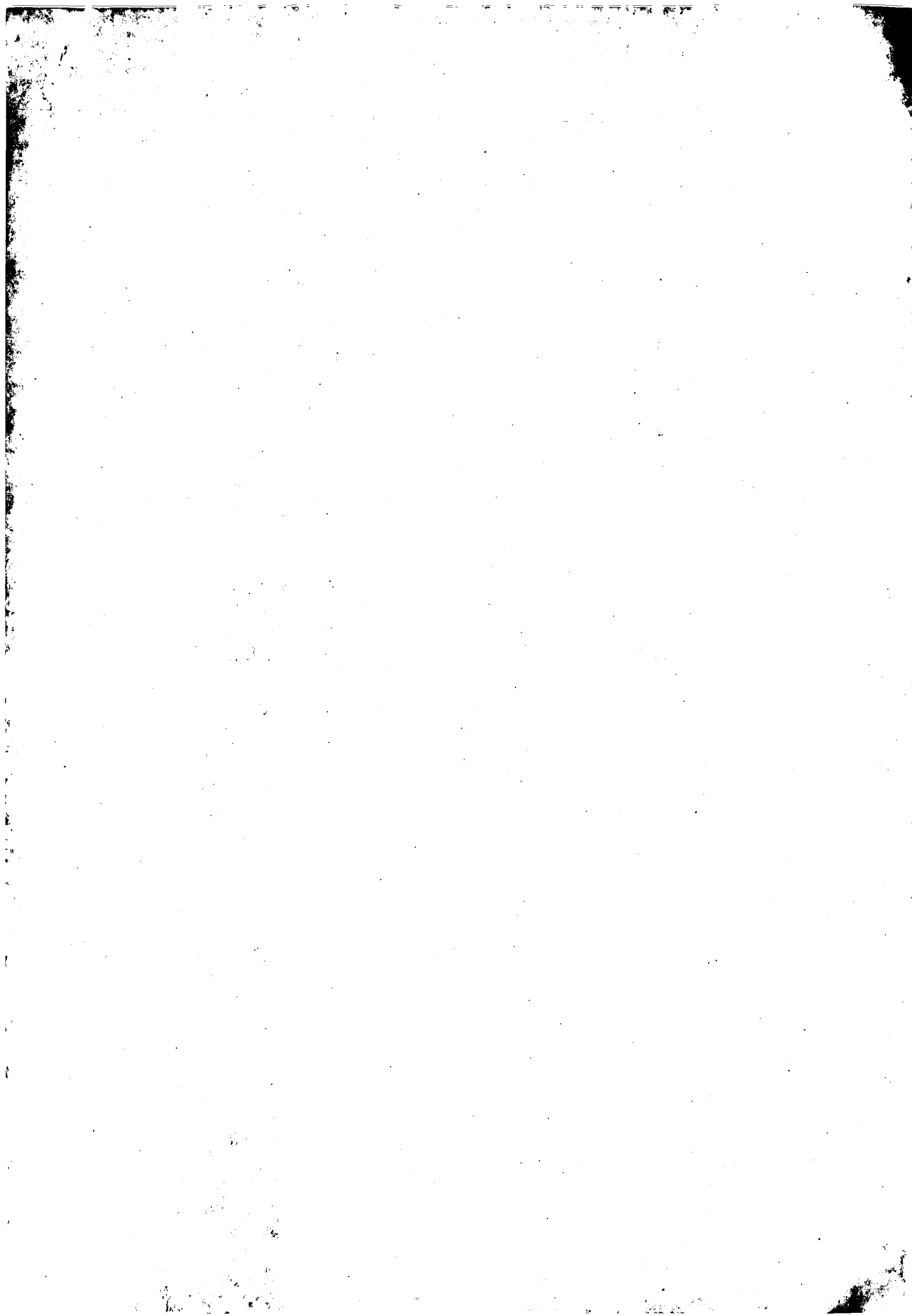
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Db 3 GCTCTAGAATG 13

RESULT 15  
PCT-US03-04088-520/c  
; Sequence 520, Application PC/TUS0304088  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene  
; FILE REFERENCE: 02-708-A (400/080)  
; CURRENT APPLICATION NUMBER: PCT/US03/04088  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/396,600  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 626  
; SOFTWARE: Patent version 3.2  
; SEQ ID NO 520  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
; PCT-US03-04088-520

Query Match 100.0%; Score 11; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATG 11  
|||  
Db 23 GCTCTAGAATG 13

Search completed: June 23, 2003, 19:12:13  
Job time: 483.861 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 922.598 Seconds  
(without alignments)  
299.770 Million cell updates/sec

Title: US-08-770-564A-11  
Perfect score: 11  
Sequence: 1 GCTCTGAAATG 11

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database :

Pending Patents\_NA\_Main:\*

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2: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq:\*  
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Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	PCT-US97-23619-11	Sequence 11, Appl
2	11	100.0	11	US-08-770-564A-11	Sequence 11, Appl
3	11	100.0	11	US-09-540-119B-11	Sequence 11, Appl
4	11	100.0	13	US-09-540-119B-12	Sequence 12, Appl
5	11	100.0	15	PCT-US97-23619-10	Sequence 10, Appl
6	11	100.0	15	US-08-770-564A-10	Sequence 10, Appl
7	11	100.0	18	US-08-974-549-543	Sequence 543, App
8	11	100.0	18	US-09-402-181A-543	Sequence 543, App
9	11	100.0	18	US-09-402-181B-543	Sequence 543, App
10	11	100.0	18	US-09-432-503-543	Sequence 543, App
11	11	100.0	18	US-09-721-477-543	Sequence 543, App
12	11	100.0	18	US-09-721-506-543	Sequence 543, App
13	11	100.0	19	PCT-US97-23619-9	Sequence 9, Appl
14	11	100.0	19	US-08-770-564A-9	Sequence 9, Appl
15	11	100.0	21	US-07-887-265A-13	Sequence 13, Appl
16	11	100.0	21	US-08-244-121-13	Sequence 13, Appl
17	11	100.0	21	US-09-997-868-13	Sequence 13, Appl
18	11	100.0	22	US-09-765-873A-5	Sequence 5, Appl
19	11	100.0	22	US-60-147-719-5	Sequence 5, Appl
20	11	100.0	23	US-09-952-522B-9	Sequence 9, Appl
21	11	100.0	23	US-09-952-522B-17	Sequence 17, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

22 11 100.0 23 36 US-09-952-522B-31 Sequence 31, Appl  
23 11 100.0 24 31 US-09-807-809-5 Sequence 5, Appl  
24 11 100.0 25 42 US-10-245-813-2 Sequence 2, Appl  
25 11 100.0 26 16 US-09-250-336A-4 Sequence 4, Appl  
26 11 100.0 27 25 US-09-642-177-4 Sequence 4, Appl  
27 11 100.0 28 36 US-09-956-604-135337 Sequence 135337  
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29 11 100.0 30 36 US-09-956-604-135337 Sequence 135337  
30 11 100.0 31 42 US-10-215-112-6862 Sequence 6862, Ap  
31 11 100.0 32 67 US-60-233-620-66031 Sequence 140656  
32 11 100.0 33 25 US-60-234-049-140656 Sequence 393144  
33 11 100.0 34 25 US-60-353-987-393144 Sequence 396066  
34 11 100.0 35 25 US-60-353-987-396066 Sequence 924166  
35 11 100.0 36 26 1 PCT-US96-14678A-27 Sequence 27, Appl  
36 11 100.0 37 26 1 PCT-US97-15394-16 Sequence 16, Appl  
37 11 100.0 38 26 1 PCT-US99-03302-4 Sequence 4, Appl  
38 11 100.0 39 26 1 PCT-US99-07533-4 Sequence 4, Appl  
39 11 100.0 40 26 1 PCT-US99-07533-4 Sequence 4, Appl  
40 11 100.0 41 26 1 PCT-US99-07533-4 Sequence 4, Appl  
41 11 100.0 42 26 6 US-08-272-102-23 Sequence 23, Appl  
42 11 100.0 43 26 7 US-08-387-524-19 Sequence 19, Appl  
43 11 100.0 44 26 8 US-08-405-496-16 Sequence 16, Appl  
44 11 100.0 45 26 8 US-08-422-711-16 Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
PCT-US97-23619-11  
Sequence 11, Application PC/TUS9723619  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
TITLE OF INVENTION: RNA Component of Telomerase  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:

LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: DNA  
FEATURE:  
NAME/KEY:  
LOCATION: 1..11  
OTHER INFORMATION: /note="oliigo 21ab2"  
PCT-US97-23619-11  
Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
US-08-770-564A-11  
Sequence 11, Application US/08770564A  
GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ron  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0300  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: DNA  
US-08-770-564A-11  
Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 11, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-11

Query Match      100.0%; Score 11; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
Db      1 GCTCTAGATG 11

RESULT 4
US-09-540-119B-12
; Sequence 12, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-12

Query Match      100.0%; Score 11; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
Db      1 GCTCTAGATG 11

RESULT 5
PCT-US97-23619-10
; Sequence 10, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
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; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..15
; OTHER INFORMATION: /note="Oligo 21ab3"
PCT-US97-23619-10

Query Match      100.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
Db      1 GCTCTAGATG 11

RESULT 6
US-08-770-564A-10
; Sequence 10, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
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REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564a-10

Query Match 100.0%; Score 11; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11

RESULT 7  
US-08-974-549-543  
Sequence 543, Application US/08974549  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 726  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTR molecule"  
US-08-974-549-543

Query Match 100.0%; Score 11; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11

RESULT 8  
US-09-402-181A-543  
Sequence 543, Application US/09402181A  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181A  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017



FILED DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausehus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTRT molecule"  
SEQUENCE DESCRIPTION: SEQ ID NO: 543:  
US-09-402-181A-543

Query Match 100.0%; Score 11; DB 18; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11

RESULT 9  
US-09-402-181B-543  
; Sequence 543, Application US/09402181B  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 633  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/402,181B  
; FILING DATE: 29-Sep-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausehus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTRT molecule"  
SEQUENCE DESCRIPTION: SEQ ID NO: 543:  
US-09-402-181B-543

Query Match 100.0%; Score 11; DB 18; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11

RESULT 10  
US-09-432-503-543  
; Sequence 543, Application US/09432503  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30

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Page 6

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /notes "antisense hTRT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-432-503-543
Query Match 100.0%; Score 11; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11
RESULT 11
US-09-721-477-543
Sequence 543, Application US/09721477
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.;
Lingner, Joachim;
Nakamura, Toru;
Chapman, Karen B.;
Morin, Gregg B.;
Harley, Calvin B.;
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
```

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COUNTRY: USA
ZIP: 94111-3634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,477
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /notes "antisense hTRT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-721-477-543
Query Match 100.0%; Score 11; DB 29; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11
RESULT 12
US-09-721-506-543
Sequence 543, Application US/09721506
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.;
Lingner, Joachim;
Nakamura, Toru;
Chapman, Karen B.;
Morin, Gregg B.;
Harley, Calvin B.;
Andrews, William H.
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TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,506  
FILING DATE: 22-Nov-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17865  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTERT molecule"  
US-09-721-506-543

Query Match 100.0%; Score 11; DB 29; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
|||||  
Db 1 GCTCTAGATG 11

RESULT 13  
PCT-US97-23619-9  
; Sequence 9, Application PC/TUS9723619  
; GENERAL INFORMATION:

APPLICANT:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: Methods for Detecting and Inhibiting the  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/23619  
FILING DATE: Not yet assigned  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,564  
FILING DATE: 20-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,565  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15389-27PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..19  
OTHER INFORMATION: /note="oligo 21ab"  
PCT-US97-23619-9

Query Match 100.0%; Score 11; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
|||||  
Db 1 GCTCTAGATG 11

RESULT 14  
US-08-770-564a-9  
; Sequence 9, Application US/08770564a  
; GENERAL INFORMATION:  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ron  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Inhibitory Polynucleotides Directed  
TITLE OF INVENTION: Against the RNA Component of Telomerase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor

Fri Jun 27 07:41:06 2003

us-08-770-564a-11.01lgo.rnpn

Page 8

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,564A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002200US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-564A-9

Query Match 100.0%; Score 11; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
DB 1 GCTCTAGATG 11

RESULT 15  
US-07-887-265A-13/C  
Sequence 13, Application US/07887265A  
GENERAL INFORMATION:  
APPLICANT: Gorman, Cornelia M.,  
APPLICANT: Maxiolet, Dave,  
APPLICANT: Groskreutz, Debyra J  
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/887,265A  
FILING DATE: 19920522  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803631  
FILING DATE: 06-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Carolyn R.  
REGISTRATION NUMBER: 32,324  
REFERENCE/DOCKET NUMBER: 748P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-2614  
TELEFAX: 415/952-9861

TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-887-265A-13

Query Match 100.0%; Score 11; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
DB 11 GCTCTAGATG 1

Search completed: June 23, 2003, 16:08:22  
Job time : 923.675 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 88.3944 Seconds  
(without alignments)  
182.610 Million cell updates/sec

Title: US-08-770-564a-11

Perfect score: 11

Sequence: 1 GCTTACGATG 11

Scoring table: OLIGO NUC  
Gapex 60.0, Gapex 60.0

Searched: 1042519 seqs, 733713590 residues

Word size: 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database: Published Applications NA.\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US05\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	100.0	21	9	US-09-997-868-13
2	11	100.0	22	10	US-09-765-873A-5
3	11	100.0	23	9	US-09-952-522B-9
4	11	100.0	23	9	US-09-952-522B-17
5	11	100.0	23	9	US-09-952-522B-31
6	11	100.0	24	9	US-10-245-813-2
7	11	100.0	25	9	US-10-215-112-6862
8	11	100.0	26	9	US-10-011-366-16
9	11	100.0	26	9	US-10-118-495-11
10	11	100.0	26	9	US-10-118-495-13
11	11	100.0	26	9	US-09-952-522B-19
12	11	100.0	26	9	US-10-044-539-312
13	11	100.0	26	10	US-09-057-351-23
14	11	100.0	27	10	US-09-784-508-8
15	11	100.0	28	10	US-09-844-006A-3
16	11	100.0	29	9	US-10-162-223-2
17	11	100.0	34	10	US-09-784-508-10
18	11	100.0	36	9	US-10-166-183-14
19	11	100.0			

Result No.	Score	Query Match	Length	ID	Description
C 20	11	100.0	36	9	US-10-127-816-18
21	11	100.0	36	10	US-09-784-508-11
22	10	90.9	21	8	US-08-913-322-3
23	10	90.9	21	10	US-09-767-479-15
24	10	90.9	22	9	US-09-981-648-11
25	10	90.9	23	9	US-09-989-706-2
26	10	90.9	23	9	US-10-071-485-49
27	10	90.9	25	9	US-10-098-263B-8894
28	10	90.9	25	9	US-10-098-263B-44593
29	10	90.9	25	9	US-10-098-263B-44594
30	10	90.9	25	9	US-10-098-263B-80109
31	10	90.9	25	9	US-10-098-263B-80110
32	10	90.9	26	10	US-09-954-695-10
33	10	90.9	26	10	US-09-954-695-14
34	10	90.9	26	10	US-09-954-695-18
35	10	90.9	26	10	US-09-954-695-38
36	10	90.9	26	10	US-09-954-695-42
37	10	90.9	26	10	US-09-954-586-10
38	10	90.9	26	10	US-09-954-586-14
39	10	90.9	26	10	US-09-954-586-18
40	10	90.9	26	10	US-09-954-586-42
41	10	90.9	29	9	US-10-117-846-27
42	10	90.9	29	9	US-10-083-590-4
43	10	90.9	30	9	US-09-987-021-13
44	10	90.9	30	9	US-09-987-021-17
45	10	90.9	30	10	US-09-957-485-13

## ALIGNMENTS

RESULT 1  
US-09-997-868-13/c  
Sequence 13, Application US/09997868  
Publication No. US20030031654A1  
GENERAL INFORMATION:  
APPLICANT: Gorman, Cornelia M.,  
Groskreutz, Debrya J.  
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/997,868  
FILING DATE: 12-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/887265  
FILING DATE: 22-May-1992  
APPLICATION NUMBER: 07/803631  
FILING DATE: 06-Dec-1992  
APPLICATION NUMBER: PCT/US92/10621  
FILING DATE: 04-Dec-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P0748P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-997-868-13

Query Match 100.0%; Score 11; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 11 GCTCTAGATG 1

## RESULT 2

US-09-765-873A-5  
Sequence 5, Application US/09765873A  
Patent No. US20010053847A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Xiao-Song  
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID  
FILE REFERENCE: BC1009 US CIP  
CURRENT APPLICATION NUMBER: US/09/765,873A  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: US 09/627,216  
PRIOR FILING DATE: 2000-07-27  
PRIOR APPLICATION NUMBER: US 60/147,719  
PRIOR FILING DATE: 1999-08-06  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 5  
LENGTH: 22  
TYPE: DNA  
ORGANISM: primer  
US-09-765-873A-5

Query Match 100.0%; Score 11; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 3 GCTCTAGATG 13

## RESULT 3

US-09-952-522B-9  
Sequence 9, Application US/09952522B  
Publication No. US20030082152A1  
GENERAL INFORMATION:  
APPLICANT: Katz, Adam J.  
APPLICANT: Lull, Ramon  
APPLICANT: Futrell, J. William  
APPLICANT: Hedrick, Marc H.  
APPLICANT: Benham, Prosper  
APPLICANT: Lorenz, Hermann Peter  
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
FILE REFERENCE: 30448, 77US11  
CURRENT APPLICATION NUMBER: US/09/952,522B  
PRIOR FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: PCT/US00/06232  
PRIOR FILING DATE: 2000-03-10  
PRIOR APPLICATION NUMBER: 60/123,711  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/162,462  
PRIOR FILING DATE: 1999-10-29  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 9  
LENGTH: 23

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: human  
OTHER INFORMATION: osteocalcin forward primer  
US-09-952-522B-9

Query Match 100.0%; Score 11; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 1 GCTCTAGATG 11

## RESULT 4

US-09-952-522B-17  
Sequence 17, Application US/09952522B  
Publication No. US20030082152A1  
GENERAL INFORMATION:  
APPLICANT: Katz, Adam J.  
APPLICANT: Lull, Ramon  
APPLICANT: Futrell, J. William  
APPLICANT: Hedrick, Marc H.  
APPLICANT: Benham, Prosper  
APPLICANT: Lorenz, Hermann Peter  
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
FILE REFERENCE: 30448, 77US11  
CURRENT APPLICATION NUMBER: US/09/952,522B  
PRIOR FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: PCT/US00/06232  
PRIOR FILING DATE: 2000-03-10  
PRIOR APPLICATION NUMBER: 60/123,711  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/162,462  
PRIOR FILING DATE: 1999-10-29  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 17  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Osteopontin  
OTHER INFORMATION: forward primer  
US-09-952-522B-17

Query Match 100.0%; Score 11; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
Db 1 GCTCTAGATG 11

## RESULT 5

US-09-952-522B-31  
Sequence 31, Application US/09952522B  
Publication No. US20030082152A1  
GENERAL INFORMATION:  
APPLICANT: Katz, Adam J.  
APPLICANT: Lull, Ramon  
APPLICANT: Futrell, J. William  
APPLICANT: Hedrick, Marc H.  
APPLICANT: Benham, Prosper  
APPLICANT: Lorenz, Hermann Peter  
APPLICANT: Zhu, Min  
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
FILE REFERENCE: 30448, 77US11  
CURRENT APPLICATION NUMBER: US/09/952,522B

;; CURRENT FILING DATE: 2001-09-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/06232  
;; PRIOR FILING DATE: 2000-03-10  
;; PRIOR APPLICATION NUMBER: 60/123,711  
;; PRIOR FILING DATE: 1999-03-10  
;; PRIOR APPLICATION NUMBER: 60/162,462  
;; PRIOR FILING DATE: 1999-10-29  
;; NUMBER OF SEQ ID NOS: 58  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 31  
;; LENGTH: 23  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1  
US-09-952-522B-31

Query Match 100.0%; Score 11; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
Db 1 GCTCTAGATG 11

RESULT 6  
US-10-245-813-2  
;; Sequence 2, Application US/10245813  
;; Publication No. US20030060443A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gyun Min Lee  
;; TITLE OF INVENTION: INHIBITION OF APOPTOSIS BY THE  
;; FILE REFERENCE: 118.19-US-01  
;; CURRENT APPLICATION NUMBER: US/10/245,813  
;; CURRENT FILING DATE: 2002-09-17  
;; PRIOR APPLICATION NUMBER: 2001-57353  
;; PRIOR FILING DATE: 2001-09-17  
;; NUMBER OF SEQ ID NOS: 5  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 24  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: casp3L primer  
US-10-245-813-2

Query Match 100.0%; Score 11; DB 9; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
Db 1 GCTCTAGATG 11

RESULT 7  
US-10-215-112-6862/c  
;; Sequence 6862, Application US/10215112  
;; Publication No. US20030082596A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Michael Wittmann  
;; TITLE OF INVENTION: Method of Genetic Analysis of Probes:  
;; FILE REFERENCE: 3119  
;; CURRENT APPLICATION NUMBER: US/10/215,112  
;; CURRENT FILING DATE: 2002-08-08  
;; NUMBER OF SEQ ID NOS: 14936  
;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 6862  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-215-112-6862

Query Match 100.0%; Score 11; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
Db 15 GCTCTAGATG 5

RESULT 8  
US-10-011-366-16  
;; Sequence 16, Application US/10011366  
;; Publication No. US20030054493A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Williams, James A.  
;; TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES  
;; OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE  
DISEASE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Medlen & Carroll  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/011,366  
FILING DATE: 16-NO. US20030054493A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/957,310  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 08/329,154  
FILING DATE: 24-OCT-1994  
APPLICATION NUMBER: US 08/161,907  
FILING DATE: 02-DEC-1993  
APPLICATION NUMBER: US 07/985,321  
FILING DATE: 04-DEC-1992  
APPLICATION NUMBER: US 07/429,791  
FILING DATE: 31-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: OPND-01121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-011-366-16  
Query Match 100.0%; Score 11; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
|||||  
DB 1 GCTCTAGATG 11

RESULT 9  
US-10-118-495-11

/ Sequence 11, Application US/10118495  
/ Publication No. US20030074688A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Benning, Christoph  
/ APPLICANT: Riekhof, Wayne  
/ APPLICANT: Kling, Rouven  
/ TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids  
/ FILE REFERENCE: MSU-06897  
/ CURRENT APPLICATION NUMBER: US/10/118,495  
/ CURRENT FILING DATE: 2002-04-08  
/ PRIOR APPLICATION NUMBER: 60/283,812  
/ PRIOR FILING DATE: 2001-04-13  
/ NUMBER OF SEQ ID NOS: 42  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 11  
/ LENGTH: 26  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic  
US-10-118-495-11

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
|||||  
DB 1 GCTCTAGATG 11

RESULT 10  
US-10-118-495-13

/ Sequence 13, Application US/10118495  
/ Publication No. US20030074688A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Benning, Christoph  
/ APPLICANT: Riekhof, Wayne  
/ APPLICANT: Kling, Rouven  
/ TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids  
/ FILE REFERENCE: MSU-06897  
/ CURRENT APPLICATION NUMBER: US/10/118,495  
/ CURRENT FILING DATE: 2002-04-08  
/ PRIOR APPLICATION NUMBER: 60/283,812  
/ PRIOR FILING DATE: 2001-04-13  
/ NUMBER OF SEQ ID NOS: 42  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 13  
/ LENGTH: 26  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic  
US-10-118-495-13

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
|||||  
DB 1 GCTCTAGATG 11

RESULT 11  
US-09-952-522B-19

/ Sequence 19, Application US/09952522B  
/ Publication No. US20030082152A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Katz, Adam J.  
/ APPLICANT: Lluil, Ramon  
/ APPLICANT: Furell, J. William  
/ APPLICANT: Hedrick, Marc H.  
/ APPLICANT: Benham, Prosper  
/ APPLICANT: Lorenz, Hermann Peter  
/ APPLICANT: Zhu, Min  
/ TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES  
/ FILE REFERENCE: 30448.77US11  
/ CURRENT APPLICATION NUMBER: US/09/952,522B  
/ CURRENT FILING DATE: 2001-09-10  
/ PRIOR APPLICATION NUMBER: PCT/US00/06232  
/ PRIOR FILING DATE: 2000-03-10  
/ PRIOR APPLICATION NUMBER: 60/123,711  
/ PRIOR FILING DATE: 1999-03-10  
/ PRIOR APPLICATION NUMBER: 60/162,462  
/ PRIOR FILING DATE: 1999-10-29  
/ NUMBER OF SEQ ID NOS: 58  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 19  
/ LENGTH: 26  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Bone  
US-09-952-522B-19

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
|||||  
DB 1 GCTCTAGATG 11

RESULT 12  
US-10-044-692-312

/ Sequence 312, Application US/10044692  
/ Publication No. US20030096344A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ APPLICANT: Lingner, Joachim  
/ APPLICANT: Nakamura, Toru  
/ APPLICANT: Chapman, Karen B.  
/ APPLICANT: Morin, Gregg B.  
/ APPLICANT: Harley, Calvin  
/ APPLICANT: Andrews, William H.  
/ TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS  
/ NUMBER OF SEQUENCES: 335  
/ CORRESPONDENCE ADDRESSES:  
/ ADDRESSEE: Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/10/044,692  
/ FILING DATE: 11-Jan-2002



CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/912,951  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 312:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 312:  
US-10-044-692-312

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
DB 5 GCTCTAGATG 15

RESULT 13  
US-10-044-539-312  
Sequence 312, Application US/10044539  
Publication No. US2003010093A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 335  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/044,539  
FILING DATE: 11-Jan-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 312:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 312:  
US-10-044-539-312

Query Match 100.0%; Score 11; DB 9; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
DB 5 GCTCTAGATG 15

RESULT 14  
US-09-057-351-23  
Sequence 23, Application US/09057351  
Patent No. US20010034439A1  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
Feng, Junli  
APPLICANT: Funk, Walter  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995

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Page 6

ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000821US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-057-351-23

Query Match 100.0%; Score 11; DB 10; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTAGATG 11  
|||  
Db 5 GCTTAGATG 15

RESULT 15  
US-09-784-508-8  
Sequence 8, Application US/09784508  
Patent No. US20020046417A1  
GENERAL INFORMATION:  
APPLICANT: Martin, Robert R.  
APPLICANT: Mathews, Helena  
APPLICANT: Keller, Karen  
APPLICANT: Kellogg, Jill A.  
APPLICANT: Wagner, Ry  
TITLE OF INVENTION: Development of Resistance to Raspberry  
FILE REFERENCE: 4257-0024.31  
CURRENT APPLICATION NUMBER: US/09/784,508  
CURRENT FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: US 09/737,719  
PRIOR FILING DATE: 2000-12-15  
PRIOR APPLICATION NUMBER: US 60/171,018  
PRIOR FILING DATE: 1999-01-25  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer  
US-09-784-508-8

Query Match 100.0%; Score 11; DB 10; Length 27;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTAGATG 11  
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Db 2 GCTTAGATG 12

Search completed: June 23, 2003, 20:01:33  
Job time : 89.3944 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 17.2231 Seconds  
(without alignments)  
195.867 Million cell updates/sec

Title: US-08-770-564A-11

Perfect score: 11  
Sequence: 1 GCTCTAGATG 11

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database :

Issued Patents NA:\*  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfillseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	2	US-08-770-565-11
2	11	100.0	15	2	US-08-770-565-10
3	11	100.0	18	4	US-08-770-549A-543
4	11	100.0	19	2	US-08-770-565-9
5	11	100.0	21	4	US-08-026-143B-13
6	11	100.0	21	5	PCT-US92-10621-13
7	11	100.0	21	5	PCT-US94-02233-13
8	11	100.0	22	4	US-09-627-216A-5
9	11	100.0	23	3	US-08-973-068-46
10	11	100.0	23	3	US-08-330-123A-23
11	11	100.0	26	1	US-08-480-604A-16
12	11	100.0	26	1	US-08-482-115B-23
13	11	100.0	26	2	US-08-660-678A-23
14	11	100.0	26	2	US-08-710-249-26
15	11	100.0	26	2	US-08-485-778-19
16	11	100.0	26	2	US-08-405-496A-16
17	11	100.0	26	2	US-08-472-802C-24
18	11	100.0	26	3	US-08-520-550A-19
19	11	100.0	26	3	US-08-898-443-23
20	11	100.0	26	4	US-08-874-549A-558
21	11	100.0	26	4	US-09-060-523-23
22	11	100.0	26	4	US-08-915-136-16
23	11	100.0	26	4	US-09-220-157A-26
24	11	100.0	26	4	US-09-286-959B-4
25	11	100.0	26	4	US-09-580-517-23
26	11	100.0	26	4	US-09-153-310-4
27	11	100.0	26	4	US-08-957-310-16

28	11	100.0	27	2	US-08-770-565-26	Sequence 26, Appl
29	11	100.0	27	3	US-08-630-172-24	Sequence 24, Appl
30	11	100.0	27	4	US-09-375-419-24	Sequence 8, Appl
31	11	100.0	30	2	US-08-770-565-8	Sequence 7, Appl
32	11	100.0	30	2	US-08-995-927-7	Sequence 5, Appl
33	11	100.0	30	4	US-09-349-627-5	Sequence 22, Appl
34	11	100.0	30	4	US-09-582-096-7	Sequence 22, Appl
35	11	100.0	33	3	US-08-630-172-22	Sequence 3, Appl
36	11	100.0	33	4	US-09-375-419-22	Sequence 12, Appl
37	11	100.0	37	3	US-08-815-190A-3	Sequence 9, Appl
38	11	100.0	39	4	US-09-091-305-3	Sequence 11, App
39	11	100.0	40	1	US-08-395-800A-12	Sequence 11, App
40	10	90.9	15	2	US-08-624-601-13	Sequence 14, App
41	10	90.9	16	4	US-08-687-580B-9	Sequence 11, App
42	10	90.9	20	4	US-08-964-722-7	Sequence 11, App
43	10	90.9	21	1	US-07-956-700B-114	Sequence 11, App
44	10	90.9	21	1	US-08-476-537-114	Sequence 11, App
45	10	90.9	21	1	US-08-485-607-114	Sequence 11, App

#### ALIGNMENTS

RESULT 1  
US-08-770-565-11  
; Sequence 11, Application US/08770565  
; Patent No. 5846723  
GENERAL INFORMATION:  
; APPLICANT: Kim, Nam Woo  
; APPLICANT: Wu, Fred  
; APPLICANT: Kealey, James T.  
; APPLICANT: Pruzan, Ronald  
; APPLICANT: Weinrich, Scott L.  
; TITLE OF INVENTION: Methods for Detecting the RNA Component of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,565  
; FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-770-565-11  
Query Match 100.0%; Score 11; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. NO. 2.8e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCTAGATG 11

Fri Jun 27 07:41:05 2003

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Page 2

Db 1 GCTCTAGATG 11

RESULT 2  
US-08-770-565-10  
Sequence 10, Application US/0870565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
NUMBER OF SEQUENCES: 26  
TITLE OF INVENTION: Telomerase  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-10  
Query Match 100.0%; Score 11; DB 2; Length 15;  
Best Local Similarity 100.0%; Fred. No. 2.7e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..18  
OTHER INFORMATION: /note="antisense hTERT molecule"  
US-08-974-549A-543  
Query Match 100.0%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Fred. No. 2.6e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
US-08-770-565-9  
Sequence 9, Application US/08770565  
Patent No. 5846723  
GENERAL INFORMATION:  
APPLICANT: Kim, Nam Woo  
APPLICANT: Wu, Fred  
APPLICANT: Kealey, James T.  
APPLICANT: Pruzan, Ronald  
APPLICANT: Weinrich, Scott L.  
TITLE OF INVENTION: Methods for Detecting the RNA Component of  
TITLE OF INVENTION: Telomerase  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,565  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-002300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-770-565-9

Query Match 100.0%; Score 11; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGAATG 11  
|||||  
Db 1 GCTCTGAATG 11

RESULT 5  
US-08-026-143B-13/c  
Sequence 13, Application US/08026143B  
Patent No. 6348327  
GENERAL INFORMATION:  
APPLICANT: Gorman, Cornelia M.,  
Groskreutz, Debrya J.  
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and  
Polypeptide Synthesis  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/026,143B  
FILING DATE: 01-Mar-1993  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/887265  
FILING DATE: 22-MAY-1992  
APPLICATION NUMBER: 07/803631  
FILING DATE: 06-DEC-1992  
APPLICATION NUMBER: PCT/US92/10621  
FILING DATE: 04-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P0748P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-08-026-143B-13

Query Match 100.0%; Score 11; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGAATG 11  
|||||  
Db 11 GCTCTGAATG 1

RESULT 6  
PCT-US92-10621-13/c  
Sequence 13, Application PC/TUS9210621  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Gorman, Cornelia M.,  
APPLICANT: Mariotte, Dave,  
APPLICANT: Groskreutz, Debrya J.  
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10621  
FILING DATE: 19921204  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/887265  
FILING DATE: 22-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/803631  
FILING DATE: 06-DEC-1992  
ATTORNEY/AGENT INFORMATION:

```

NAME: Adler, Carolyn R.
REGISTRATION NUMBER: 32,324
REFERENCE/DOCKET NUMBER: 748P2.PCT
TELEPHONE: 415/225-2614
TELEFAX: 415/952-9881
TELEX: 91/371-7168
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-10621-13

Query Match          100.0%; Score 11; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 11 GCTCTAGATG 1

RESULT 7
PCT-US94-02233-13/C
Sequence 13, Application PC/TUS9402233
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 748P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-02233-13

Query Match          100.0%; Score 11; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 11 GCTCTAGATG 1

RESULT 8
US-09-627-216A-5
Sequence 5, Application US/09627216A
Patent No. 668837
GENERAL INFORMATION:
APPLICANT: Sarisanti, Sima F
APPLICANT: Gang, Xue-Song
APPLICANT: O'Neil, Wei
APPLICANT: Vannelli, Todd
APPLICANT: Garenby, Anthony
TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
FILE REFERENCE: BCI009 US NA
CURRENT APPLICATION NUMBER: US/09/627,216A
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-627-216A-5

Query Match          100.0%; Score 11; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 3 GCTCTAGATG 13

RESULT 9
US-08-973-068-46
Sequence 46, Application US/08973068
Patent No. 6127604
GENERAL INFORMATION:
APPLICANT: Dale, James Langham
APPLICANT: Harding, Robert Maxwell
APPLICANT: Dugdale, Benjamin
APPLICANT: Beetham, Peter Ronald
APPLICANT: Hafner, Gregory John
APPLICANT: Becker, Douglas Kenneth
TITLE OF INVENTION: INTERGENIC REGIONS OF BANANA BUNCHY TOP VIRUS
FILE REFERENCE: 09657/002001
CURRENT APPLICATION NUMBER: US/08/973,068
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: PCT/AU96/00335
EARLIER FILING DATE: 1996-05-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 46
LENGTH: 23
TYPE: DNA
ORGANISM: Banana Bunchy Top Virus (BBTV)
US-08-973-068-46

Query Match          100.0%; Score 11; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

RESULT 10
US-08-330-123A-23
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Sequence 23, Application US/08330123A  
Patent No. 5583016  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/330,123A  
FILING DATE: 27-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000810  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-330-123A-23

Query Match 100.0%; Score 11; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
|||||  
DB 5 GCTCTAGATG 15

RESULT 11  
US-08-480-604A-16  
Sequence 16, Application US/08480604A  
Patent No. 5736139  
GENERAL INFORMATION:  
APPLICANT: KINK, JOHN A.  
APPLICANT: THALLEY, BRUCE S.  
APPLICANT: PADHYE, NISHA V.  
APPLICANT: FIRCA, JOSEPH R.  
APPLICANT: STAPFORD, DOUGLAS C.  
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND  
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,604A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/422,711  
FILING DATE: 14-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/405,496  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/329,154  
FILING DATE: 25-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,907  
FILING DATE: 02-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/985,321  
FILING DATE: 04-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/429,791  
FILING DATE: 31-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: INGOLIA, DIANE E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: OPHD-01763  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-480-604A-16

Query Match 100.0%; Score 11; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
|||||  
DB 1 GCTCTAGATG 11

RESULT 12  
US-08-482-115B-23  
Sequence 23, Application US/08482115B  
Patent No. 5776679  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Assays for the RNA Component of Human  
TITLE OF INVENTION: Telomerase  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,115B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000830US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-482-115B-23

Query Match 100.0%; Score 11; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
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Db 5 GCTCTAGATG 15

RESULT 13  
US-08-660-678A-23  
Sequence 23, Application US/08660678A  
Patent No. 5837857  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Peng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,678A  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.

REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000811US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-660-678A-23

Query Match 100.0%; Score 11; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11  
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Db 5 GCTCTAGATG 15

RESULT 14  
US-08-710-249-26  
Sequence 26, Application US/08710249  
Patent No. 5858777  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Peng, Junli  
APPLICANT: Andrews, William H.  
APPLICANT: Adams, Robert R.  
TITLE OF INVENTION: Methods and Reagents for Regulating  
TITLE OF INVENTION: Telomere Length and Telomerase Activity  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,249  
FILING DATE: 13-SEP-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/583,808  
FILING DATE: 05-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/003,492  
FILING DATE: 08-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001220US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-710-249-26



Query Match 100.0%; Score 11; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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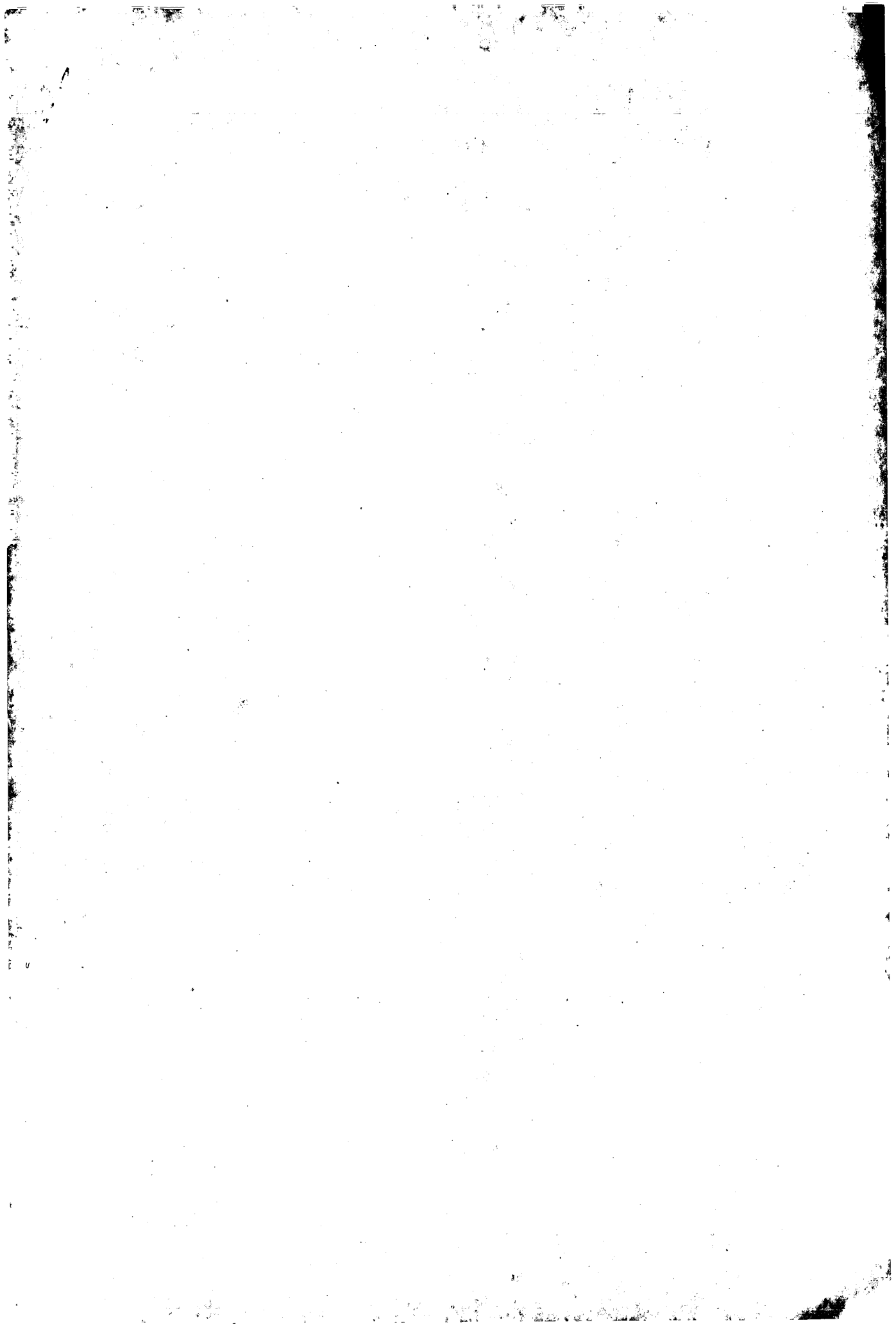
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DB 5 GCTCTGAATG 15

RESULT 15  
US-08-485-778-19  
; Sequence 19, Application US/08485778  
; Patent No. 5876979  
; GENERAL INFORMATION:  
; APPLICANT: Andrews, William H.  
; APPLICANT: Avillion, Ariel Athena  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Greider, Carol  
; APPLICANT: Marhuenda, Maria Antonia Blasco  
; APPLICANT: Villeponteau, Bryant  
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Releasee #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,778  
; FILING DATE: 07-JE-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/387,524  
; FILING DATE: 13-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHJ94-05A4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-485-778-19

Query Match 100.0%; Score 11; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAATG 11  
|||||  
DB 5 GCTCTGAATG 15

Search completed: June 23, 2003, 10:17:07



GenCore version 5.1.6  
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OM nucleic - nucleic search, using bw model

Run on: June 22, 2003, 18:09:32 ; Search time 73.0996 Seconds  
(without alignments)  
338.880 Million cell updates/sec

Title: US-08-770-564A-11  
Perfect score: 11  
Sequence: 1 GCTCTAGATG 11

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size: 0  
Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database: N.Geneseq\_101002.\*

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24:	/SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	11	100.0	11	23	AA515929
3	11	100.0	13	23	AA515930
4	11	100.0	15	19	AAV41177
5	11	100.0	17	22	AA57369
6	11	100.0	19	19	AAV41176
7	11	100.0	19	22	AAH43421
8	11	100.0	21	14	AAQ43258
9	11	100.0	21	14	AAQ43257

C	10	11	100.0	21	15	AAQ71457
	11	11	100.0	22	24	AAD33073
	12	11	100.0	22	24	AAD26921
	13	11	100.0	23	18	AAT49421
	14	11	100.0	24	20	AA563470
	15	11	100.0	25	20	AAZ08704
	16	11	100.0	26	17	AAT10304
	17	11	100.0	26	17	AAT10299
	18	11	100.0	26	17	AAT29258
	19	11	100.0	26	17	AAT11044
	20	11	100.0	26	18	AAT58811
	21	11	100.0	26	19	AAV30567
	22	11	100.0	26	19	AAV19489
	23	11	100.0	26	19	AAV17033
	24	11	100.0	26	20	AAV90788
	25	11	100.0	26	20	AAV74402
	26	11	100.0	26	20	AAV01542
	27	11	100.0	26	21	ABK09963
	28	11	100.0	26	21	AAA88250
	29	11	100.0	26	21	AAA08601
	30	11	100.0	26	24	ABK48024
	31	11	100.0	26	24	AAD24246
	32	11	100.0	27	18	AAT97049
	33	11	100.0	27	19	AAV41193
	34	11	100.0	27	22	AAH22533
	35	11	100.0	27	24	ABA95497
	36	11	100.0	28	17	AAT43859
	37	11	100.0	28	19	AAV57587
	38	11	100.0	28	21	AAV95720
	39	11	100.0	28	21	ABA04366
	40	11	100.0	29	21	AAV65568
	41	11	100.0	29	22	AAH45090
	42	11	100.0	29	24	ABK89026
	43	11	100.0	30	18	AAT91844
	44	11	100.0	30	19	AAV63649
	45	11	100.0	30	19	AAV41175

## ALIGNMENTS

RESULT 1  
AAV41178  
ID AAV41178 standard; DNA; 11 BP.  
XX AAV41178;  
AC 08-OCT-1998 (first entry)  
XX  
DT RNA component of human telomerase (hTR) antisense oligo 21ab2.  
DE  
XX  
XX RNA component; human telomerase; antisense oligonucleotide; infection;  
XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;  
XX contraction; sterility; immunosuppression; therapeutic; hTR;  
XX immune system down-regulation; anti-inflammatory therapy; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9828442-A1.  
XX  
XX 02-JUL-1998.  
XX  
XX  
XX 19-DEC-1997; 97WO-US23619.  
XX  
XX 20-DEC-1996; 96US-0770565.  
XX 20-DEC-1996; 96US-0770564.  
XX  
XX (GERO-) GERON CORP.  
XX  
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;  
XX  
XX WPI; 1998-377670/32.  
XX  
XX

Rx 2,4 protelaxin  
Phenylalanine ammo  
Rhodoporphyrin for  
Banana bunchy top  
Oligonucleotide Cl  
RNA component of h  
RNA component of h  
C. difficile toxin  
Primer for product  
Human telomerase P  
Clostridium diffic  
Human hTR gene RT-  
Telomerase PCR pri  
Human telomerase R  
Human telomerase R  
PCR primer for Hum  
Novel recombinant  
Human telomerase R  
PCR primer #4 to a  
Human telomerase-a  
Human telomerase (a  
Sense primer for h  
RNA component of h  
RBDV movement prot  
Human telomerase R  
Mouse ob gene for  
HER-A cDNA amplify  
B. subtilis KatB g  
CRT C-domain-green  
Human FGFR-1 PCR p  
Murine interleukin  
PCR primer, pF83H,  
Human inhibitory k  
Antisense oligonuc  
RNA component of h

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XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contrereception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contrereception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. Yeast,
CC parasites or fungi.
XX
SQ Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 other;
XX
Query Match 100.0%; Score 11; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11
    |||||
    1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

```

RESULT 2  
AAS15929  
ID AAS15929 standard; DNA; 11 BP.  
XX AAS15929;  
AC  
XX  
XX 27-FEB-2002 (first entry)  
DT  
XX  
XX Human telomerase polynucleotide inhibitor #10.  
DE  
XX  
XX Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;  
KW breast; prostate; colon; mixed cell leukemia; Hodgkin's disease;  
KW fertility; inflammatory condition; tumour; cancer; veterinary;  
KW immunosuppression; telomerase inhibitor; ss.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH 1..11  
FT modified\_base  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "N3'-P5' phosphoramidate linkages"  
XX  
XX WO200174136-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US10476.  
XX  
XX 31-MAR-2000; 2000US-0540119.  
XX  
XX (GERO-) GERON CORP.  
PA

```

XX Gryaznov SM, Pruzan R, Weinrich SL;
XX WPI; 2001-656955/75.
XX
XX New polynucleotide useful for inhibiting telomerase activity in cells,
PT or for treating telomerase-mediated condition or disease, such as
PT cancers, tumours, Hodgkin's disease, or inflammatory conditions -
XX
XX Example 3; Page 32; 48pp; English.
XX
XX The invention relates to polynucleotide inhibitors (I) and methods for
CC inhibiting telomerase activity. (II) are useful in inhibiting telomerase
CC activity and proliferation of a telomerase positive cell, and in
CC manufacturing a medicament for inhibiting telomerase activity in a cell
CC and in treating telomerase-mediated condition or disease, such as
CC adenocarcinoma of breast, prostate or colon, mixed cell leukemia,
CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also
CC useful in treating a tumour or in manufacturing a medicament for the
CC treatment of tumour. The polynucleotide inhibitors may also be used in
CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
CC activity in cells in vivo is useful in prophylactic and therapeutic
CC methods of treating cancer and other disorders involving inappropriate
CC expression of telomerase, and in treating veterinary proliferative
CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
CC for immunosuppression and for selectively down-regulating specific
CC branches of the immune system. The present sequence represents
CC human telomerase polynucleotide inhibitor #10, as described in the
CC method of the invention.
XX
SQ Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 other;
XX
Query Match 100.0%; Score 11; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11
    |||||
    1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

```

RESULT 3  
AAS15930  
ID AAS15930 standard; DNA; 13 BP.  
XX AAS15930;  
AC  
XX  
XX 27-FEB-2002 (first entry)  
DT  
XX  
XX Human telomerase polynucleotide inhibitor #11.  
DE  
XX  
XX Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;  
KW breast; prostate; colon; mixed cell leukemia; Hodgkin's disease;  
KW fertility; inflammatory condition; tumour; cancer; veterinary;  
KW immunosuppression; telomerase inhibitor; ss.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH 1..13  
FT modified\_base  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "N3'-P5' phosphoramidate linkages"  
XX  
XX WO200174136-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US10476.  
XX  
XX 31-MAR-2000; 2000US-0540119.  
XX  
XX (GERO-) GERON CORP.  
PA

PA (GERO-) GERON CORP.  
 XX  
 PI Gryaznov SM, Pruzan R, Weinrich SL;  
 XX  
 PT WPI; 2001-656955/75.  
 DR  
 XX  
 PT New polynucleotide useful for inhibiting telomerase activity in cells,  
 PT or for treating telomerase-mediated condition or disease, such as  
 PT cancers, tumours, Hodgkin's disease, or inflammatory conditions -  
 XX  
 PS Example 3; Page 32; 48pp; English.  
 XX  
 CC The invention relates to polynucleotide inhibitors (I) and methods for  
 CC inhibiting telomerase activity. (I) are useful in inhibiting telomerase  
 CC activity and proliferation of a telomerase positive cell, and in  
 CC manufacturing a medicament for inhibiting telomerase activity in a cell  
 CC and in treating telomerase-mediated condition or disease, such as  
 CC adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,  
 CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also  
 CC useful in treating a tumour or in manufacturing a medicament for the  
 CC treatment of tumour. The polynucleotide inhibitors may also be used in  
 CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase  
 CC activity in cells in vivo is useful in prophylactic and therapeutic  
 CC methods of treating cancer and other disorders involving inappropriate  
 CC expression of telomerase, and in treating veterinary proliferative  
 CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful  
 CC for immunosuppression and for selectively down-regulating specific  
 CC branches of the immune system. The present sequence represents  
 CC human telomerase polynucleotide inhibitor #11, as described in the  
 CC method of the invention.  
 CC  
 SQ Sequence 13 BP; 5 A; 2 C; 3 G; 3 T; 0 other;  
 XX  
 XX  
 Query Match 100.0%; Score 11; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTCTAGATG 11  
 Db 1 GCTCTAGATG 11

RESULT 4  
 AAV41177  
 ID AAV41177 standard; DNA; 15 BP.  
 XX  
 AC AAV41177;  
 XX  
 DT 08-OCT-1998 (first entry)  
 XX  
 DE RNA component of human telomerase (hTR) antisense oligo 21ab3.  
 XX  
 KW RNA component; human telomerase; antisense oligonucleotide; infection;  
 KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;  
 KW contraception; sterilisation; immunosuppression; therapeutic; hTR;  
 KW immune system down-regulation; anti-inflammatory therapy; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 OS  
 PN WO9828442-A1.  
 XX  
 PD 02-JUL-1998.  
 XX  
 PF 19-DEC-1997; 97WO-US23619.  
 XX  
 XX 20-DEC-1996; 96US-0770565.  
 PR 20-DEC-1996; 96US-0770564.  
 XX  
 PA (GERO-) GERON CORP.  
 XX  
 XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F,  
 PI  
 PT

DR WPI; 1998-377670/32.  
 XX  
 PT New polynucleotide(s) antisense to human telomerase - used for  
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,  
 PT contraception, immuno-suppression or treating infection  
 XX  
 PS Claim 11; Page 65; 80pp; English.  
 XX  
 CC Sequences shown in AAV41169 to AAV41181 represent antisense  
 CC oligonucleotides to the RNA component of human telomerase (hTR). These  
 CC antisense oligonucleotides specifically hybridise to a nucleotide  
 CC sequence within an accessible region of the hTR, but that does not  
 CC hybridise to a sequence within the template region of hTR. These  
 CC oligonucleotides may specifically be used for detection of an RNA  
 CC component of human telomerase in a sample. This is useful for diagnosing  
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),  
 CC and providing prognosis for a cancer patient. The inhibitory  
 CC oligonucleotides can inhibit the telomerase activity level in a cell by  
 CC interfering with transcription of the RNA component, decreasing the  
 CC half-life of the telomerase RNA component transcript, inhibiting assembly  
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the  
 CC polymerase activity of telomerase. These antisense oligonucleotides can  
 CC be used for inhibiting telomerase activity in both cultured cells and in  
 CC cells in vivo. They can be used in therapeutics for treating or  
 CC preventing cancer, for contraception or sterilisation, for  
 CC immunosuppression, and for selectively down-regulating specific branches  
 CC of the immune system, e.g. a specific subset of T-cells, in  
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,  
 CC parasites or fungi.  
 CC  
 SQ Sequence 15 BP; 5 A; 3 C; 4 G; 3 T; 0 other;  
 XX  
 XX  
 Query Match 100.0%; Score 11; DB 19; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTCTAGATG 11  
 Db 1 GCTCTAGATG 11

RESULT 5  
 AAF57369  
 ID AAF57369 standard; DNA; 17 BP.  
 XX  
 AC AAF57369;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Murine Cdc25A intron 7/exon 8 splice junction sequence.  
 XX  
 KW Cdc25; Cdc25 phosphatase; transcription; modulator; murine; CDC25A;  
 KW exon; intron; ds.  
 KW  
 OS Mus sp.  
 XX  
 PN WO200120034-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 11-SEP-2000; 2000WO-US24838.  
 XX  
 PR 13-SEP-1999; 99US-0153639.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 XX Voss J, Timm J;  
 PI  
 XX WPI; 2001-244825/25.  
 DR  
 XX Assay for screening modulators of Cdc25 activity by using a cell having  
 PT a recombinant Cdc25 phosphatase gene whose expression alters the  
 PT transcription of a selected gene in the presence of a modulator -

XX Example 1; Page 15; 55pp; English.

XX The invention relates to a method of identifying a modulator of Cdc25

XX activity that comprises contacting a test cell having a recombinant Cdc25

XX phosphatase gene whose expression alters transcription of a selected

XX gene, with a compound under conditions where recombinant Cdc25

XX phosphatase gene is expressed and alters the transcription of a selected

XX gene as an indication of the compound being a modulator of Cdc25-mediated

XX transcription. The method is useful for identifying modulators of Cdc25

XX activity. Sequences AAF57363-376 represent intron/exon splice junction

XX sequences of the murine Cdc25a gene.

XX Sequence 17 BP; 4 A; 3 C; 4 G; 6 T; 0 other;

SO Query Match 100.0%; Score 11; DB 22; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGGAATG 11

Db 4 GCTCTGGAATG 14

RESULT 6

AAV41176

ID AAV41176 standard; DNA; 19 BP.

XX AAV41176;

AC 08-OCT-1998 (first entry)

DT RNA component of human telomerase (hTR) antisense oligo 21ab.

DE RNA component; human telomerase; antisense oligonucleotide; infection;

KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;

KM contraction; sterility; immunosuppression; therapeutic; hTR;

KX immune system down-regulation; anti-inflammatory therapy; ss.

XX Synthetic.

OS Homo sapiens.

XX MO9828442-A1.

PN 02-JUL-1998.

XX 19-DEC-1997; 97MO-US23619.

PF 20-DEC-1996; 96US-0770565.

PR 20-DEC-1996; 96US-0770564.

XX (GERO-) GERON CORP.

PA Kealey JT, Klm JW, Pruzan R, Weinrich SL, Wu F;

XX WPI; 1998-377670/32.

DR New polynucleotide(s) anti-sense to human telomerase - used for

XX detecting or inhibiting human telomerase, e.g. for treating cancers,

PT contraction, immuno-suppression or treating infection

XX Claim 11; Page 65; 80pp; English.

PS Sequences shown in AAV41169 to AAV41181 represent antisense

CC oligonucleotides to the RNA component of human telomerase (hTR). These

CC antisense oligonucleotides specifically hybridize to a nucleotide

CC sequence within an accessible region of the hTR, but that does not

CC hybridize to a sequence within the template region of hTR. These

CC oligonucleotides may specifically be used for detection of an RNA

CC component of human telomerase in a sample. This is useful for diagnosing

CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),

CC and providing prognosis for a cancer patient. The inhibitory

CC oligonucleotides can inhibit the telomerase activity level in a cell by

CC interfering with transcription of the RNA component, decreasing the

CC half-life of the telomerase RNA component transcript, inhibiting assembly

CC of the RNA component into the telomerase holoenzyme, or inhibiting the

CC polymerase activity of telomerase. These antisense oligonucleotides can

CC be used for inhibiting telomerase activity in both cultured cells and in

CC cells in vivo. They can be used in therapeutics for treating or

CC preventing cancer, for contraception or sterilization, for

CC immunosuppression, and for selectively down-regulating specific branches

CC of the immune system, e.g. a specific subset of T-cells, in

CC anti-inflammatory therapies or for treating infections by, e.g. yeast,

CC parasites or fungi.

XX Sequence 19 BP; 5 A; 3 C; 7 G; 4 T; 0 other;

SO Query Match 100.0%; Score 11; DB 19; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGGAATG 11

Db 1 GCTCTGGAATG 11

RESULT 7

AAH43421

ID AAH43421 standard; DNA; 19 BP.

XX AAH43421;

AC 04-DEC-2001 (first entry)

DT ISA3 reverse primer.

DE European; infectious Salmon anaemia; ISA; antigen; RNA segment 3;

KW virus; ISA; nucleoprotein; vaccine; fish; infection; primer; amplify;

KX polymerase chain reaction; PCR; ss.

XX Synthetic.

OS WO200165569-A1.

PN 13-SEP-2001.

PD 08-MAR-2001; 2001WO-GB01013.

PE 08-MAR-2000; 2000GB-0005457.

PR 14-MAR-2000; 2000GB-0005960.

PR 01-DEC-2000; 2000GB-0029409.

XX (UYAB-) UNIV ABERDEEN.

PA Melvin WT, Breeman S, Labus MB;

XX WPI; 2001-589927/66.

DR Vaccinating fish against infectious Salmon Anemia (ISA) virus infection

XX using European ISA virus antigen polypeptides -

XX Claim 34; Page 34; 41pp; English.

PS The sequences given in AAH43407-21 are primers which were used in

CC the amplification and cloning of the cDNA encoding the European

CC infectious Salmon anaemia (ISA) antigen polypeptide. The antigen is

CC cloned from RNA segment 3 of ISA virus (ISAV) and is believed to be

CC a major cell culture antigen of the virus, which may be a nucleoprotein.

CC The ISA antigen, or a fragment of it, may be used to vaccinate fish

CC against ISAV infection. It may also be used to screen fish for ISA

CC virus infection.

XX Sequence 19 BP; 5 A; 4 C; 4 G; 6 T; 0 other;

SO Query Match 100.0%; Score 11; DB 22; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 11, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 GCTCTAGATG 11  
 |||||  
 XX  
 DB 1 GCTCTAGATG 11

RESULT 8  
 AAQ43258/c  
 ID AAQ43258 standard; DNA; 21 BP.

XX AC AAQ43258;

XX DT 24-SEP-1993 (first entry)

XX DE Sequence encoding the C-chain/A-chain junction prorelaxin (Rx)  
 DE mutant Rx 2.4 at the prohormone convertase cleavage site.

XX KW Prohormone convertase; enzyme; cleavage; prorelaxin; hormone; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT CDS 1..21

XX FT /\*tag= a

XX PN MO9311247-A.

XX PD 10-JUN-1993.

XX PF 04-DEC-1992; 92WO-US10621.

XX PR 06-DEC-1991; 91US-0803631.

XX PR 22-MAY-1992; 92US-0887265.

XX PA (GETH ) GENENTECH INC.

XX PI Gorman CM, Groskreutz DJ, Marriot D;

XX DR WPI; 1993-197065/24.

XX DR P-PSDB; AAR37621.

XX PT Heterologous polypeptide factor prep. - by introducing into

XX PT polypeptide factor dependent host cell nucleic acid, and then

XX PT culturing host cell, etc.

XX PS Example; Page 54; 134pp; English.

XX CC The inventors describe the production of mammalian cells expressing

XX CC prohormone convertase which facilitates the processing of prohormone

XX CC precursors to active hormones. More specifically the cleavage site

XX CC is the prohormone convertase cleavage site given in AAR37632-35. In

XX CC order to define murine prohormone convertase 1 specifically

XX CC prorelaxin alanine mutations of the basic residues K and R were

XX CC constructed. The following mutations were tested for substrate

XX CC specificity to murine prohormone convertase: 1.4, 2.4, 3.2, 4.3,

XX CC 7.2 and 8.6 (see AAQ43256-63; AAR37619-26).

XX CC Sequence 21 BP; 10 A; 4 C; 4 G; 3 T; 0 other;

XX CC Query Match 100.0%; Score 11; DB 14; Length 21;

XX CC Best Local Similarity 100.0%; Pred. No. 1.2e+03;

XX CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX CC QY 1 GCTCTAGATG 11

XX CC |||||

XX CC DB 11 GCTCTAGATG 1

XX CC RESULT 9

XX CC AAQ43257/c

XX CC ID AAQ43257 standard; DNA; 21 BP.

XX CC XX

AC AAQ43257;

XX DT 24-SEP-1993 (first entry)

XX DE Sequence encoding the C-chain/A-chain junction prorelaxin (Rx)

XX DE mutant Rx 1.4 at the prohormone convertase cleavage site.

XX KW Prohormone convertase; enzyme; cleavage; prorelaxin; hormone; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT CDS 1..21

XX FT /\*tag= a

XX PN MO9311247-A.

XX PD 10-JUN-1993.

XX PF 04-DEC-1992; 92WO-US10621.

XX PR 06-DEC-1991; 91US-0803631.

XX PR 22-MAY-1992; 92US-0887265.

XX PA (GETH ) GENENTECH INC.

XX PI Gorman CM, Groskreutz DJ, Marriot D;

XX DR WPI; 1993-197065/24.

XX DR P-PSDB; AAR37620.

XX PT Heterologous polypeptide factor prep. - by introducing into

XX PT polypeptide factor dependent host cell nucleic acid, and then

XX PT culturing host cell, etc.

XX PS Example; Page 54; 134pp; English.

XX CC The inventors describe the production of mammalian cells expressing

XX CC prohormone convertase which facilitates the processing of prohormone

XX CC precursors to active hormones. More specifically the cleavage site

XX CC is the prohormone convertase cleavage site given in AAR37632-35. In

XX CC order to define murine prohormone convertase 1 specifically

XX CC prorelaxin alanine mutations of the basic residues K and R were

XX CC constructed. The following mutations were tested for substrate

XX CC specificity to murine prohormone convertase: 1.4, 2.4, 3.2, 4.3,

XX CC 7.2 and 8.6 (see AAQ43256-63; AAR37619-26).

XX CC Sequence 21 BP; 10 A; 4 C; 4 G; 3 T; 0 other;

XX CC Query Match 100.0%; Score 11; DB 14; Length 21;

XX CC Best Local Similarity 100.0%; Pred. No. 1.2e+03;

XX CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX CC QY 1 GCTCTAGATG 11

XX CC |||||

XX CC DB 11 GCTCTAGATG 1

XX CC RESULT 10

XX CC AAQ71457/c

XX CC ID AAQ71457 standard; DNA; 21 BP.

XX CC XX

XX CC AC AAQ71457;

XX CC DT 26-APR-1995 (first entry)

XX CC DE Rx 2.4 prorelaxin C/A chain junction mutant cleavage site.

XX CC KW prohormone; convertase; insulin; proinsulin; factor; growth;

XX CC precursors; transgenic; mammal; prorelaxin; cleavage; ss.

XX CC OS Synthetic.

XX CC XX

PN WO9420624-A.  
 XX 15-SEP-1994.  
 PD  
 XX  
 PF 01-MAR-1994; 94WO-US02223.  
 XX  
 PR 01-MAR-1993; 93US-0026143.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Gorman CM, Groekreutz DJ,  
 XX  
 DR WPI; 1994-303031/37.  
 DR P-PSDB; AAR60585.  
 XX  
 PT Treating insulin-dependent disorders in mammals - by introducing  
 FT a nucleic acid encoding a variant proinsulin into a host cell,  
 PT with a constitutive pathway of protein secretion, or a plasmid,  
 PT and introducing the cell or plasmid to the mammal  
 XX  
 PS Example 3; Page 52; 117pp; English.  
 XX  
 CC A series of natural or mutated cDNAs for the prohormone convertase (PC)  
 CC cleavage sites in human prorelaxin protein between the C and A chains  
 CC (AAQ74455-59 corresponding to AAR60583-7) or in the B and C chains  
 CC (AAQ74460-63 corresponding to AAR60588-90). The natural cleavage sites  
 CC contain two dibasic residues, Lys-Arg, both of which are required for  
 CC cleavage. The mutant sites have replacements of either residues with an  
 CC Ala. This confers specificity to murine PC1. In this particular mutant,  
 CC the Lys residue at the fourth position of the cleavage site has been  
 CC replaced by a Ala residue. Relaxin is an ovarian hormonal peptide  
 CC responsible for remodelling the reproductive tract prior to parturition.  
 CC The cells containing both the prohormone convertase gene and the required  
 CC precursor to be expressed can be injected into a mammal.  
 CC  
 SQ Sequence 21 BP; 10 A; 4 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 11; DB 15; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
 |||||  
 DB 11 GCTCTAGATG 1

RESULT 11  
 AAD33073  
 ID AAD33073 standard; DNA; 22 BP.  
 XX  
 AC AAD33073;  
 XX  
 DT 01-JUN-2002 (first entry)  
 XX  
 DE Phenylalanine ammonia lyase (PAL) gene amplifying forward PCR primer.  
 XX  
 KW Para-hydroxycinnamic acid; PHCA; food packaging; electronic connector;  
 KW phenylalanine ammonia lyase; PAL; glucose; tyrosine ammonia lyase; TNL;  
 KW cytochrome P-450; cytochrome P-450 reductase; liquid crystal polymer;  
 KW LCP; telecommunication; medical device; aerospace application;  
 KW biocatalyst; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200210407-A1.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PR 23-JAN-2001; 2001WO-US02099.  
 XX  
 DR 27-JUL-2000; 2000US-0627216.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.

XX  
 PI Gatenby AA, Sariafani FS, Tang X, Qi WW, Vannelli T;  
 XX  
 DR WPI; 2002-280635/32.  
 XX  
 PT Novel nucleic acid encoding truncated mutant tyrosine ammonia lyase  
 PT (PAL) polypeptide, or mutant TAL polypeptide, useful for producing  
 PT parahydroxycinnamic acid in recombinant host cell lacking cinamate  
 PT hydroxylase  
 XX  
 PS Example 9; Page 51; 139pp; English.  
 XX

CC The invention relates to methods for biological production of para-  
 CC hydroxycinnamic acid (PHCA). The invention relates to developing of a new  
 CC biocatalyst for conversion of glucose to PHCA by incorporation of the  
 CC wild type phenylalanine ammonia lyase (PAL; EC 4.3.1.5) from the yeast  
 CC Rhodotorula glutinis into Escherichia coli underlying the ability of the  
 CC wildtype PAL to convert tyrosine to PHCA. The invention is also directed  
 CC to developing a new biocatalyst for conversion of glucose to PHCA by  
 CC incorporation of the wildtype PAL which possesses enhanced tyrosine  
 CC ammonia lyase (TAL) activity from the yeast Rhodotorula glutinis plus the  
 CC plant cytochrome P-450 and the cytochrome P-450 reductase into E. coli.  
 CC Nucleic acid encoding mutant TAL enzyme is useful for producing PHCA by  
 CC recombinant techniques. The recombinantly produced PHCA may be used as a  
 CC monomer for production of liquid crystal polymers (LCP). LCP may be used  
 CC in electronic connectors and telecommunication and aerospace  
 CC applications. LCP resistance to sterilizing radiation has also enabled  
 CC these materials to be used in medical devices as well as chemical, and  
 CC food packaging applications. The present sequence is a PCR primer used  
 CC to amplify PAL gene.  
 CC  
 SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 11; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
 |||||  
 DB 3 GCTCTAGATG 13

RESULT 12  
 AAD26921  
 ID AAD26921 standard; DNA; 22 BP.  
 XX  
 AC AAD26921;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Rhodospiridium toruloides PAL gene amplifying PCR primer A.  
 XX  
 KW Phenylalanine ammonia-lyase; PAL; enzyme; cinamate; food packing; PHCA;  
 KW para-hydroxycinnamic acid; tyrosine ammonia-lyase; TAL; medical device;  
 KW liquid crystal Polymer; LCP; electronic connector; telecommunication;  
 KW aerospace application; chemical; red yeast; PCR primer; ss.  
 XX  
 OS Rhodospiridium toruloides.  
 XX  
 PN WO200111071-A2.  
 XX  
 PD 15-FEB-2001.  
 XX  
 PR 03-AUG-2000; 2000WO-US21156.  
 XX  
 DR 06-AUG-1999; 99US-147719P.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Tang X, Vannelli TM, Qi WW, Sariafani S, Gatenby AA;  
 XX  
 DR WPI; 2002-121549/16.  
 XX



PT Producing para-hydroxycinnamic acid for producing liquid crystal  
 PT polymer, comprises converting cinnamate to PHCA, glucose to PHCA by  
 PT phenyl ammonia-lyase route, or generating a biocatalyst with tyrosine  
 PT ammonia-lyase activity -  
 XX  
 PS Example 9; Page 45; 75pp; English.  
 XX  
 CC The invention relates to a method for producing para-hydroxycinnamic  
 CC acid (PHCA). The method comprises converting cinnamate to PHCA by  
 CC converting glucose to phenylalanine to PHCA through the phenyl  
 CC ammonia-lyase (PAL) route or by generating a new biocatalyst possessing  
 CC enhanced tyrosine ammonia-lyase (TAL) activity. The method is useful for  
 CC the biological production of PHCA which is useful as a monomer for the  
 CC production of liquid crystal polymers (LCP), where the LCP is used in  
 CC electronic connectors, telecommunications and aerospace applications.  
 CC LCP is also useful in medical devices, as well as chemical, and food  
 CC packing applications due to its resistance to sterilising radiation. The  
 CC present sequence is a PCR primer used for amplifying red yeast  
 CC (Rhodospiridium toruloides) PAL gene.  
 XX  
 SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;  
 XX  
 QY Query Match 100.0%; Score 11; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Db 1 GCTCTAGAATG 11  
 3 GCTCTAGAATG 13  
 XX  
 RESULT 13  
 AAT49421  
 ID AAT49421 standard; DNA; 23 BP.  
 XX  
 AC AAT49421;  
 XX  
 DT 24-AUG-1997 (first entry)  
 XX  
 DE Banana bunchy top virus DNA component 4 promoter PCR primer BT4.1.  
 XX  
 KW Banana bunchy top virus; BBTV; intergenic region; promoter;  
 KW transgenic plant; polymerase chain reaction; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9638554-A1.  
 XX  
 PD 05-DEC-1996.  
 XX  
 PF 31-MAY-1996; 96MO-AU00335.  
 XX  
 PR 31-MAY-1995; 95AU-0003285.  
 XX  
 PA (UYOU-) UNIV QUEENSLAND TECHNOLOGY.  
 XX  
 PI Becker DK, Beetham PR, Dale JL, Dugdale B, Hafner GJ;  
 PI Harding RM;  
 XX  
 DR WPI; 1997-034368/03.  
 XX  
 PT DNA from intergenic region of banana bunchy top virus DNA component  
 PT - useful for promoting, enhancing, regulating or modifying  
 PT transcription of a non-BBTV gene in transgenic plants  
 XX  
 PS Example 2; Page 22; 80pp; English.  
 XX  
 CC PCR primers BT4.1 (+662) (AAT49421) and BT4.2 (+278) (AAT49422) were  
 CC used to amplify the intergenic region of banana bunchy top virus  
 CC (BBTV) DNA component 4 (see also AAT49386) from BBTV infected banana  
 CC nucleic extract. The 659 bp intergenic region was subcloned as a  
 CC XbaI and BamHI fragment into pGEM4.1 (+). It was then  
 CC cloned from pGEM4.1 as a XbaI and BamHI fragment into pBI101.3

CC (pBT4.1). The component 4 intergenic region insert in pBT4.1 is  
 CC given in AAT49400.  
 XX  
 SQ Sequence 23 BP; 6 A; 2 C; 7 G; 8 T; 0 other;  
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 QY Query Match 100.0%; Score 11; DB 18; Length 23;  
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 XX  
 Db 1 GCTCTAGAATG 11  
 1 GCTCTAGAATG 11  
 XX  
 RESULT 14  
 AAF63470  
 ID AAF63470 standard; DNA; 24 BP.  
 XX  
 AC AAF63470;  
 XX  
 DT 11-MAY-2001 (first entry)  
 XX  
 DE Oligonucleotide CMH3.  
 XX  
 KW Baculovirus expression system; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112829-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 14-AUG-2000; 2000WO-GB03144.  
 XX  
 PR 18-AUG-1999; 99GB-0019409.  
 XX  
 PA (UYOX-) UNIV OXFORD BROOKES.  
 PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.  
 XX  
 PI Possee RD, King LA;  
 XX  
 DR WPI; 2001-202870/20.  
 XX  
 PT Method for cloning a gene, especially useful for expressing thousands  
 PT of genes in alternative hosts, comprises employing a  
 PT replication-deficient baculovirus vector and a rescue vector and  
 PT causing the vectors to recombine -  
 XX  
 PS Disclosure; Page 14; 54pp; English.  
 XX  
 CC The present invention relates to a method for cloning a gene. The method  
 CC comprises employing a replication-deficient baculovirus vector and a  
 CC rescue vector, and causing the vectors to recombine to produce a  
 CC replication-enabled baculovirus vector having at least one gene to be  
 CC cloned. The present sequence is an oligonucleotide used in the present  
 CC invention. The method of the present invention is especially useful for  
 CC expressing thousands of genes in alternative hosts (e.g. insect cells) to  
 CC derive sufficient material for determining protein function.  
 XX  
 SQ Sequence 24 BP; 6 A; 6 C; 7 G; 5 T; 0 other;  
 XX  
 QY Query Match 100.0%; Score 11; DB 22; Length 24;  
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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Db 1 GCTCTAGAATG 11  
 3 GCTCTAGAATG 13  
 XX  
 RESULT 15  
 AAZ08704  
 ID AAZ08704 standard; DNA; 25 BP.

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XX AA08704;
XX 20-OCT-1999 (first entry)
XX
XX Human telomerase RNA template PCR primer R3C.
XX
XX Telomerase; body fluid; cancer; tumour; screening; TRAP; diagnosis;
XX telomeric repeat amplification protocol; detection; PCR primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX MO9941406-A1.
XX 19-AUG-1999.
XX
XX 16-FEB-1999; 99MO-US03302.
XX
XX 16-FEB-1998; 98US-0074793.
XX
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX
XX Abruzzo LV, Highsmith E, Stenberg J, Strovel JW;
XX WPI; 1999-508655/42.
XX
XX Detecting telomerase activity in non-cellular body fluid using a
XX modified telomeric repeat amplification protocol
XX
XX Disclosure; Page 16; 32pp; English.
XX
XX A method has been developed for detecting telomerase activity in a
XX non-cellular portion of body fluid from a cancer patient using a
XX modified telomeric repeat amplification protocol (TRAP). A method for
XX detecting cancer comprises: (a) removing the cellular portion of a body
XX fluid specimen from the patient; (b) preparing a protein extract from
XX the body fluid remainder; (c) assaying the extract for the presence and
XX quantity of telomerase RNA or telomerase activity; and (d) comparing the
XX results with normal levels, to determine the presence of cancer. The
XX methods are used in cancer diagnosis and prognosis, and also to monitor
XX cancer therapy effectiveness. Unlike prior art telomerase activity
XX assays in cancer patients, the method allows noninvasive sample
XX collection. The methods are also more reliable and less tumour specific
XX than other methods which detect circulating tumour markers. The present
XX sequence represents a human telomerase RNA template PCR primer used in
XX the exemplification of the present invention.
XX
XX SQ Sequence 25 BP; 7 A; 3 C; 9 G; 6 T; 0 other;
XX
XX Query Match 100.0%; Score 11; DB 20; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GCTCTAGATG 11
XX |||||
XX 4 GCTCTAGATG 14
XX
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Search completed: June 23, 2003, 05:43:39  
Job time : 73.4073 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 127.924 Seconds  
(without alignments)  
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Title: US-08-770-564a-11  
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Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

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GenEmbl:  
1: gb\_ba:  
2: gb\_hcg:  
3: gb\_in:  
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14: gb\_vl:  
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17: em\_hum:  
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27: em\_scs:  
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32: em\_hcg\_other:  
33: em\_hcg\_mus:  
34: em\_hcg\_pln:  
35: em\_hcg\_rdn:  
36: em\_hcg\_mam:  
37: em\_hcg\_vrt:  
38: em\_sy:  
39: em\_hcg\_hum:  
40: em\_hcg\_mus:  
41: em\_hcg\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	6	AR063835
2	11	100.0	15	6	AR063834
3	11	100.0	17	6	AX099957
4	11	100.0	18	6	BD011244
5	11	100.0	18	6	E36993
6	11	100.0	19	6	AR063833
7	11	100.0	19	6	AX244257
8	11	100.0	21	6	AR193717
9	11	100.0	22	6	AR205029
10	11	100.0	22	6	AX082540
11	11	100.0	22	6	AX370655
12	11	100.0	23	6	AR112025
13	11	100.0	24	6	AX085592
14	11	100.0	26	6	A94988
15	11	100.0	26	6	AR000025
16	11	100.0	26	6	AR016055
17	11	100.0	26	6	AR028786
18	11	100.0	26	6	AR059216
19	11	100.0	26	6	AR075527
20	11	100.0	26	6	AR161925
21	11	100.0	26	6	AR169136
22	11	100.0	26	6	AR179447
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24	11	100.0	26	6	AX022187
25	11	100.0	26	6	AX033377
26	11	100.0	26	6	AX036237
27	11	100.0	26	6	AX468455
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30	11	100.0	26	6	E37046
31	11	100.0	26	6	I31770
32	11	100.0	27	6	AR063850
33	11	100.0	27	6	AX175102
34	11	100.0	27	6	AX317989
35	11	100.0	28	6	AX298137
36	11	100.0	30	6	AR063832
37	11	100.0	30	6	AR134697
38	11	100.0	30	6	AX465471
39	11	100.0	34	6	AX175104
40	11	100.0	36	6	AX175105
41	11	100.0	39	6	A63531
42	11	100.0	39	6	AR122907
43	11	100.0	40	6	AR039082
44	10	90.9	12	6	AX456436
45	10	90.9	15	6	I07861

#### ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1	AR063835	Sequence 11 from patent US 5846723.	AR063835	AR063835.1	GI:5993143	Unknown.	Unknown.	1 (bases 1 to 11)	Kim,N.Moo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.	Methods for detecting the RNA component of telomerase	Patent: US 5846723-A 11 08-DEC-1998;	Location/Qualifiers
1	AR063835	Sequence 11 from patent US 5846723.	AR063835	AR063835.1	GI:5993143	Unknown.	Unknown.	11 bp		DNA	linear	PAT 29-SHP-1999

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Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCTCTAGATG 11

RESULT 2
LOCUS AR063834 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5846723.
ACCESSION AR063834
VERSION AR063834.1 GI:5933142
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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BASE COUNT 5 a 3 c 4 g 3 t
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Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 3
LOCUS AX099957 17 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 17 from Patent WO0120034.
ACCESSION AX099957
VERSION AX099957.1 GI:13538967
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source 1.17
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Best Local Similarity 100.0%; Pred. No. 1e+04;
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Qy 1 GCTCTAGATG 11
Db 4 GCTCTAGATG 14

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RESULT 4
LOCUS BD011244 18 bp DNA linear PAT 31-JAN-2002
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011244
VERSION BD011244.1 GI:18639617
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS
PN JP 2001081042-A/201
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643, 18-APR-1997 US 08/844419 PR
25-APR-1997 US 08/846017, 06-MAY-1997 US 08/851843 PR
09-MAY-1997 US 08/854050, 14-AUG-1997 US 08/91312 PR
14-AUG-1997 US 08/912951, 14-AUG-1997 US 08/915503 PI
R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI
MORIN, CALVIN B HARLEY, WILLIAM H ANDREWS
PI CALVIN B HARLEY, WILLIAM H ANDREWS
PC A61K38/00, A61K31/7088, A61K39/00, A61P35/00, A61P43/00,
PC C07K5/10, C07K5/107, C07K5/117, C07K7/06, C07K16/40, C12N9/12, PC
C12N15/08, C12N15/02, C12N14/8, C12N1/68, G01N33/15, G01N33/50, G01N33/53, PC
G01N33/53, G01N33/56, G01N33/573//C12P21/08, A61K37/02, C12N15/00 CC
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CC Topology: Linear;
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FT /organism="unidentified".
FEATURES
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Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 5
LOCUS E36993 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36993
VERSION E36993.1 GI:13022956
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS
PN JP 1999253177-A/201
PD 1999-06-01
PF 1999-06-01
PR 1999-06-01
R THOMAS, R.S., JOCHIMU, R., TORU, N., KAREN, B.C., GREG, B.M.,
CALVIN, B.H. and WILLIAM, H.A.
PI THOMAS, R.S., JOCHIMU, R., TORU, N., KAREN, B.C., GREG, B.M.,
CALVIN, B.H. and WILLIAM, H.A.
PC Human telomerase catalytic subunit promoter
Patent: JP 1999253177-A 201 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP

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COMMENT OS Unidentified  
 PN JP 1999253177-A/201  
 PD 21-SEP-1999  
 PR 15-OCT-1998 JP 1998320169  
 PR 01-OCT-1996 US 08/722,643,18-APR-1997 US 08/844,419, PR  
 25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR  
 09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR  
 14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503, PI THOMAS  
 R SECHI, JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B  
 MORIN,  
 PI CALVIN B HARRI, WILLIAM H ANDREWS  
 PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,  
 PC C12Q1/02,  
 PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC  
 C07K16/40,  
 PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,C12N1/19, PC  
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 PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),  
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 Db 1 GCTCTAGATG 11  
 RESULT 6  
 AR063833 19 bp DNA linear PAT 29-SEP-1999  
 LOCUS AR063833  
 DEFINITION Sequence 9 from patent US 5846723.  
 ACCESSION AR063833  
 VERSION AR063833.1 GI:5993141  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Prizan,R. and Weinrich,S.L.  
 TITLE Methods for detecting the RNA component of telomerase  
 JOURNAL Patent: US 5846723-A 9 08-DEC-1998;  
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 QY 1 GCTCTAGATG 11  
 Db 1 GCTCTAGATG 11  
 RESULT 7  
 AX244257 19 bp DNA linear PAT 28-SEP-2001  
 LOCUS AX244257  
 DEFINITION Sequence 19 from Patent WO0166569.

ACCESSION AX244257 GI:15859305  
 VERSION AX244257.1  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Melvin,W.T., Breeman,S. and Labus,M.B.  
 TITLE Viral antigen and vaccine against Isav (infectious salmon anaemia virus)  
 JOURNAL Patent: WO 0166569-A 19 13-SEP-2001;  
 The University Court of The University of Aberdeen (GB)  
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 Db 1 GCTCTAGATG 11  
 RESULT 8  
 AR193717/c 21 bp DNA linear PAT 20-APR-2002  
 LOCUS AR193717  
 DEFINITION Sequence 13 from patent US 6348327.  
 ACCESSION AR193717  
 VERSION AR193717.1 GI:20240309  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Gorman,C.M. and Groskreutz,D.J.  
 TITLE Non-endocrine animal host cells capable of expressing variant  
 proinsulin and processing the same to form active, mature insulin  
 and methods of culturing such cells  
 JOURNAL Patent: US 6348327-A 13 19-FEB-2002;  
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 ACCESSION AR205029  
 VERSION AR205029.1 GI:21502506  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Gatenby,A.A., Sarrafian,S., Tang,X.-S., Qi,W.Wei. and Vannelli,T.  
 TITLE Bioproduction of para-hydroxycinnamic acid

JOURNAL Patent: US 6368837-A 5 09-APR-2002;  
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QY 1 GCTCTAGATG 11  
11  
3 GCTCTAGATG 13

Db

RESULT 10  
AX082540 22 bp DNA linear PAT 28-FEB-2001  
LOCUS  
DEFINITION Sequence 5 from Patent WO011071.  
AX082540  
ACCESSION AX082540.1 GI:13184654  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequences.  
REFERENCE  
1 (bases 1 to 22)  
AUTHORS Tang, X.S., Vannelli, T.M., Qi, W.W., Sariassani, S. and Gatenby, A.A.  
TITLE Bioproduction of para-hydroxycinnamic acid  
JOURNAL Patent: WO 011071-A 5 15-FEB-2001;  
E.I. DU PONT DE NEMOURS & COMPANY INCORPORATED (US)  
Location/Qualifiers  
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11  
3 GCTCTAGATG 13

Db

RESULT 11  
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LOCUS  
DEFINITION Sequence 5 from Patent WO0210407.  
AX370655  
ACCESSION AX370655.1 GI:19186820  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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artificial sequences.  
REFERENCE  
1  
AUTHORS Gatenby, A.A., Sariassani, F.S., Tang, X.S., Qi, W.W. and Vannelli, T.  
TITLE Bioproduction of para-hydroxycinnamic acid  
JOURNAL Patent: WO 0210407-A 5 07-FEB-2002;  
E.I. DUPONT DE NEMOURS AND COMPANY (US)  
Location/Qualifiers  
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source /organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="primer"

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
11  
3 GCTCTAGATG 13

Db

RESULT 12  
AR112025 23 bp DNA linear PAT 14-FEB-2001  
LOCUS  
DEFINITION Sequence 46 from patent US 6127604.  
AR112025  
ACCESSION AR112025.1 GI:12828873  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 23)  
AUTHORS Dale, J. Langham, J., Harding, R., Maxwell, J., Dugdale, B., Beetham, P., Ronald, J., Halmer, G., John, J., and Becker, D., Kenneth.  
TITLE Intergenic regions of banana bunchy top virus  
JOURNAL Patent: US 6127604-A 46 03-OCT-2000;  
Location/Qualifiers  
1..23  
source /organism="unknown"

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Db

RESULT 13  
AX085592 24 bp DNA linear PAT 09-MAR-2001  
LOCUS  
DEFINITION Sequence 5 from Patent WO0112829.  
AX085592  
ACCESSION AX085592.1 GI:13275601  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
unidentified baculovirus.  
unidentified baculovirus.  
Viruses; dsDNA viruses, no RNA stage; Baculoviridae.  
REFERENCE  
1 (bases 1 to 24)  
AUTHORS Posee, R.D. and King, L.A.  
TITLE Replication deficient baculovirus expression system  
JOURNAL Patent: WO 0112829-A 5 22-FEB-2001;  
OXFORD BROOKES UNIVERSITY (GB) ; NATURAL ENVIRONMENT RESEARCH COUNCIL (GB)  
Location/Qualifiers  
1..24  
source /organism="unidentified baculovirus"  
/db\_xref="taxon:10469"

BASE COUNT 6 a 6 c 7 g 5 t  
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11  
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3 GCTCTAGATG 13

Db

RESULT 14  
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LOCUS  
DEFINITION Sequence 2 from Patent EP0926245.  
A94988

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ACCESSION      A94988
VERSION        A94988.1 GI:6779168
KEYWORDS
SOURCE         unidentified.
ORGANISM       unidentified.
REFERENCE      1 (bases 1 to 26)
AUTHORS        Emrich,T.D.
TITLE          Method for detection of carcinoma of the urinary bladder within a
               urine sample
JOURNAL        Patent: EP 0926245-A 2 30-JUN-1999;
               ROCHE DIAGNOSTICS GMBH (DE)
FEATURES
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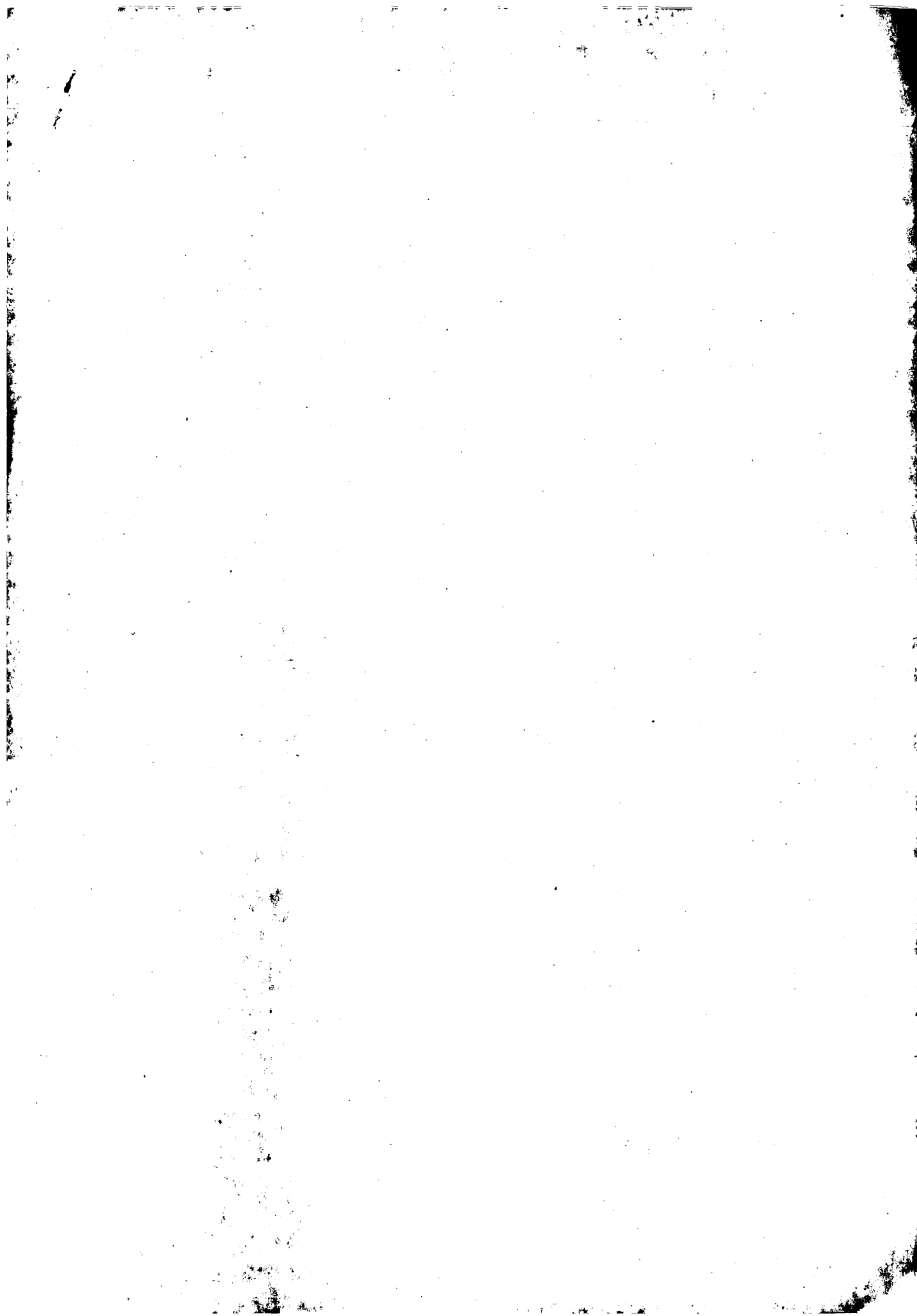
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Db 5 GCTCTGAATG 15

RESULT 15
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ACCESSION      AR000025
VERSION        AR000025.1 GI:3962556
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 26)
AUTHORS        Kink,J.A., Thalley,B.S., Stafford,D.C., Pirca,J.R. and Padhye,N.V.
TITLE          Treatment of Clostridium difficile induced disease
JOURNAL        Patent: US 5736139-A 16 07-APR-1998;
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FEATURES
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Search completed: June 23, 2003, 06:34:21  
 Job time : 128.386 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 167.219 Seconds  
(without alignments)  
292.710 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7

Sequence: 1 GCTTCAG 7

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	7	100.0	10	9	US-10-329-465-53	Sequence 53, Appl
C 2	7	100.0	10	10	US-10-293-222-131	Sequence 131, Appl
C 3	7	100.0	11	9	US-10-314-322-34	Sequence 34, Appl
C 4	7	100.0	12	9	US-10-240-580-38	Sequence 38, Appl
C 5	7	100.0	13	9	US-10-106-799-13	Sequence 13, Appl
C 6	7	100.0	13	9	US-10-106-799-14	Sequence 14, Appl
C 7	7	100.0	13	9	US-10-146-505-84	Sequence 84, Appl
C 8	7	100.0	14	9	US-10-303-778-13859	Sequence 13859, A
C 9	7	100.0	15	9	US-10-294-035-747	Sequence 747, Appl
C 10	7	100.0	15	9	US-10-294-035-748	Sequence 748, Appl
C 11	7	100.0	15	9	US-10-294-035-940	Sequence 940, Appl
C 12	7	100.0	15	9	US-10-294-038-1008	Sequence 1008, Appl
C 13	7	100.0	15	9	US-10-294-038-2682	Sequence 2682, Appl
C 14	7	100.0	15	9	US-10-294-038-4251	Sequence 4251, Appl
C 15	7	100.0	15	9	US-10-287-822-1580	Sequence 1580, Appl
C 16	7	100.0	15	9	US-10-310-188-33324	Sequence 33324, A
C 17	7	100.0	15	9	US-10-310-188-72013	Sequence 72013, A
C 18	7	100.0	15	9	US-10-305-273-169	Sequence 169, Appl
C 19	7	100.0	15	9	US-10-305-273-1191	Sequence 1191, Appl
C 20	7	100.0	15	9	US-10-305-275-550	Sequence 550, Appl

C 21	7	100.0	15	9	US-10-316-956-1230	Sequence 1230, Appl
C 22	7	100.0	15	9	US-10-316-956-1239	Sequence 1239, Appl
C 23	7	100.0	15	9	US-10-316-956-1250	Sequence 1250, Appl
C 24	7	100.0	15	9	US-10-316-956-1251	Sequence 1251, Appl
C 25	7	100.0	15	9	US-10-316-956-1252	Sequence 1252, Appl
C 26	7	100.0	15	9	US-10-316-954-413	Sequence 413, Appl
C 27	7	100.0	15	9	US-10-316-954-1307	Sequence 1307, Appl
C 28	7	100.0	15	9	US-10-316-954-2852	Sequence 2852, Appl
C 29	7	100.0	15	9	US-10-316-954-2853	Sequence 2853, Appl
C 30	7	100.0	15	9	US-10-316-954-3393	Sequence 3393, Appl
C 31	7	100.0	15	9	US-10-316-954-4902	Sequence 4902, Appl
C 32	7	100.0	15	9	US-10-316-954-4903	Sequence 4903, Appl
C 33	7	100.0	15	9	US-10-321-854-1864	Sequence 1864, Appl
C 34	7	100.0	15	9	US-10-321-854-3261	Sequence 3261, Appl
C 35	7	100.0	15	9	US-10-310-157-1213	Sequence 1213, Appl
C 36	7	100.0	15	9	US-10-310-157-1214	Sequence 1214, Appl
C 37	7	100.0	15	9	US-10-310-157-3289	Sequence 3289, Appl
C 38	7	100.0	15	9	US-10-310-157-4486	Sequence 4486, Appl
C 39	7	100.0	15	9	US-10-310-157-55923	Sequence 55923, Appl
C 40	7	100.0	15	9	US-10-310-157-55935	Sequence 55935, Appl
C 41	7	100.0	15	9	US-10-310-157-6009	Sequence 6009, Appl
C 42	7	100.0	15	9	US-10-305-273A-169	Sequence 169, Appl
C 43	7	100.0	15	9	US-10-305-273A-1191	Sequence 1191, Appl
C 44	7	100.0	15	9	US-10-305-275A-550	Sequence 550, Appl
C 45	7	100.0	15	10	US-10-367-892-657	Sequence 657, Appl

## ALIGNMENTS

RESULT 1  
US-10-329-465-53/c  
; Sequence 53, Application US/10329465  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL  
; FILE REFERENCE: 27373/37928A  
; CURRENT APPLICATION NUMBER: US/10/329,465  
; PRIOR FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: US 607343, 826  
; PRIOR FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-329-465-53

Query Match 100.0%; Score 7; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 GCTTCAG 1

RESULT 2  
US-10-293-222-131/c  
; Sequence 131, Application US/10293222  
; GENERAL INFORMATION:  
; APPLICANT: Versteeg, Rogier  
; APPLICANT: Caron, Hubertus N.  
; TITLE OF INVENTION: MYC targets  
; FILE REFERENCE: 2183-5580US  
; CURRENT APPLICATION NUMBER: US/10/293,222  
; PRIOR FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: PCT/NL01/00361  
; PRIOR FILING DATE: 2001-05-11

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Page 2

PRIOR APPLICATION NUMBER: BP 00201698.8  
PRIOR FILING DATE: 2000-05-11  
PRIOR APPLICATION NUMBER: BP 00202284.6  
PRIOR FILING DATE: 2000-06-29  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: Patentn Ver. 2.1  
SEQ ID NO 131  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-293-222-131

Query Match 100.0%; Score 7; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
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RESULT 3  
US-10-314-322-34/c  
Sequence 34, Application US/10314322  
GENERAL INFORMATION:  
APPLICANT: Heber-Katz, Ellen  
TITLE OF INVENTION: Compositions and Methods for Wound  
FILE REFERENCE: 000486.00016  
CURRENT APPLICATION NUMBER: US/10/314,322  
PRIOR FILING DATE: 2002-12-09  
PRIOR APPLICATION NUMBER: US 60/074,737  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/097,937  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: US 60/102,051  
PRIOR FILING DATE: 1998-09-28  
PRIOR APPLICATION NUMBER: US 09/249,155  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 346  
SOFTWARE: PatSeq for Windows Version 4.0  
SEQ ID NO 34  
LENGTH: 11  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-314-322-34

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Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 10 GCTTCAG 4

RESULT 4  
US-10-240-580-38  
Sequence 38, Application US/10240580  
GENERAL INFORMATION:  
APPLICANT: Inoue, Takashi  
TITLE OF INVENTION: METHOD AND APPARATUS FOR MICROORGANISM DISCRIMINATION METHOD OF  
TITLE OF INVENTION: DATABASE FOR MICROORGANISM DISCRIMINATION, AND MICROORGANISM DIS  
TITLE OF INVENTION: PROGRAM AND RECORDING MEDIUM ON WHICH SUCH PROGRAM IS RECORDED  
FILE REFERENCE: 9982-24  
CURRENT APPLICATION NUMBER: US/10/240,580  
PRIOR FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: PCT/JP01/02516  
PRIOR FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: JP 2000-99482  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: Patentn version 3.1

SEQ ID NO 38  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-10-240-580-38

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Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 4 GCTTCAG 10

RESULT 5  
US-10-106-799-13  
Sequence 13, Application US/10106799  
GENERAL INFORMATION:  
APPLICANT: Council of Scientific and Industrial Research  
TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran  
TITLE OF INVENTION: Method thereof  
FILE REFERENCE: US 673  
CURRENT APPLICATION NUMBER: US/10/106,799  
PRIOR FILING DATE: 2002-10-31  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patentn version 3.1  
SEQ ID NO 13  
LENGTH: 13  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Ap34 arbitrary primer for differential display  
US-10-106-799-13

Query Match 100.0%; Score 7; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 3 GCTTCAG 9

RESULT 6  
US-10-106-799-14  
Sequence 14, Application US/10106799  
GENERAL INFORMATION:  
APPLICANT: Council of Scientific and Industrial Research  
TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran  
TITLE OF INVENTION: Method thereof  
FILE REFERENCE: US 673  
CURRENT APPLICATION NUMBER: US/10/106,799  
PRIOR FILING DATE: 2002-10-31  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patentn version 3.1  
SEQ ID NO 14  
LENGTH: 13  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Ap35 arbitrary primer for differential display  
US-10-106-799-14

Query Match 100.0%; Score 7; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7  
Db 3 GCTTCAG 9

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RESULT 7
US-10-146-505-84/c
; Sequence 84, Application US/10146505
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: F220
; OTHER INFORMATION: The sequence TGAGCTCTGTG is deleted
US-10-146-505-84

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```

Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTTCAG 7
Db 7 GCTTCAG 1

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RESULT 8
US-10-303-778-13859/c
; Sequence 13859, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-13859

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Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTTCAG 7
Db 8 GCTTCAG 2

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RESULT 9
US-10-294-035-747/c
; Sequence 747, Application US/10294035
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,035
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: Proprietary
; SEQ ID NO 747
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Mycobacterium leprae strain TN complete genome.
; FEATURE:
; LOCATION: (1626549)...(1626563)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 104
US-10-294-035-747

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Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTTCAG 7
Db 12 GCTTCAG 6

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```

RESULT 10
US-10-294-035-748/c
; Sequence 748, Application US/10294035
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,035
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: Proprietary
; SEQ ID NO 748
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Mycobacterium leprae strain TN complete genome.
; FEATURE:
; LOCATION: (1626549)...(1626563)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 104
US-10-294-035-748

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Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTTCAG 7
Db 12 GCTTCAG 6

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RESULT 11
US-10-294-035-940/c
; Sequence 940, Application US/10294035
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,035
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: Proprietary
; SEQ ID NO 940
; LENGTH: 15
; TYPE: DNA

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Page 4

ORGANISM: Mycobacterium leprae strain TN complete genome.  
FEATURE:  
LOCATION: (2080233)...(2080248)  
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 1297  
US-10-294-035-940

Query Match  
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;  
Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
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DB 7 GCTTCAG 1

RESULT 12

Sequence 1008 Application US/10294038  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g  
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/294,038  
CURRENT FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 5372  
SOFTWARE: Proprietary  
SEQ ID NO 1008  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g  
FEATURE:  
LOCATION: (371601)...(371615)  
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 1249  
US-10-294-038-1008

Query Match  
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;  
Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
DB 8 GCTTCAG 14

RESULT 13

Sequence 2682 Application US/10294038  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g  
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/294,038  
CURRENT FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 5372  
SOFTWARE: Proprietary  
SEQ ID NO 2682  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g  
FEATURE:  
LOCATION: (1117875)...(1117888)  
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectorObjectNumber = 3354  
US-10-294-038-2682

Query Match  
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;  
Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
DB 1 GCTTCAG 7

RESULT 14  
Sequence 4251 Application US/10294038

GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g  
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/294,038  
CURRENT FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 5372  
SOFTWARE: Proprietary  
SEQ ID NO 4251  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g  
FEATURE:  
LOCATION: (1902455)...(1902469)  
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 531  
US-10-294-038-4251

Query Match  
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;  
Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
DB 8 GCTTCAG 14

RESULT 15

Sequence 1580 Application US/10287822  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Synecocystis PCC6803 complete genome.  
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/287,822  
CURRENT FILING DATE: 2002-11-05  
NUMBER OF SEQ ID NOS: 5726  
SOFTWARE: Proprietary  
SEQ ID NO 1580  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Synecocystis PCC6803 complete genome.  
FEATURE:  
LOCATION: (959678)...(959693)  
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 208  
US-10-287-822-1580

Query Match  
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;  
Pred. No. 2.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
DB 11 GCTTCAG 5

Search completed: June 26, 2003, 04:15:21  
Job time: 168.527 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 593.968 Seconds  
(without alignments)  
296.308 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7

Sequence: 1 GCTTCAG 7

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
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19: /cgn2\_6/ptodata/2/pna/US095A\_COMB.seq.\*  
20: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq.\*  
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22: /cgn2\_6/ptodata/2/pna/US095D\_COMB.seq.\*  
23: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq.\*  
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27: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq.\*  
28: /cgn2\_6/ptodata/2/pna/US097A\_COMB.seq.\*  
29: /cgn2\_6/ptodata/2/pna/US097B\_COMB.seq.\*  
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36: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq.\*  
37: /cgn2\_6/ptodata/2/pna/US099D\_COMB.seq.\*  
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41: /cgn2\_6/ptodata/2/pna/US101B\_COMB.seq.\*  
42: /cgn2\_6/ptodata/2/pna/US102A\_COMB.seq.\*  
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Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	11 US-08-770-564A-12	Sequence 12, Appl
2	7	100.0	8	10 US-08-632-782-86	Sequence 86, Appl
3	7	100.0	10	1 PCT-US00-04606-65	Sequence 65, Appl
4	7	100.0	10	1 PCT-US01-10743A-43	Sequence 43, Appl
5	7	100.0	10	1 PCT-US01-10743A-44	Sequence 44, Appl
6	7	100.0	10	1 PCT-US01-18814-44	Sequence 44, Appl
7	7	100.0	10	1 PCT-US01-18814-49	Sequence 49, Appl
8	7	100.0	10	1 PCT-US01-21306-130	Sequence 130, App
9	7	100.0	10	1 PCT-US01-23100-118	Sequence 118, App
10	7	100.0	10	1 PCT-US01-29207-36	Sequence 36, Appl
11	7	100.0	10	1 PCT-US01-42727-58	Sequence 58, Appl
12	7	100.0	10	1 PCT-US02-24250-52	Sequence 52, Appl
13	7	100.0	10	1 PCT-US97-13001-10	Sequence 10, Appl
14	7	100.0	10	1 PCT-US99-13800-226	Sequence 226, Appl
15	7	100.0	10	1 PCT-US99-13800-1449	Sequence 1449, Ap
16	7	100.0	10	8 US-08-458-785-49	Sequence 49, Appl
17	7	100.0	10	8 US-08-459-444-49	Sequence 49, Appl
18	7	100.0	10	8 US-08-459-448-49	Sequence 49, Appl
19	7	100.0	10	8 US-08-459-504-49	Sequence 49, Appl
20	7	100.0	10	8 US-08-459-504A-49	Sequence 49, Appl
21	7	100.0	10	8 US-08-459-595-49	Sequence 49, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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22 7 100.0 10 8 US-08-460-408-49 Sequence 49, Appl
23 7 100.0 10 17 US-09-335-032-369 Sequence 369, App
24 7 100.0 10 17 US-09-335-032-2641 Sequence 2641, Ap
25 7 100.0 10 17 US-09-335-032-2931 Sequence 2931, Ap
26 7 100.0 10 17 US-09-335-032-4373 Sequence 4373, Ap
27 7 100.0 10 17 US-09-335-032-8177 Sequence 8177, Ap
28 7 100.0 10 17 US-09-335-032-8178 Sequence 8178, Ap
29 7 100.0 10 17 US-09-336-376-1613 Sequence 1613, Ap
30 7 100.0 10 17 US-09-336-376-1701 Sequence 1701, Ap
31 7 100.0 10 17 US-09-336-376-4067 Sequence 4067, Ap
32 7 100.0 10 17 US-09-816-763-61 Sequence 61, Appl
33 7 100.0 10 31 US-09-988-462-49 Sequence 49, Appl
34 7 100.0 10 37 US-10-033-145-226 Sequence 226, App
35 7 100.0 10 38 US-10-033-145-1449 Sequence 1449, Ap
36 7 100.0 11 1 PCT-US02-13093A-81 Sequence 81, Appl
37 7 100.0 11 16 US-09-249-155A-34 Sequence 34, Appl
38 7 100.0 11 16 US-08-864-765A-3 Sequence 34, Appl
39 7 100.0 12 12 US-09-267-332-20 Sequence 20, Appl
40 7 100.0 12 16 US-09-424-521-9 Sequence 3, Appl
41 7 100.0 12 18 US-09-528-209A-2823 Sequence 2823, Ap
42 7 100.0 12 19 US-09-528-209A-7616 Sequence 7616, Ap
43 7 100.0 12 19 US-09-528-209A-7616 Sequence 25, Appl
44 7 100.0 12 19 US-09-528-209A-7616
45 7 100.0 12 33 US-09-868-605-45

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## ALIGNMENTS

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RESULT 1
US-08-770-564A-12
; Sequence 12, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-564A-12
Query Match 100.0%; Score 7; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+09;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
Db 1 GCTTCAG 7
RESULT 2
US-08-632-782-86
; Sequence 86, Application US/08632782
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramtin
; APPLICANT: Hardin, Paul B.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,782
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5525
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-632-782-86
Query Match 100.0%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
Db 1 GCTTCAG 7
RESULT 3
PCT-US00-04606-65/c
; Sequence 65, Application PC/TUS0004606
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Schulz, Vincent P
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Chew, Anne
; TITLE OF INVENTION: Drug Target Isoforms: Polymorphisms in the Tumor
; TITLE OF INVENTION: Necrosis Factor Receptor I Gene
; FILE REFERENCE: MMH03030PCT

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CURRENT APPLICATION NUMBER: PCT/US00/04606  
CURRENT FILING DATE: 2000-02-23  
EARLIER APPLICATION NUMBER: 60/121,314  
EARLIER FILING DATE: 1999-02-23  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 65  
LENGTH: 10  
TYPE: DNA  
ORGANISM: HOMO SAPIENS  
PCT-US00-04606-65

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
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Db 9 GCTTCAG 3

RESULT 4  
PCT-US01-10743A-43/C  
Sequence 43, Application PC/TUS0110743A  
GENERAL INFORMATION:  
APPLICANT: Genaisance Pharmaceuticals, Inc.  
APPLICANT: Chew, Anne  
APPLICANT: Choi, Julie Y.  
APPLICANT: Koshy, Beena  
TITLE OF INVENTION: Haplotypes of the SCN2B Gene  
FILE REFERENCE: MMH-0481PCT SCN2B  
CURRENT APPLICATION NUMBER: PCT/US01/10743A  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/196,597  
PRIOR FILING DATE: 2000-04-13  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapien  
PCT-US01-10743A-43

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
Db 7 GCTTCAG 1

RESULT 5  
PCT-US01-10743A-44  
Sequence 44, Application PC/TUS0110743A  
GENERAL INFORMATION:  
APPLICANT: Genaisance Pharmaceuticals, Inc.  
APPLICANT: Chew, Anne  
APPLICANT: Choi, Julie Y.  
APPLICANT: Koshy, Beena  
TITLE OF INVENTION: Haplotypes of the SCN2B Gene  
FILE REFERENCE: MMH-0481PCT SCN2B  
CURRENT APPLICATION NUMBER: PCT/US01/10743A  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/196,597  
PRIOR FILING DATE: 2000-04-13  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 44  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapien  
PCT-US01-10743A-44

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
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Db 3 GCTTCAG 9

RESULT 6  
PCT-US01-18814-44/C  
Sequence 44, Application PC/TUS0118814  
GENERAL INFORMATION:  
APPLICANT: Genaisance Pharmaceuticals, Inc.  
APPLICANT: Choi, Julie Y.  
APPLICANT: Koshy, Beena  
APPLICANT: Sanchez, Angela  
APPLICANT: Saueker, Elizabeth Ann  
TITLE OF INVENTION: HAPLOTYPES OF THE PKG2 GENE  
FILE REFERENCE: MMH-0770PCT PKG2  
CURRENT APPLICATION NUMBER: PCT/US01/18814  
CURRENT FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 60/210,568  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 44  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US01-18814-44

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
Db 10 GCTTCAG 4

RESULT 7  
PCT-US01-18814-49  
Sequence 49, Application PC/TUS0118814  
GENERAL INFORMATION:  
APPLICANT: Genaisance Pharmaceuticals, Inc.  
APPLICANT: Choi, Julie Y.  
APPLICANT: Koshy, Beena  
APPLICANT: Sanchez, Angela  
APPLICANT: Saueker, Elizabeth Ann  
TITLE OF INVENTION: HAPLOTYPES OF THE PKG2 GENE  
FILE REFERENCE: MMH-0770PCT PKG2  
CURRENT APPLICATION NUMBER: PCT/US01/18814  
CURRENT FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 60/210,568  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 49  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US01-18814-49

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
| | | | |  
Db 4 GCTTCAG 10

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RESULT 8
PCT-US01-23306-130
; Sequence 130, Application PC/TUS0123306
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C
; APPLICANT: Bielecki, Karyn M.
; APPLICANT: Kazem, Amir
; APPLICANT: Koshy, Beena
; TITLE OF INVENTION: Haplotypes of the ETRB Gene
; FILE REFERENCE: MMH-0902PCT ETRB
; CURRENT APPLICATION NUMBER: PCT/US01/23306
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/215,984
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-23306-130

Query Match          100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
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Db 3 GCTTCAG 9

RESULT 9
PCT-US01-23100-118
; Sequence 118, Application PC/TUS0123100
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Duda, Amy
; APPLICANT: Koshy, Beena
; APPLICANT: Sanchis, Angela
; TITLE OF INVENTION: Haplotypes of the CHRNA1 Gene
; FILE REFERENCE: MMH-071PCT CHRNA1
; CURRENT APPLICATION NUMBER: PCT/US01/23100
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,538
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-23100-118

Query Match          100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
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Db 2 GCTTCAG 8

RESULT 10
PCT-US01-29207-36
; Sequence 36, Application PC/TUS0129207
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Koshy, Beena
; APPLICANT: Sanchis, Angela
; APPLICANT: Tirrell, Charles
; TITLE OF INVENTION: Haplotypes of the GPR7 Gene
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; FILE REFERENCE: MMH-1293PCT
; CURRENT APPLICATION NUMBER: PCT/US01/29207
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/232,900
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-29207-36

Query Match          100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
    |||||
Db 1 GCTTCAG 7

RESULT 11
PCT-US01-42727-58/c
; Sequence 58, Application PC/TUS0142727
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Chew, Anne
; APPLICANT: Han, Jin-Hua
; APPLICANT: Sanchis, Angela
; TITLE OF INVENTION: HAPLOTYPES OF THE CYP27A1 GENE
; FILE REFERENCE: CYP27A1 MMH-1279PCT
; CURRENT APPLICATION NUMBER: PCT/US01/42727
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,942
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-42727-58

Query Match          100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
    |||||
Db 7 GCTTCAG 1

RESULT 12
PCT-US02-24250-52/c
; Sequence 52, Application PC/TUS0224250
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Denton, R. Rex
; APPLICANT: Drysdale, Connie M.
; APPLICANT: Hoffman, Michael
; APPLICANT: Judson, Richard S.
; APPLICANT: Maertz, Manfred
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stack Catherine B.
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Vanden Bog, Rodi
; APPLICANT: Winkelman, Bernhard R.
; TITLE OF INVENTION: Association of Low Density Lipoprotein Receptor (LDLR) Gene Haplot;
; FILE REFERENCE: MMH-2889PCT LDLR
```



CURRENT APPLICATION NUMBER: PCT/US02/24250  
CURRENT FILING DATE: 2002-07-30  
PRIOR APPLICATION NUMBER: US 60/308,688  
PRIOR FILING DATE: 2001-07-30  
NUMBER OF SEQ ID NOS: 103  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 52  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-24250-52

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 10 GCTTCAG 4

RESULT 13  
PCT-US97-13001-10/c  
Sequence 10, Application PC/TUS9713001  
GENERAL INFORMATION:  
APPLICANT: Toothman, Penelope  
TITLE OF INVENTION: Method of Identifying Aloe Using  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratechun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM pc compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/13001  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/022,611  
FILING DATE: 26-JULY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: UNI.07/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3433  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE:  
PCT-US97-13001-10

Query Match 100.0%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7  
DB 7 GCTTCAG 1

RESULT 14

PCT-US99-13800-226/c  
Sequence 226, Application PC/TUS9913800  
GENERAL INFORMATION:  
APPLICANT: Genzyme Corporation  
APPLICANT: Roberts, Bruce L.  
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
FILE REFERENCE: 68126881206940  
CURRENT APPLICATION NUMBER: PCT/US99/13800  
EARLIER FILING DATE: 1999-06-18  
EARLIER APPLICATION NUMBER: 60/090,039  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,040  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,041  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,853  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,997  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,079  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,035  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,993  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,992  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,072  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,878  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,991  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,000  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,048  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,999  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,043  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,042  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,036  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,044  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,844  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,080  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,833  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/089,994  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,077  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,078  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,047  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,076  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/090,045  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: 60/111,715  
EARLIER FILING DATE: 1998-12-08  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 226  
LENGTH: 10  
TYPE: DNA

Fri Jun 27 07:41:19 2003

us-08-770-564a-12.rmpm

Page 6

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; ORGANISM: Homo sapiens
PCT-US99-13800-226

Query Match      100.0%; Score 7; DB 1; Length 10;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 1449, Application PC/TUS9913800
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce L.
; APPLICANT: Shankara, Srinivas
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: 68126891206940
; CURRENT APPLICATION NUMBER: PCT/US99/13800
; CURRENT FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/090,039
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,040
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,041
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,853
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,997
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,079
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,035
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,993
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,992
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,072
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,878
; EARLIER FILING DATE: 1998-06-19
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; EARLIER APPLICATION NUMBER: 60/090,044
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; EARLIER APPLICATION NUMBER: 60/089,844
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,080
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,833
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,994
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,077
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,078
; EARLIER FILING DATE: 1998-06-19
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; EARLIER APPLICATION NUMBER: 60/090,047
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,076
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; EARLIER APPLICATION NUMBER: 60/111,715
; EARLIER FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 2138
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1449
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-13800-1449

Query Match      100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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       10 CCTTCAG 4
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Job time : 595.583 secs